Abstract 6917

Molecular pathogen identification and resistance gene detection from positive blood cultures

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Background: The gold standard for pathogen detection in blood is the inoculation of blood culture (BC) bottles and subsequent identification of microbes using mass spectrometry (MS). Rapid identification of the causative pathogen, and possible inherent antibiotic resistances, is crucial for appropriate treatment of severe infections.

Rapid pathogen identification is hampered as: (1) certain bacterial species proliferate very slowly under BC conditions (e.g. *Bacteroides spp.*, *Propionibacterium acnes*); (2) in mixed infections, faster proliferating species overgrow slower ones, which might then be missed; (3) treatment with antibiotics prior to blood draw prolongs/inhibits bacterial growth; (4) antibiotic resistance(s) are determined by (time-consuming) plating.

This work compares pathogen identification from positive BC by state-of-the-art MS and Cube Dx' molecular test: *LINA compact sequencing*, which uses a diluted sample of BC directly in a PCR reaction. After the PCR pathogens are identified using Cube Dx' *compact sequencing*, covering 101 targets (bacterial-, resistance- and fungal genes).

Materials/methods: In total, 277 blinded BC samples (178 positive, 99 negative) were analysed at Unilabs by conventional culture and MS in parallel to *LINA compact sequencing,* respectively.

Results: Among the positive samples both methods identified identical bacterial species/genus in 166/178 cases (93%). Seventeen samples (ff6%) yielded discordant results. In 3 cases *compact sequencing* did not report a bacterial species. Interestingly, in 4 positive samples, *compact sequencing* yielded a result whereas MS did not, and in 9 cases more than one species was detected – indicating that molecular diagnostics reveals mixed infections, even if one species might be predominant in culture. As an example, 3 samples contained bacteria of the *Acinetobacter baumannii complex* and *Escherichia coli* according to *compact sequencing*, where MS only detected *E.coli*.

Conclusions: Results for positive BC samples with *LINA compact sequencing* were obtained within 3 hours. *LINA* detected almost all positive blood cultures concordantly with current established methods resulting in a sensitivity of 98%. In addition, several mixed infections and slow growing bacteria were identified which were missed by MS, including *Acinetobacter species* which are highly relevant carriers of antibiotic resistance genes, resulting in a specificity of 88%.

		Culture	
		positive	negative
Cube	positive	166	13
	negative	4	94

Sensitivity	Specificity
98%	88%

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