The optimalisation of the MALDI-TOF MS database for the identification of anaerobic bacteria

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Introduction

The MALDI-TOF MS database needs optimalisation for the identification of anaerobic bacteria. The European Network for the Rapid Idenfication of Anaerobes (ENRIA) aims to have at least 5 Main Spectral Profiles (MSPs) present in the database of each anaerobic species recovered from human clinical specimens. The project is initiated by the ESCMID study groups ESGAI and ESGEM, and consists of 7 expertise laboratories in Europe.

Material and methods

Human clinical anaerobes were collected by the expertise laboratories and sent to the University Medical Center Groningen, The Netherlands. Strains were subcultured and subjected to 16S rRNA gene sequencing for definititive identification. Only of strains with >98,7% sequence similarity were included in the ENRIA project. MSPs were created of 110 gram-positivie anaerobic cocci (GPAC) isolates. Validation of the optimized database was performed using 129 sequenced GPAC clinical isolates.

Table 1. MALDI-TOF MS identification results of GPAC clinical isolates compared with the Bruker database and with the Bruker database supplemented with MSPs of well characterized GPAC species.

	Bruker database			Bruker database + ENRIA GPAC database			
	score ≥2	score >1.7 - <2	score ≤1.7	score ≥2	score >1.7 - <2	score ≤1.7	no. of strains with higher score
P. harei (n=28)	19	8	1	28	0	0	26
F. magna (n=25)[a]	16	8	1	16	8	1	0
P. micra (n=27)[a]	25	2	0	25	2	0	0
A. vaginalis (n=8)	0	2	6	8	0	0	8
A. murdochii (n=5)	4	1	0	5	0	0	1
A. hydrogenalis (n=2)	0	0	2	0	2	0	2
A. obesiensis (n=2)	0	0	2	0	0	2	0
P. anaerobius (n=8)	7	1	0	8	0	0	8
P. stomatis (n=2)[b]	0	0	2	1	1	0	2
M. asaccharolytica (n=2)[b]	0	0	2	2	0	0	2
P. lacrimalis (n=2)[b]	0	0	2	2	0	0	2
P. grossensis (n=2) [b]	0	1	1	1	1	0	2
different GPAC species (n=7)	0	1	6	7	0	0	7
GPAC (9)	2	0	7	2	1	6	2
% of all strains	**56,6%**	**18,6%**	**24,8%**	**81,4%**	**11,6%**	**7,0%**	**48,1%**

[a] No additional reference spectra were added to the MALDI-TOF MS database.
[b] Species was not present in the MALDI-TOF MS database.

Results

± 650 strains were collected, representing 258 different species. Of these species, 75 species were not yet represented in the database. MSPs were created of 110 gram-positive anaerobic cocci (GPAC) isolates. Results of the validation are presented in Table1. By comparing the obtained spectra of the strains used for validation, with the Bruker database and the optimized database, we observed an increase of reliable species identification from 56,6% to 81,4%. GPAC strains which could not be identified decreased from 24,8% to 7,0%. For 48,1% of the strains a higher log score was obtained.

Conclusion

Optimalisation of the MALDI-TOF MS database is expected to result in a higher number of anaerobic clinical isolates which can be reliably identified. After optimalisation, GPAC are represented in the database by 33 species, of which 16 species were not present in the Bruker database. Eventhough, 17 species are still under represented (<5 MSPs) in the database, the number of strains which could be reliably identified at the species level increased from 56,6% to 81,4%.

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