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.*, 2001; Speert *et al.*, 2002), indicating the differences among the genomovars in virulence factors and in the ability of person-to-person transmissibility. Most of the virulent and epidemic strains have been identified within genomovar III-A (Mahenthiralingam *et al.*, 2001; 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 several Western CF populations (Canada 80 %, Speert *et al.*, 2002; Italy 73 %, Agodi *et al.*, 2001), the high rate of *B. stabilis* found in the CF population in Slovakia is a unique observation. Although the low numbers of patients do not permit conclusions to be drawn on the causes of this phenomenon in Slovakia, we can speculate that this may be caused either by unique strains acquired separately by each patient, or by transmission of an as yet unknown epidemic clone of *B. stabilis*. To test the hypotheses, we performed randomly amplified polymorphic DNA (RAPD) fingerprinting (Mahenthiralingam *et al.*, 1996), a widely used genotyping method for BCC strain analyses. Thirteen Slovak

B. stabilis isolates showed patterns indistinguishable among all the isolates (data not shown). If such an RAPD result was obtained in genomovars other than *B. stabilis*, it would suggest clonality of the isolates. However, as genomic variability among *B. stabilis* strains is remarkably restricted (Vandamme *et al.*, 2000), the result does not allow exclusion of either of the hypotheses, and further analyses to confirm or refute the relationship of the isolates are needed.

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

Country	Total no. of patients	No. of patients infected with genomovar [<i>n</i> (%)]*							
		I	<i>B. multivorans</i>	III-A	III-B	<i>B. stabilis</i>	<i>B. vietnamiensis</i> VI	<i>B. ambifaria</i>	Unidentified genomovar†
Czech Republic	61 (100 %)	0	3	55 (90 %)	1	1	0	0	1
Slovak Republic	24 (100 %)	0	0	7 (29 %)	3	13 (54 %)	0	0	1

**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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