

COMPARISON OF THE WORLDWIDE TRANSMISSIBLE *PSEUDOMONAS AERUGINOSA* WITH ISOLATES FROM BRAZILIAN CYSTIC FIBROSIS PATIENTS

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ABSTRACT

Cross-infection with *Pseudomonas aeruginosa* among cystic fibrosis (CF) patients is a rare occurrence. However, the emergence of transmissible strains has been reported between unrelated individuals. We analyzed the genetic relationship among *P. aeruginosa* isolates from Brazilian CF patients and transmissible clones which are worldwide spread. The data does not indicate the presence of closely related variant clones.

Key words: *Pseudomonas aeruginosa*, Epidemic strain, Cystic fibrosis.

Pseudomonas aeruginosa is a common cause of chronic pulmonary infection in patients with cystic fibrosis (CF). These infections contribute considerably for morbidity and mortality of CF patients due to an intense host inflammatory response which leads to an irreversible loss of lung function (7). Many studies indicate that the same CF patients may harbour distinct strains in their respiratory tract, suggesting that may be a relatively high heterogeneity of strains of *P. aeruginosa* in the CF pulmonary microbiota. It is also known that chronic CF patients are colonized by unique strains, and cross-infection was considered to be rare (11). More recently, the emergence of transmissible *P. aeruginosa* has been reported with increasing frequency among unrelated individuals which constitute an emerging threat to patients with CF (3,5). The presence of common clones circulating among different CF

patients was described in Europe and the United States of America (1, 6). The first major transmissible *P. aeruginosa* CF strain (Liverpool Epidemic Strain – “LES”) was identified in Liverpool - UK (1), where it occasionally “superinfected” individuals and eventually replaced their original strains (6). Moreover, the “Midlands 1” strain was originally isolated in Birmingham - UK and was identified as the second most common clone in the UK (10). A multiresistant transmissible strain (“Manchester clone”) has also been identified in adults at a CF treatment center in Manchester - UK (2).

Although the presence of transmissible strains of *P. aeruginosa* is not related to increased morbidity, it may lead to treatment burden for infected patient in contrast to the patients who harbor a unique, non-transmissible strains (9). Römmling et al. (8) have reported the spread of an epidemic clone (clone C)

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with dissemination over several countries on two continents with higher prevalence in the aquatic environment and with the potential to infect CF patients. The occurrence of these transmissible strains has provoked debate on infection control issues and the management of CF patients. It remains controversial, however, whether patients harboring transmissible strains of *P. aeruginosa* should be segregated from those colonized with non-transmissible strains. This study consisted of a analysis of the genetic relationship of *P. aeruginosa* isolates from Brazilian CF patients and the transmissible strains which are spread worldwide. A total of 179 *P. aeruginosa* from 20 CF patients were investigated. The clinical isolates were recovered from adult and paediatric CF patients admitted at the Hospital Universitário Pedro Ernesto (HUPE) and at the Instituto Fernandes Figueira (IFF FioCruz), respectively, two reference centres for cystic fibrosis treatment located in Rio de Janeiro, Brazil. All patients presented chronic respiratory infection due to *P. aeruginosa*. Initially, we have employed RAPD-PCR, using the primer 208 – 5' ACGGCCGACC 3'(4). We found 49 different profiles among the 179 clinical isolates indicating a considerable genetic heterogeneity. Nevertheless, we have observed, eventually, the presence of the same strain in different patients. We have selected one isolated belonging to each of the 49 RAPD profiles for the second stage of the study which consisted of PFGE following digestion of intact genomic DNA with SpeI (Roche Indianapolis IN USA) as previously described (10). DNA fragment analysis was performed with BioNumerics version 5.3 (Applied Maths, St. Marten-Latem, Belgium) and clusters were defined using the Dice coefficient of similarity. UPGMA dendrograms were drawn with a position tolerance of 1.00% and optimization of 1.00%. The following transmissible strains were compared with the clinical isolates: “clone C” (8), “LES” (1), “Manchester” (2) and “Midlands” (10). No similarity were found among the Brazilian clinical CF isolates and the transmissible strains from other countries. It has to be considered that the population of CF patients evaluated in this study is representative of only two hospitals in Brazil and, therefore, a national surveillance is warranted to confirm the

presence or absence of transmissible *P. aeruginosa* strains among CF patients in Brazil. Strain typing is important for the detection of sources or routes of infections, identification between endemic and epidemic strains and prevention of transmission between patients. We have observed that there is no genetic relatedness among the *P. aeruginosa* from CF patients from Rio de Janeiro - Brazil, when compared with the widespread clones of *P. aeruginosa* from CF patients around the world.

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