Brief communication

Genetic similarity of *Burkholderia cenocepacia* from cystic fibrosis patients

Luana Pretto\(^a\), Fernanda de-Paris\(^b,\,*\), Alice Beatriz Mombach Pinheiro Machado\(^b\), Andrea Francisco Martins\(^b\), Afonso Luis Barth\(^a,\,*\)

\(^a\) Universidade Federal do Rio Grande do Sul, Porto Alegre, RS, Brazil
\(^b\) Hospital de Clínicas de Porto Alegre, Serviço de Patologia Clínica, Unidade de Microbiologia e Biologia Molecular, Porto Alegre, RS, Brazil

**A R T I C L E   I N F O**

Article history:
Received 9 May 2012
Accepted 15 September 2012
Available online 1 January 2013

**Keywords:**
*Burkholderia cenocepacia*
Cystic fibrosis
PFGE
Genetic similarity

**A B S T R A C T**

*Burkholderia cenocepacia* may cause serious infections in patients with cystic fibrosis, and this microorganism can be highly transmissible. Pulsed-field gel electrophoresis is widely used to study the dynamics of strain spread in cystic fibrosis patients. The aim of this work was to perform pulsed-field gel electrophoresis-based molecular typing of *B. cenocepacia* isolates to evaluate the epidemiology of this species at our hospital. A total of 28 isolates from 23 cystic fibrosis patients were analyzed. Initially, we compared isolates obtained from the same patient at different periods of time. We then compared the pulsed-field gel electrophoresis profiles of 15 IIIA isolates, and in a third analysis, evaluated the genetic profile of 8 IIIB isolates from different patients. The pulsed-field gel electrophoresis profiles of isolates from the same patient indicated that they are genetically indistinguishable. Analysis of isolates from different patients revealed the presence of multiple clonal groups. These results do not indicate cross-transmission of a unique clone of *B. cenocepacia* among cystic fibrosis patients, although this has been observed in some patients. Our findings highlight the importance of adequate patient follow-up at cystic fibrosis centers and adherence to management and segregation measures in cystic fibrosis patients colonized with *B. cenocepacia*.

© 2013 Elsevier Editora Ltda. Open access under CC BY-NC-ND license.
centers have begun to adopt policies for segregation of “B. cenocepacia-positive” and “negative” patients to prevent B. cenocepacia infection.6

Within this context, studies of the epidemiology of B. cenocepacia play an essential role in guiding infection control measures at CF centers. Consequently, the objective of this study was to perform molecular typing by DNA macrorestriction followed by pulsed-field gel electrophoresis (PFGE) of B. cenocepacia isolates in order to evaluate the epidemiology of this pathogen in CF patients at Hospital de Clínicas de Porto Alegre (HCPA), a tertiary-level university hospital with more than 800 beds in Porto Alegre, Brazil. The HCPA CF Reference Center provides care to nearly 250 CF patients. The hospital has a segregation program in place for BCC-colonized CF patients: colonized outpatients are seen on different days of the week than non-colonized CF patients, and colonized inpatients are admitted to isolation wards.

This study evaluated 28 B. cenocepacia isolates obtained from the sputum of 23 CF patients seen during the year 2008. During the same period, Leite and coworkers studied a total of 244 CF patients from HCPA and observed a prevalence rate of BCC of 10.6%. B. cenocepacia accounted for most BCC isolates (60%; 77.5% IIIA and 22.5% IIIB).8

Isolates were identified by phenotypic testing (characteristic growth on BCSA medium, polymyxin B resistance, pyrrolidonyl arylamidase [PYR] negativity) and with the miniAPI semi-automated ID/AST system, using the 32GN card (BioMérieux). B. cenocepacia identification was confirmed by nested PCR using primers for recA as described by Drevinek et al. B. cenocepacia was also used to identify phylogenetic subgroups IIIA and IIIB.10 The majority of our isolates (67.8%) were identified as genovar IIIA (data not shown).

For PFGE analysis, DNA restriction was carried out with the SpeI enzyme and electrophoresis was performed in CHEF-DRII equipment (Bio-Rad Laboratories). Run conditions were as described by Kutty et al. Profiles were analyzed in the BioNumerics software environment (Applied Maths). The percentages of similarity of the test isolates were identified on a dendrogram derived from the UPGMA algorithm and based on the Dice coefficient. A similarity coefficient of 80% was used to define pulsed-field type clusters.12

Three different analyses of isolates were performed on the basis of PFGE profiles. We first compared isolate profiles within the same patient (using a subsample of 5 patients and 10 isolates) at different points in time (4–6 months apart). These isolates showed the same DNA macrorestriction profile (100% genetic similarity – Fig. 1). On the basis of this finding, we decided to include only one isolate from each patient for analysis of isolate similarity among different patients.

The second analysis included 15 IIIA isolates from different patients. Nine different clonal groups (represented by letters A to I) were established (Fig. 2). Groups A, C, F, G, H, and I included only one isolate; group B included 3 isolates that displayed 100% genetic similarity; group D included 4 isolates, 3 of which exhibited 100% similarity; and group E included 2 isolates also displaying 100% similarity. Notably, we found that the B. cenocepacia IIIA isolates from CF patients in our sample exhibited little genetic similarity with the ET12 strain.

The third analysis included 8 IIIB isolates from different patients and showed the presence of five distinct clonal groups (designated J to O) (Fig. 2). Groups L, N and O included only one isolate; group J included two isolates (710 and 768) that displayed 100% genetic similarity; and group M included 3 isolates (642, 656 and 706).

PFGE analysis revealed the presence of clonal groups formed by isolates with 100% genetic similarity and other groups with a similarity of >80%. We observed many different pulsortypes, most of which comprised only one isolate. These findings suggest the occurrence of multiple B. cenocepacia clonal groups among CF patients treated at HCPA, and, therefore, indicate absence of cross-transmission of a unique B. cenocepacia clone among CF patients, although this phenomenon has been observed in some patients (e.g. with clonal group D). Indeed, there were instances of different patients in the sample being colonized by the same strain. Several epidemiological studies have shown most cases of BCC infection transmitted between CF patients involved B. cenocepacia strains.11 The most dramatic clinical pictures were associated with the ET12 strain.14 Apparently, ET12 is an endemic strain isolated predominantly at CF centers in North America and Europe. However, our findings show that, on PFGE analysis, the DNA macrorestriction profile of ET12 strain isolates is quite distinct from that of B. cenocepacia IIIA isolates obtained from CF patients treated at HCPA. Our study also showed the persistence of particular genotype profiles in the same patients over time. In five patients, we observed the same B. cenocepacia clone in isolates collected 4–6 months apart. This suggests that, even during courses of antibiotic therapy, the original strain may not be eradicated from some patients.15 Genotyping studies have shown that chronic infection in CF patients is typically associated with a single BCC strain. Transient coinfec tion with two different BCC species or two strains of the same species may occur, but this phenomenon is rare and found mainly in early infection.16

In summary, we demonstrated the presence of multiple B. cenocepacia clonal groups among CF patients treated at Hospital de Clínicas de Porto Alegre. Our findings highlight the importance of adequate patient follow-up at CF centers and
adherence to management and segregation measures in CF patients colonized with *B. cepacia*.

**Conflict of interest**

The authors have no conflicts of interest to declare.

**Acknowledgements**

The authors would like to honor the memory of Ms. Maria Izote Vieira (Unidade de Microbiologia e Biologia Molecular – Hospital de Clínicas de Porto Alegre) and acknowledge her technical support. We also thank Ms. Odelta dos Santos (Universidade Federal de Ciências da Saúde de Porto Alegre – UFCSPA) for her assistance with BioNumerics software analysis. This work was supported by Fundo de Incentivo à Pesquisa e Ensino, Hospital de Clínicas de Porto Alegre (FIFE/HCPA), Fundação de Amparo à Pesquisa do Estado do Rio Grande do Sul (FAERG) and the Brazilian National Council for Scientific and Technological Development (CNPq).

**REFERENCES**

1. Mahenthiralingam E, Baldwin A, Dowson CG. *Burkholderia cepacia* complex bacteria: opportunistic pathogens with important natural biology. J Appl Microbiol. 2008;104:1539–51.
2. Vanlaere E, Baldwin A, Gevers D, et al. Taxon K, a complex within the *Burkholderia cepacia* complex, comprises at least two novel species, *Burkholderia contaminans* sp. nov. and *Burkholderia latza* sp. nov. Int J Syst Evol Microbiol. 2009;59:102–11.
3. Drevinek P, Mahenthiralingam E. *Burkholderia cepacia* in cystic fibrosis: epidemiology and molecular mechanisms of virulence. Clin Microbiol Infect. 2010;16:821–30.
4. McDowell A, Mahenthiralingam E, Dunbar KEA, Moore JE, Crowe M, Elborn JS. Epidemiology of *Burkholderia cepacia* complex species recovered from cystic fibrosis patients: issues related to patient segregation. J Med Microbiol. 2004;53:663–8.
5. Correia S, Nascimento C, Pereira L, Cunha MV, Sa-Correia I, Barreto C. The clinical course of *Burkholderia cepacia* complex bacteria respiratory infection in cystic fibrosis patients. Rev Port Pneumol. 2008;14:5–26.
6. Holden MT, Seth-Smith HM, Crossman LC, et al. The genome of *Burkholderia cepacia* J2315, an epidemic pathogen of cystic fibrosis patients. J Bacteriol. 2009;191:261–77.
7. Grandorge A, Menard A, Neto M, et al. Epidemiology and molecular characterization of a clone of *Burkholderia cepacia* responsible for nosocomial pulmonary tract infections in a French intensive care unit. Diag Microbiol Infect Dis. 2010;66:29–40.
8. Saiman L, Siegel J. Infection control in cystic fibrosis. Clin Microbiol Rev. 2004;17:57–71.
9. Leite FC, Machado ABMP, Lutz L, Vieira MI, Barth AL. Molecular identification of *Burkholderia cepacia* complex and species distribution among cystic fibrosis patients seen at the reference center in Southern Brazil. Rev HCPA. 2011;31:138–44.
10. Drevinek P, Hrbáčková H, Cinek O, et al. Direct PCR detection of *Burkholderia cepacia* complex and identification of its genovars by using sputum as source of DNA. J Clin Microbiol. 2002;40:3485–8.
11. Kutty PK, Moody B, Guillson JS, et al. Multistate outbreak of *Burkholderia cepacia* colonization and infection associated with the use of intrinsically contaminated alcohol-free mouthwash. Chest. 2007;132:1825–31.
12. Singh A, Goering RV, Simjee S, Foley SL, Zervos MJ. Application of molecular techniques to the study of hospital infection. Clin Microbiol Rev. 2006;19:512–30.
13. Kidd TJ, Douglas JM, Bergh HA, Coulter C, Bell SC. *Burkholderia cepacia* complex epidemiology in persons with cystic fibrosis.

**Fig. 2 – Dendrogram of percent similarity among pulsed-field gel electrophoresis (PFGE) profiles of IIA and IIIB isolates from different patients.** B. *cepacia* ET12 was considered a highly virulent external strain.
from Australia and New Zealand. Res Microbiol. 2008;159:194–9.

14. Turton JF, O’Brien E, Megson B, Kaufmann ME, Pitt TL. Strains of *Burkholderia cenocepacia* genomovar IIIA possessing the cblA gene that are distinct from ET12. Diag Microbiol Infect Dis. 2009;64:94–7.

15. Silbert S, Barth AL, Sader HS. Heterogeneity of *Pseudomonas aeruginosa* in Brazilian cystic fibrosis patients. J Clin Microbiol. 2001;39:3976–81.

16. Yang JH, Spilker T, LiPuma JJ. Simultaneous coinfection by multiple strains during *Burkholderia cepacia* complex infection in cystic fibrosis. Diag Microbiol Infect Dis. 2006;54:95–8.