Genomovar distribution of the *Burkholderia cepacia* complex differs significantly between Czech and Slovak patients with cystic fibrosis

The morbidity and mortality rates in cystic fibrosis (CF) patients are significantly affected by infections with organisms from the *Burkholderia cepacia* complex (BCC). The complex currently includes nine genomic species (genomovars): *Burkholderia cepacia* (genomovar I), *Burkholderia multivorans* (genomovar II), genomovar III (divided into two recA clusters, III-A and III-B; Mahenthiralingam et al., 2000), *Burkholderia stabilis* (genomovar IV), *Burkholderia vietnamiensis* (genomovar V), genomovar VI, *Burkholderia ambifaria* (genomovar VII), *Burkholderia anthina* (genomovar VIII) and *Burkholderia pyrrocinia* (genomovar IX) (Vandamme, 2002). Although all genomovars have been isolated from clinical sources, their occurrence varies significantly (Agodi et al., 2002). We compared the BCC genomovar distribution in CF patients from the Czech Republic and CF patients from the Slovak Republic. BCC isolates from 61 Czech CF patients attending the Prague CF centre and from 24 Slovak CF patients attending three different Slovak CF centres were collected during the year 2001. The BCC was recovered in sputum cultures and verified by means of a nested-PCR assay (Drevinek et al., 2002). The genomovar status of BCC was then determined using a set of eight recA gene sequence-specific PCRs distinguishing all the genomovars with the exception of *B. anthina* and *B. pyrrocinia*.

The BCC genomovar distribution in the Czech and Slovak CF populations is shown in Table 1. Whereas genomovar III-A was predominant in the Czech CF community (90 %), in Slovakia the most frequently identified genomovar was *B. stabilis* (54 %) (P of the difference < 10^{-4}). This result is in marked contrast to what might be expected in two neighbouring populations which had formed the Czechoslovak federation until the end of 1992. While the high prevalence of genomovar III-A in the Czechs has its counterparts in *B. stabilis* in Slovakia, we can speculate that this may be drawn on the causes of this phenomenon in Slovakia, Most of the virulent and epidemic strains have been identified within genomovar III-A (Mahenthiralingam et al., 2001; Agodi et al., 2002).

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In conclusion, the difference in genomovar distribution between two closely related populations is a surprising result as is the high percentage of genomovar III-A in the Czech Republic and of *B. stabilis* in Slovakia.

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**Table 1. Genomovar distribution of the BCC in Czech and Slovak CF patients**

<table>
<thead>
<tr>
<th>Country</th>
<th>Total no. of patients</th>
<th>I B. multivorans</th>
<th>III-A</th>
<th>III-B</th>
<th>B. stabilis</th>
<th>B. vietnamiensis VI</th>
<th>B. ambifaria</th>
<th>Unidentified genomovar</th>
</tr>
</thead>
<tbody>
<tr>
<td>Czech Republic</td>
<td>61 (100 %)</td>
<td>0</td>
<td>3</td>
<td>55 (90 %)</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Slovak Republic</td>
<td>24 (100 %)</td>
<td>0</td>
<td>0</td>
<td>7 (29 %)</td>
<td>3</td>
<td>13 (54 %)</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

*P of the difference (Kolmogorov–Smirnov test) < 10^{-4}.
†No genomovar-specific reaction was positive, indicating the possible presence of another genomovar from the BCC.
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