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Burkholderia respiratory tract infections in Italian patients with cystic fibrosis: Molecular characterization

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Summary Objectives: To characterize by molecular techniques Burkholderia strains responsible for respiratory tract infections in cystic fibrosis (CF) patients (children and adults), to assign the Burkholderia cepacia complex (Bcc) isolates to a genomovar and to assess the presence of cblA and esmR genes in bacteria. Unique or sequential Burkholderia isolates (n = 48) that had been collected from eight CF children and 17 adults over several (4–6) years were investigated; moreover 11 reference strains were analyzed.

Methods: The microorganisms were identified by using biochemical methods, genotyped by pulse field gel electrophoresis (PFGE) and random-amplified polymorphic DNA fingerprinting—PCR (RAPD—PCR), and assessed by PCR assays for the genomovar and cblA and esmR genes of Bcc.

Results: Among isolates 70.8% were identified as Bcc genomovar III-A; one child was infected by Burkholderia ambifaria and four adults were colonized with Burkholderia gladioli. The cblA gene was not detected in any of the isolates, while the esmR gene was detected in the 52.1% of the strains, all belonging to genomovar III-A.

Conclusion: Molecular analysis of strains revealed in CF patients a colonization with a persistent Burkholderia flora with strains of one genotype. The prevalence of Bcc of genomovar III-A in the two categories of patients and of B. gladioli in four adults demonstrated that transmission may have occurred between subjects. Moreover the B. ambifaria infection demonstrated in a child may be environmentally derived. © 2005 The British Infection Society. Published by Elsevier Ltd. All rights reserved.
Introduction

Burkholderia species are widely distributed in the natural environment and several species also cause disease. Correct identification of this genus is difficult, but recently a recA gene-based approach was developed to identify the entire Burkholderia genus. In this genus, closely related species, referred collectively to the Burkholderia cepacia complex (Bcc), are recognized as opportunistic human pathogens that cause numerous outbreaks, particularly among cystic fibrosis (CF) patients. They cause a rapid decline in pulmonary function, with ensuing increased morbidity and mortality. Because only a limited number of antibiotics are effective against Bcc, complete eradication of infection is rare.

Taxonomic studies based on traditional phenotypic and genotypic tests have demonstrated that Bcc includes nine genomic species or genomovars: B. cepacia (formerly genomovar I), Burkholderia multivorans (genomovar II), Burkholderia cenocepacia (genomovar III, divided into four recA clusters, III-A, III-B, III-C and III-D), Burkholderia stabilis (genomovar IV), Burkholderia vietnamiensis (genomovar V), Burkholderia dolosa (genomovar VI), Burkholderia ambifaria (genomovar VII), Burkholderia anthina (genomovar VIII) and Burkholderia pyrrhocina (genomovar IX).

Various markers have been associated with transmissible strains of Bcc, such as the cblA and esmR genes, which encode the protein for cable pilus production and the B. cepacia epidemic strain marker BCESM.

With these recent developments in genotyping techniques, we examined 48 Burkholderia strains isolated from eight children and 17 adults (over the last 4 and 6 years, respectively). These subjects were admitted to hospital for periodic controls in two different centres, one in the city of Torino (northwest Italy), the other located in Torino city outskirts. Moreover 11 reference strains were carried out as previously described with some modifications. Bacteria were incubated in Trypticase Soy Broth (Oxoid) and on Mueller Hinton agar (Oxoid) and liquid cultures effected by pulsed-field gel electrophoresis (PFGE) were assessed.

Furthermore the LMG 2216 strain (B. gladioli) was assessed.

Patients and bacterial strains

The 48 clinical (unique or sequential) isolates were obtained from the expectorates of eight children affected by CF attending the Cystic Fibrosis Centre of the Regina Margherita Hospital (Torino, Italy) and 17 adults with CF attending the Cystic Fibrosis Centre at S. Luigi Gonzaga Hospital in Orbassano (Torino, Italy), centres that are ~15 km apart. The reference Bcc strains examined were ATCC 17759 (Bcc genomovar I), kindly given by C. Van Pelt (Rotterdam), LMG 17588 (Bcc genomovar II), 13011 (Bcc genomovar III-B), 18888 (Bcc genomovar IV), 16232 (Bcc genomovar V), 18941 (Bcc genomovar VI), 19467 (Bcc genomovar VII), 16670 (Bcc genomovar VIII) and 14191 (Bcc genomovar IX), obtained from BCCM/LMG bacteria collection (Gent, Belgium), the strain CF5610 (Bcc genomovar III-A, cblA+ ET12 lineage strain, from John Govan’s collection, Edinburgh, kindly sent by F. Clode, PHLS, London). Moreover the LMG 2216 strain (B. gladioli) was assessed.

Materials and methods

Pulsed-field gel electrophoresis (PFGE)

DNA macrorestriction and PFGE of Burkholderia strains were carried out as previously described with some modifications. Bacteria were incubated in Trypticase Soy Broth, then centrifuged at 3000 rpm for 10 min; the pellet was washed in 1 ml of SE buffer (25 mM EDTA, 75 mM NaCl, pH 7.4), resuspended in 150 µl of the same buffer and diluted. The bacterial suspension was included in Trypticase Soy Broth (Oxoid) at 28 °C for 48 h; the isolates were tentatively identified as Bcc using commercial tests, including API 20NE kit (BioMérieux) and Vitek Auto Microbic System (BioMérieux).

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The strains identified as belonging to the Burkholderia genus by using biochemical methods were analyzed by the following: (I) genotyping was effected by pulsed-field gel electrophoresis (PFGE) and random-amplified polymorphic DNA fingerprinting—PCR (RAPD—PCR); (II) the genomovar of Bcc was assessed by PCR assays; and (III) the cblA and esmR genes of Bcc were detected by PCRs.

Materials and methods

Pulsed-field gel electrophoresis (PFGE)

DNA macrorestriction and PFGE of Burkholderia strains were carried out as previously described with some modifications. Bacteria were incubated in Trypticase Soy Broth, then centrifuged at 3000 rpm for 10 min; the pellet was washed in 1 ml of SE buffer (25 mM EDTA, 75 mM NaCl, pH 7.4), resuspended in 150 µl of the same buffer and diluted. The bacterial suspension was included in 150 µl 2% low melting point agarose (Bio-Rad) in SE buffer; agarose plugs were prepared and maintained at 4 °C. Bacteria were lysed by incubating the plugs in lysis solution containing 0.5 mg ml⁻¹ proteinase K (Sigma), 0.5 M EDTA, 1% N-laurylsarcosine (Sigma) for 16 h at 37 °C. Plugs were washed six times by gentle agitation for 1 h in TE buffer and stored in TE buffer at 4 °C, then incubated three times in 1 ml of pre-XbaI buffer (6 mM TrisHCl, 150 mM NaCl, 6 mM MgCl₂, 1 mM DTT, pH 7.9) for 30 min at 37 °C and treated overnight at 37 °C with 10 U XbaI (Sigma–Aldrich). The gel was...
prepared using 1% pulsed-field-certified agarose (Bio-Rad) in 0.5× TBE buffer (45 mM Tris–borate and 1 mM EDTA) and sealed with 0.75% low melting point agarose. A 50–1000 Kb molecular weight marker (Sigma) was used. PFGE was performed using the CHEF Mapper XA System (Bio-Rad). The gel run was performed at 6.0 V cm⁻¹ for 23 h at 14 °C with initial time pulse of 1 s and final time pulse of 30 s. Gel images of the genomic DNAs were digitized by using a Kodak Image Station 2000R following ethidium bromide staining. The clonality was examined according to the recommendations; i.e., isolates differing in more than six bands were considered sufficiently divergent to warrant separate pattern designations, whereas those that differ by one to three (a–c subtypes) or four to six bands should be considered, respectively, closely or possibly related. Reproducibility was checked by repeating PFGE runs.

Random-amplified polymorphic DNA (RAPD)

Template DNA was prepared from bacteria grown for 48 h at 28 °C on Müller Hinton agar plates. Crude DNA extracts were obtained by suspending five colonies in 100 μl sterile distilled water, vortexing, centrifuging at 3000 rpm for 5 min and using the supernatant. We used primers 208, 270 and 272 (5'–ACGCGCCGACC-3'; 5'–TGCGCGGGG-3'; and 5'–AGCGGCCCA-3', respectively) and the conditions described. The amplified DNA fragments were separated in a 1.5% agarose gel (Invitrogen) in 1× TBE with 0.5% ethidium bromide (10 mg ml⁻¹, Sigma) for 1 h and 40 min at 6 V cm⁻¹. RAPD fingerprints were analyzed by Kodak Image Station 2000R and the clonality was evaluated based on guidelines reported.

Isolates that differed by two or more prominent bands were assigned to different major types, whereas isolates that differed by one to two faint bands were considered minor variant types (a and b) of a given major type. Reproducibility of the random PCR patterns was assessed by repeating PCR runs.

PCR analysis

The identification of the Burkholderia genomovar status was effected by PCR using nine recA primer pairs specific for genomovars I, II, III-A, III-B, IV, V, VI, VII and VIII. For isolates whose identification remained unclear, the evaluation of 23S rDNA of the species B. gladioli by using the SS-PCR with primer pair LP1–LP4 was done. Detection by PCRs of the B. cepacia epidemic strain marker (BCESM) and cable pili subunit gene (cblA) was carried out as previously described.

Results

The analysis effectuated to determine the species or genomovar status of Burkholderia revealed (Table 1) that among the 48 isolates tested 34 (11 from seven children and 23 from 13 adults) belonged to B. cenocepacia group III-A, one strain (sequentially isolated from a child) was identified as B. ambifaria (genomovar VII), and 11 strains, obtained from four adults, were negative for all Bcc genomovars and positive to the PCR analysis for B. gladioli. Among all strains 25, four from children and 21 from adults, belonging exclusively to B. cenocepacia group III-A, were positive for esmR gene (Table 1); on the contrary, no strain was cblA-positive. By PFGE (Table 1, Fig. 1) we observed that the isolates show four distinct banding patterns: P1, P2 (including four subtypes), P3 and P4 (including P4a, that differed in one band). The pattern indicated as P2 was the most prevalent (75 and 58.8% of the bacteria collected on the first occasion of microbiological diagnosis from children and adults, respectively). The P1 and P3 profiles were noted only in strains from adults, while one, indicated as not classified (NC) because resulted not digested with XbaI, was isolated from one child alone; strains characterized as belonging to the P4 profile were observed in few isolates. The results of RAPD analysis reported were obtained using the primer 272, chosen after test screening with primers 208, 270 and 272. Four banding profiles were obtained by the analysis of isolates: R1, R2 (including two subtypes, differing in one or two minor bands), R3 and R4; the RAPD profile designated as R2 was prevalent and present both in children and adults (Table 1, Fig. 1). The Burkholderia strains with patterns P2−R2 corresponded to B. cenocepacia group III-A, those not classified (NC) by PFGE and defined as R3 by RAPD belonged to B. ambifaria (genomovar VII), and those named P1−R1 belonged to the B. gladioli species. The reference Bcc strain group III-A (CF5610) also revealed a P2–R2 profile, whereas the other reference strains tested, belonging to different Bcc genomovars, had PFGE and RAPD patterns different from the isolates tested (not reported) except for the LMG 19467 strain (Bcc genomovar VII) whose RAPD profile was similar to the isolate of the same genomovar collected from a child (Table 1).

Discussion

The poor prognosis of CF is especially associated with an early onset of respiratory tract infection with a variety of bacterial species. Among these are
included several species of the genus *Burkholderia* whose incidence appears to be increasing; of the emerging pathogens, Bcc and *B. gladioli*, also demonstrated in the present work, are prominent.\(^{16}\) Between these microorganisms there is a high degree of phenotypic similarity and accurate identification is difficult. The use of a procedure based on a species-specific PCR for the identification

<table>
<thead>
<tr>
<th>Category of patients (number of strains)</th>
<th>Patients or isolates</th>
<th>Isolation</th>
<th>BCESM</th>
<th>Species or genomovar status</th>
<th>PFGE profile</th>
<th>RAPD profile</th>
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\(^a\) NC, not classified because not restricted with XbaI enzyme.
of *B. gladioli* is useful to clarify the role of this microorganism as a human pathogen in CF.

Our results revealed that *B. cenocepacia* (genomovar III-A) is the most prevalent (70.8 and 80% of all isolates or of the firstly examined strain for patient, respectively) in the samples obtained from CF patients. This is in line with other data derived from the analysis of CF patients, but different from results reported in a Belgian study. There is evidence that genomovar III-A strains are more invasive for respiratory epithelial cells and associated with greater morbidity and mortality. Eleven strains (isolated from four different adults), that by biochemical analysis were presumptively identified as *B. cepacia*, resulted positive to the PCR assay for *B. gladioli* and revealed particular PFGE and RAPD patterns. These results confirm previous observations indicating that *B. gladioli* is the species most frequently misidentified by commercial systems as Bcc and show that this species may determine adverse clinical outcome and person-to-person transmission. Moreover one child was colonized by *B. ambifaria* (genomovar VII); infection with this species, which is common in environmental samples, has not been previously reported, to our knowledge, in strains isolated from other Italian patients, though found in small number in patients of other countries. This suggests that this species may play a role as a human pathogen and its acquisition from the environment is possible.

Following up some patients over certain time period obtaining different isolates per patient, we noted that in all cases the infection was persistent. Only little genetic differences were identified in sequential isolates of some patients (1c and 9a); this fact might be due to antibiotic resistance variations. The PFGE and RAPD profiles P3–R4 and P4–R3 noted in singular isolates from four patients might be derived from isolates harbouring more than one *Burkholderia* strain or hybrids between Bcc and *B. gladioli*, as previously reported.

Many Bcc genomovar III-A strains, isolated from patients submitted to controls in two different hospitals, were genotypically similar to the reference epidemic (ET 12 lineage) strain belonging to the same genomovar and associated with serious outbreaks among CF patients in UK. However, in the isolates tested the *cblA* gene was not demonstrated, perhaps owing to the instability of its sequence. Isolates with a P2–R2 DNA profile and positive for *esmR* gene (part of a genomic cluster encoding virulence and metabolism-associated gene) prevailed, suggesting the possibility of interpersonal transmission or nosocomial acquisition. CF patients may acquire other Bcc lineages also from the environment. In recent years, in fact, Bcc has been used in agriculture as biopesticides and bioremedial products, most notably particular strains of *B. vietnamiensis* and *B. ambifaria* because of their low incidence of isolation from CF patients.
Strategies introduced in different countries have limited the epidemic spread of Bcc\(^1,7,13,34,35\), so the implementation of stringent infection control measures is important to limit spread both within and outside hospital and epidemiological studies of Burkholderia species are critical to keep pace with the ecological and pathogenic interest in the genus.

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