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ePoster Viewing
Diagnostic bacteriology – non-culture based, including molecular and MALDI-TOF

Prevalence, colonization patterns, antibiotic susceptibility and MALDI-TOF identification of Burkholderia cepacia complex isolates from a Spanish cystic fibrosis unit

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Background: *Burkholderia cepacia* complex (BCC) species are associated with a rapid decline in lung function and high mortality in cystic fibrosis (CF) patients. Correct identification of BCC species is crucial as some of them, like *B. cenocepacia* (Bceno), are associated with poorer prognosis. *B. contaminans* (Bcont), a novel species with unknown clinical importance, has been reported as the most frequently isolated in Spain. Our objectives were: i) to study the prevalence, antibiotic susceptibility and colonization patterns of the BCC species isolated in our Hospital and ii) to compare MALDI-TOF identification of BCC (used routinely in our laboratory) with the recommended *recA* gene sequencing.

Material/methods: *Burkholderia* spp. strains isolated from CF-patients between 2010 and 2015 were recovered. Susceptibility testing was performed by automated microdilution methods (MicroScan). Clonality of the isolates was assessed by Pulse Field Gel Electrophoresis (PFGE) with *Spe*I. Identification was performed by MALDI-TOF (Bruker Daltonics. Germany) and by *recA* sequencing.

Results: A total of 313 CF-patients attended to our hospital from 2010 to 2015, 55 strains of *Burkholderia* spp. being isolated in 14 of them (4.5% prevalence). Bcont, *B. vietnamiensis* (Bv), *B. cepacia* (Bcep), *B. stabilis* (Bs) and *B. multivorans* (Bm) were seen in 36% (n=5), 29% (n=4), 14% (n=2), 7% (n=1), and 7% of the patients, respectively, being 1 patient (7%) colonized by *B. gladioli* (Bg). The most active antibiotics against BCC species were meropenem, minocycline and co-trimoxazole (76%, 65% and 59% of susceptible isolates, respectively). PFGE patterns showed that each patient harbored his own clone but a possible case of cross-transmission was identified. Chronic

colonization was found in 7 patients (50%) due to Bv (n=2), Bs (n=1), Bm (n=1), Bcep (n=1), Bcont (n=1) and Bg (n=1). MALDI-TOF identification was correct at genus and at species level in 98% and 76% of the isolates, respectively. MALDI-TOF correctly identified all Bm and Bg isolates (table) whereas always misidentified Bcont as Bceno or Bcep.

Conclusions: Bcont is the most frequent BCC species in our institution but is not frequently associated with chronic infections. MALDI-TOF misidentification could have a clinical and psychosocial impact as the most prevalent BCC species in Spain are frequently identified wrongly as Bceno. MALDI-TOF could be a rapid a promising tool for the identification of BCC species, but an increased number of BCC spectra in its database is needed.

***Rec A* Id.**	**No. Isolates**	**MALDI-TOD id.**	
		Correct, n (%)	**Incorrect, n(species)**
B. multivorans	10	10 (100)	0
B. gladioli	6	6 (100)	0
B. vietnamiensis	23	21 (91)	2 (1 *B. cenocepacia*; 1 *Brevibacillus* spp.)
B. stabilis	6	3 (50)	3 (1 *B. pyrrocinia*; 2 BCC Group)
B. cepacia	3	1 (33)	2 (*B. cenocepacia*)
B. contaminans	7	0 (0)	7 (4 *B. cepacia*; 3 *B. cenocepacia*)