EV0192

27th ECCMID Vienna, Austria 22 – 25 April 2017

Performance of Andromas and Bruker MALDI-TOF MS in the identification of *Neisseria*

Jean Winoc Decousser[2,4], Florence Morel[1,2], Marine Desroches[2,4], Hervé Jacquier[1,2,3] Vincent Fihman[4], Emmanuelle Cambau[1,2,3], Béatrice Berçot[1,2,3].

[1] Service de Bactériologie-Virologie, Hôpital Lariboisière, APHP, Paris, France ; [2] Infection, Antimicrobiens, Modélisation, Evolution (IAME), [3] Centre de Reference des gonocoques, Paris, France UMR1137, INSERM, Université Paris Diderot, Paris, France ; [4] Service de Bactériologie-Virologie, Hôpital Henri Mondor, APHP, Paris, France.

Background

The genus *Neisseria* includes two human pathogens species, *Neisseria meningitidis* and *Neisseria gonorrhoeae* and several non pathogenic *Neisseriae* species. Matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS system) is a cost effective and accurate method that provides highly reliable and rapid bacterial identifications[1,2] . The Bruker and Andromas MALDI-TOF MS systems uses the best database match of a mass spectrum for identification. To date, no study has compared the performance of Andromas with Bruker MALDI-TOF MS for the identification of *Neisseriae*.

Objective

To compare the performance of Andromas with Bruker MALDI-TOF MS for the identification of *N. gonorrhoeae*, *N. meningitidis* and non pathogenic *Neisseriae* after 24h and 48h of growth.

Methods

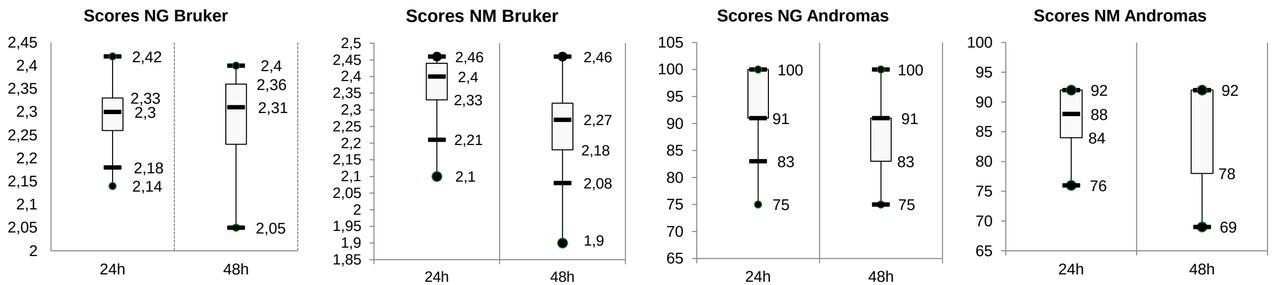
Neisseriae strains were recovered at Henri Mondor and Lariboisière hospitals, Paris, France , and were inoculated onto chocolate agars and incubated at 37C in 5% CO2.
N. meningitidis and non pathogenic *Neisseriae* had been previously identified by 16S rRNA sequencing .
Identification was carried out in duplicate using the two MALDI-TOF platforms (Andromas, Henri Mondor hospital, France and Bruker, Lariboisière Hospital, France) in parallel after 24h and 48h of growth.

Results

131 strains of *Neisseriae* tested (Henri Mondor = 33; Lariboisière = 98)

		24 h		48 h	
		Bruker	**Andromas**	**Bruker**	**Andromas**
***N. gonorrhoeae* (n=85)**	**NG**	n=85 (100%)	n=85 (100%)	n=83 (97,6%)	n=85 (100%)
	Non NG	n=0	n=0	n=0	n=0
	No peak found	n=0	n=0	n=2 (2,4%)	n=0
***N. meningitidis* (n=18)**	**NM**	n=17	n=16	n=18	n=17
	Non-NM	n=1 (N. elongata)	n=0	n=0	n=0
	No peak found	n=0	n=2	n=0	n=1

NG = *N. gonorrhoeae*
NM = *N. meningitidis*



Conclusions

Bruker and Andromas platforms have both shown good performances in *N. gonorrhoeae* and *N. meningitidis* identification. They were better after 24h of growth (median scores >2,2 for Bruker and >85% for Andromas) than after 48h of growth. MALDI-TOF identification eliminated the option of N. gonorrhoeae or N. meningitidis in 96% and 100% of non-pathogenic Neisseriae cases for Bruker and Andromas platforms respectively. Misidentification of *N. polysaccharaea* as *N. meningitidis* has been previously described in several studies [3,4] . In contrast to them, *N. cinerea* was well identified by Bruker and Andromas mass spectrometers.

Non pathogenic *Neisseriae* (n=28)	**Bruker**		**Andromas**	
16S rRNA sequencing	**Ident.**	**Score**	**Ident.**	**Score (%)**
***N. subflava/perflava* (n=13)**	*N.sp*	2,05	*N. flava/perflava/sicca*	76
	N.flavescens	1,93	*N. flava/perflava/sicca /subflava*	73
	N.flavescens	2,12	*N. flava/perflava/sicca*	92
	N.flavescens	2,16	*N. flava/perflava/sicca*	84
	N.flavescens	2,09	*N. subflava*	80
	N.flavescens	2,09	*N. subflava*	80
	N.flavescens	2,14	*N. subflava*	66
	N.flavescens	2,15	*N. subflava*	86
	N.perflava	2,1	*N. mucosa*	72
	N.perflava	2,28	*N. flava/perflava/sicca*	84
	N.flavescens	2,13	*N. subflava*	93
	N.flavescens	2,11	*N. flava/perflava/sicca*	76
	N.flavescens	2,03	*N. flava/perflava/sicca*	76
***N. mucosa* (n=3)**	*N. macae*	2,19	*N. mucosa*	100
	N. mucosa	2,06	*N. mucosa*	100
	N. mucosa	2,14	*N. mucosa*	100
***N. macacae/mucosa/sicca* (n=3)**	*N.macacae*	2,16	*N. mucosa*	100
	N.mucosa	1,91	*N. mucosa*	90
	N.macacae	1,93	*N. mucosa*	81
***N. elongata* (n=3)**	*N. elongata*	1,98	*N. elongata*	71
	N. elongata	2	*N. elongata*	76
	N. elongata	1,84	*N. elongata*	76
***N. cinerea* (n=2)**	*N. cinerea*	1,81	*N. cinerea*	100
	N. cinerea	1,77	*N. cinerea*	91
N. bacilliformis	*N.bacilliformis*	2,04	*N. bacilliformis*	85
N. polysaccharea	*N.meningitidis*	2,1	-	-
N. wadsworthi	-	-	-	-
N. wearveri / animalis	*N.weaveri*	2,04	*N. weaveri*	84

1, Bizzini A, and al. Matrix-assisted laser desorption ionization time-of-flight mass spectrometry, a revolution in clinical microbial identification. Clin Microbiol Infect 2010;16:1614–9
2, Tan KE, and al. Prospective Evaluation of a Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry System in a Hospital Clinical Microbiology Laboratory for Identification of Bacteria and Yeasts: a Bench-by-Bench Study for Assessing the Impact on Time to Identification and Cost-Effectiveness. J Clin Microbiol 2012;50:3301–8..
3. Vironneau P, and al, 2013. *Neisseria polysaccharea* and *Neisseria cinerea* identified like *Neisseria meningitidis* by MALDITOF abstr P172. Abstr. 23rd Meet. Eur. Congr. Clin. Microbiol. Infect. Dis., Berlin, Germany.
4. Cunningham SA, and al. Misidentification of Neisseria polysaccharea as Neisseria meningitidis with the use of matrix-assisted laser desorption ionization-time of flight mass spectrometry. J Clin Microbiol. 2014 Jun;52(6):2270-1.