O188
Oral Session
Non-molecular diagnosis of central nervous system and bloodstream infections

HIGHLY ACCURATE MALDI-TOF IDENTIFICATION USING THE VITEK MS PLUS SYSTEM WHEN CHALLENGED WITH INTENTIONAL MIXTURES PREPARED FROM BACTERIA AND YEAST COLONIES

B.M. Willey[1], E. Ramoutar[1], P. Lo[1], S.M. Poutanen[2]

[1]Microbiology, Mount Sinai Hospital/University Health Network, Toronto Ontario, Canada ; [2]Microbiology, Mount Sinai Hospital/University Health Network/University of Toronto, Toronto Ontario, Canada

Objectives: Identification (ID) from short-incubation cultures (3-6h) is a strategy to provide fast turn-around-times for organism IDs from positive blood cultures (BC). Since positive BC may be poly-microbial, the accuracy of MALDI-TOF in this setting has been questioned. By intentionally subjecting mixed organisms to MALDI-TOF, this study challenged the ability of bioMérieux's VITEK MS PLUS system to produce accurate ID regardless of the purity of the culture tested.

Methods: Freshly cultivated ATCC strains were used to perform 432 mixed ID tests in a range of predetermined proportions using standard application techniques on VITEK MS PLUS. Of these, 376 (87%) comprised bacterial mixtures (BM) of 2 (n=243) to 3 (n=133) distinct strains/test, while 56 (13%) comprised *Candida* mixtures (CM) of 2 species/test. BM included 24 species (*A. aphrophilus, C. jeikeium, C. species not jeikeium, E. faecalis, E. faecium, E. gallinarum, E. coli, H. influenzae, K. pneumoniae, L. mesenteroides, M. catarrhalis, N. gonorrhoeae, N. meningitidis, P. mirabilis, P. vulgaris, P. aeruginosa, S. aureus, S. epidermidis, S. lugdunensis, S. saprophyticus, S. agalactiae, S. equi ssp. equi, S. pneumoniae,* and *S. pyogenes*), while CM included 7 species (*C. albicans, C. glabrata, C. guillerimondii, C. krusei, C. lusitaniae, C. parapsilosis,* and *C. tropicalis*). Statistics were calculated using www.graphpad.quickcalcs.com.

Results: Of the 376 BM tests, 31 (8.3%; 95%CI: 5.8-11.5) produced 'Bad spectrum during analyses' or 'No ID' results. Of the 345 BM with ID, 340 (98.6%; 95%CI: 96.6-99.5) produced high-confidence correct ID [single-species correct ID (n=293: 186 from 2-strain mixes, 107 from 3-strain mixes) or 2-species correct IDs (n=47: 38 from 2-strain mixes, 9 from 3-strain mixes)] and 5 (1.5%; 95%CI: 0.5-3.5%) produced low-confidence ID that would be rejected. No misidentifications occurred with high confidence. Of the 56 CM tests, 6 (10.7%; 95% CI: 4.7-21.8) produced 'Bad spectrum during analyses' or 'No ID' results. Of the 50 CM with ID, 49 (98%; 95%CI: 88.5->99.9) produced high-confidence correct ID (n=39 single-species correct ID; n=10 both species correct), while 1 (2%; 95%CI: <0.01-11.5) resulted in an incorrect ID of *Debaryomyces polymorphus* with 98% confidence. Notably, this species is not typically isolated from human specimens and would not likely be reported until confirmation or repeat testing was completed in most laboratories.
Conclusions: This challenge of the VITEK MS PLUS system using intentionally mixed colonies for MALDI-TOF ID produced reassuring results. 98.6% of BM and 98% of CM that had an associated ID from MALDI-TOF produced correct ID with high confidence. Only 0.2% of all tests with an ID produced an incorrect ID with high confidence. Overall, these data suggest that VITEK MS PLUS ID obtained with high % confidence from short-incubation cultures from positive blood cultures will be highly accurate even in the setting of mixed cultures.