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**Clinical and microbiological characteristics of bacteraemia caused by *Burkholderia cepacia* complex species**

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**Background:** This study investigated the clinical characteristics and outcomes of bacteraemia due to *Burkholderia cepacia* complex (BCC) species among patients without cystic fibrosis

**Material/methods:** BCC isolates were identified to the species level by the Bruker Biotyper MALDI-TOF MS system and by sequencing analysis of the 16S rRNA and *recA* genes. Antimicrobial susceptibilities of the isolates were determined by the agar dilution method.

**Results:** From January 2013 to February 2015, we identified 54 patients with bacteraemia due to BCC complex species. Sequencing of the *recA* gene in the 54 blood isolates revealed 37 (68.5%) isolates of *B. cenocepacia*, 9 (16.7%) *B. cepacia*, 4 (7.4%) isolates of *B. multivorans* and one isolate each of *B. arboris*, *B. pseudomultivorans*, *B. seminalis*, and *B. vietnamiensis*. The overall performance of the Bruker Biotyper MALDI-TOF MS system for correctly identifying the 54 BCC isolates to the species level was 79.6%. Bacteraemic pneumonia (n=23, 42.6%) and catheter-related bacteraemia (n=21, 38.9%) were the most common types of infection. Higher rates of ceftazidime and meropenem resistance were found in *B. cepacia* isolates (33.3% and 22.2%, respectively) than in isolates of *B. cenocepacia* (21.6% and 10.8%, respectively) and other species (12.5% and 12.5%, respectively). Overall, the 30-day mortality rate was 38.9% (21/54). Bacteraemia caused by BCC

species other than *B. cenocepacia* and *B. cepacia* (adjusted odds ratio [aOR] 20.005,  $P=0.024$ ) and high SOFA score (aOR 1.412,  $P=0.003$ ) were predictive of higher 30-day mortality.

**Conclusions:** Different BCC complex species are associated with different outcomes of bacteraemia and exhibit different susceptibility patterns.