Comparison of Autof MS1000 and Bruker biotyper in the identification of a number of randomized clinical isolates

[Abstract] Objective: To compare the use of two matrix-assisted laser desorption ionization time of flight mass spectrometry (MALDI-TOF-MS) systems, Bruker MALDI Biotyper system (Bruker biotyper system) and MALDI-TOF-MS of Autobio (Autof MS1000 system) in the identification of clinical isolates. **Methods:** A selection of 210 clinical isolates tested in this study, representing 93 Gram-negative bacillus、18 Gram-negative cocci、26 Gram-positive bacillus、60 Gram-positive cocci and 13 Candida were isolated between February to July 2017 from the second Hospital of Nanning. All isolates were analyzed in parallel by Autof MS1000 and Bruker biotyper, which was compared with the identification by traditional biochemical test system (compact Vitek 2, BioMerieux). Discordant results among the three systems were resolved with 16/18S rDNA gene sequencing. **Results:** Of the 210 isolates, 91.0% were correctly identified to the species level by Autof MS1000 system and 85.7% by Bruker biotyper system, the difference was not statistically significant ($P>0.05$); 98.6% were correctly identified to the genus level by Autof MS1000 system and 91.4% by Bruker biotyper system, the difference was statistically significant ($P<0.01$).

Conclusions: According to the statistical results show that the identification accuracy of Autof MS 1000 was higher than that of Bruker biotyper, and the identification accuracy at the genus level was significantly with Bruker biotyper, we can predict Autof MS 1000 will become a powerful tool for clinical identification of bacteria.

Key words: bacteria identification, Atlas, strains, substrates

Identification Results:

Of the 210 isolates, 91.0% (191/210) were correctly identified to the species level and 98.6% (207/210) were correctly identified to the genus level by Autof MS1000 system. Of the 210 isolates, 85.7% (180/210) were correctly identified to the species level and 91.4% (192/210) were correctly identified to the genus level by Bruker biotyper. At the species level, the statistical results show the correction value X^2 is 2.31, P=0.1285 (>0.05), the difference is not significant. At the genus level, the statistical results show the correction value X^2 is 0.9824, P=0.0017 (<0.01), the difference is significant in statistical. Comparison of statistical results in Table 1, Variance analysis in Table 2.

Table 1. Camparison of statistical results between Autof MS1000 and Bruker biotyper

Isolates	Quantity	Autof MS1000		Bruker biotyper	
		Correct at the genus level	Correct at the species level	Correct at the genus level	Correct at the species level
A's yeast Trichosporon	1	1	1	1	1
Enterobacter asburiae	1	1	1	1	1
Staphylococcus arlettae	1	1	1	1	1
Streptococcus lutetiensis	1	1	1	1	1
Candida albicans	6	6	6	5	5
Acinetobacter baumannii	4	4	3	4	3
Staphylococcus epidermidis	3	3	3	3	3
Listeria monocytogenes	8	8	8	8	8
Enterobacter aerogenes	2	2	2	2	2
Klebsiella oxytoca	2	2	2	2	2
Pantoea agglomerans	1	1	1	1	1
Escherichia coli	16	16	16	16	16
Bacillus pumilus	3	2	1	2	1
Burkholderia multivorans	2	2	2	2	2
Klebsiella pneumoniae	6	6	6	6	6
Streptococcus pneumoniae	4	4	4	1	1
Alcaligenes faecalis	8	8	8	8	8
Enterococcus faecalis	5	5	5	5	5
Citrobacter braakii	1	1	0	1	0

Shewanella putrefaciens	1	1	1	1	1
Lactobacillus casei	2	2	2	2	2
candida glabrata	2	2	2	1	1
Escherichia hermannii	2	2	2	2	2
Monkey Neisseria	1	1	1	1	1
Streptococcus mitis	2	2	2	2	2
Enterococcus gallinarum	1	1	1	1	1
Staphylococcus gallinarum	1	1	1	0	0
Clostridium difficile	1	1	1	1	1
Paenibacillus amylolyticus	1	1	1	1	1
Raoultella planticola	4	4	0	4	1
Exiguobacterium aurantiacum	2	2	1	2	1
Staphylococcus aureus	6	6	6	6	6
Moraxella catarrhalis	16	15	15	14	14
Staphylococcus cohnii	1	1	1	1	1
Citrobacter koseri	2	2	2	2	2
Staphylococcus lugdunensis	2	2	2	2	2
Aeromonas veronii	1	0	0	1	1
Candida rugosa lipases	1	0	0	0	0
Morganella morganii	4	4	4	4	4
Achromobacter xylosoxidans	7	7	7	7	7
Pale yellow Neisseria	1	1	0	1	1
Elizabethkingia meningoseptica	2	2	2	2	2
Chryseobacterium gleum	1	1	1	1	1
Streptococcus pyogenes	1	1	1	1	1
Actinomyces neuii	1	1	1	0	0
Petri Acinetobacter	1	1	1	1	1
Candida lusitaniae	1	1	1	0	0
Proteus vulgaris	1	1	1	1	1
Proteus mirabilis	1	1	1	1	1
candida tropicalis	2	2	2	2	2
Staphylococcus hominis	1	1	1	1	0
Staphylococcus haemolyticus	5	5	4	2	2
Salmonella	2	2	1	1	0

Serratia rubidaea	2	2	2	2	2
Enterobacter cancerogenus	4	4	4	4	3
Stenotrophomonas maltophilia	3	3	3	3	3
Aeromonas hydrophila	4	4	3	4	2
Staphylococcus sciuri	5	5	5	5	5
Burkholderia pseudomallei	1	1	0	1	0
Micrococcus luteus	4	4	4	4	4
Pseudomonas aeruginosa	4	4	4	4	4
Staphylococcus capitis	2	2	2	2	2
Lactobacillus salivarius	2	2	2	2	2
Corynebacterium striatum	3	3	3	3	3
Streptococcus agalactiae	6	6	6	6	6
Lactobacillus pentosus	1	1	1	1	1
Hippocrates Enterococcus	3	3	3	3	3
Streptococcus constellation	2	2	0	2	2
Nocardia asteroides	1	1	1	0	0
Streptococcus anginosus	1	1	1	1	1
Serratia marcescens	4	4	4	4	4
Lactobacillus plantarum	1	1	1	1	1
Staphylococcus intermedius	1	1	1	0	0
Enterococcus faecium	1	1	1	1	1
Total	210	207	191	192	180

Table 2 Variance analysis

	Correct at the genus level	X^2	P	Correct at the species level	X^2	P
Bruker biotyper	192			180		
		0.9824	0.0017		2.31	0.1285
Autof MS1000	207			191		

No results and incorrect identification results statistics
See no results and incorrect identification results statistics in Table 3.

There are 19 isolates got incorrect identification results or not able to identify by Autof MS 1000 system, among them 16 got correct identification result at the genus level, only 3 isolates completely got incorrect identification result or no result. There are 30 isolates got incorrect identification results or not able to identify by Bruker biotyper system, among them 12 got correct identification result at the genus level, 18 isolates completely got incorrect identification result or no result.

Both Autof MS 1000 system and Bruker biotyper system got 99% (92/93) accuracy rate at the genus level of Gram-negative isolates, the difference is not statistically significant (P=0.447>0.05), the accuracy rates at the species level are 92.5%（86/93）and 90.3%（84/93）respectively, the difference is also not statistically significant (P=0.794>0.05), see Table 4.

While identifying Gram-positive isolates, Autof MS 1000 system and Bruker biotyper system got accuracy rate of 95%（57/60）and 85%（51/60）respectively at the genus level which difference was not statistically significant（P=0.128>0.05）, and accuracy rate of 100%（60/60）and 86.7%（52/60）respectively at the species level which difference was statistically significant (P=0.0104<0.05). See Table 5.

While identifying 26 isolates of Gram-positive bacilli, Autof MS 1000 got incorrect identification result of 3 isolates, 2 of the 3 got correct identification result at the genus level. Bruker biotyper got incorrect identification result of 5 isolates, 2 of the 5 got correct identification result at the genus level.

While identifying 18 isolates of Gram-negative cocci, Autof MS 1000 incorrectly identified 1 isolate of *Moraxella catarrhalis* into *Serratia marcescens;* Bruker biotyper could not provide identification result of 2 isolates of *Moraxella catarrhalis.*

While identifying 13 isolates of *Candida*, Autof MS 1000 could not provide identification result of 1 isolate of *Candida rugosa.* Bruker biotyper could not provide identification result of 4 isolates *Candida rugosa, Candida lusitaniae, Candida glabrata, Candida albicans.*

Table 3 Incorrect identified isolates

16/18S rDNA identification and No.	Incorrect identification by 2 MALDI TOF	
	Autof MS1000	Bruker biotyper
MS1518 Citrobacter braakii	Citrobacter freundii	Citrobacter freundii

MS755 Bacillus pumilus	Bacillus altitudinis	Bacillus altitudinis
MS538 Candida glabrata	—	?
MS2178 Staphylococcus gallinarum	—	?
MS1323 Raoultella planticola	Raoultella ornithinolytica	Raoultella ornithinolytica
MS1862 Raoultella planticola	Raoultella ornithinolytica	Raoultella ornithinolytica
MS2300 Raoultella planticola	Raoultella ornithinolytica	—
MS2265 Raoultella planticola	Raoultella ornithinolytica	Raoultella ornithinolytica
MS391 Exiguobacterium aurantiacum	Achromobacter xylosoxidans	Achromobacter xylosoxidans
MS519 Moraxella catarrhalis	—	?
MS494 Aeromonas veronii	?	—
MS539 Candida rugosa	?	?
MS414 Pale yellow Neisseria	Neisseria	—
MS440 Actinomyces neuii	—	?
MS602 Candida lusitaniae	—	?
MS545 Staphylococcus hominis	—	Staphylococcus haemolyticus
MS426 Staphylococcus haemolyticus	—	?
MS100 Staphylococcus haemolyticus	—	?
MS1129 Staphylococcus haemolyticus	Staphylococcus hominis	?
MS407 Moraxella catarrhalis	Serratia rubidaea	?
MS493 Aeromonas hydrophila	Aeromonas hydrophila subsp. Caviae	—
MS732 Burkholderia pseudomallei	Burkholderia thailandensis	Burkholderia thailandensis
MS431 Nocardia asteroide	—	?
MS385 Staphylococcus intermedius	—	?
MS466 Salmonella	Salmonella choleraesuis	?
MS536 Candida albicans	—	?
MS1906 Acinetobacter Bauman complex	Petri Acinetobacter	Petri Acinetobacter
MS98 Streptococcus pneumoniae	—	?
MS455 Streptococcus pneumoniae	—	?
MS201 Streptococcus pneumoniae	—	?
MS676 Enterobacter cancerogenus	—	Enterobacter cloacae/cancerogenus
MS711Aeromonas hydrophila	—	Aeromonas hydrophila subsp. Caviae
MS710 Aeromonas hydrophila	—	Aeromonas hydrophila subsp. Caviae
MS1903 Streptococcus constellatus	Streptococcus constellatus	—

	subsp.pharyngis		
MS1904 Streptococcus constellatus	Streptococcus constellatus subsp.pharyngis	—	
MS757 Bacillus pumilus	?	?	

Note: "—" means correct identification result

"?" means not able to provide identification result or no spectrum collected

Table 4. Difference analysis of Gram-negative isolates by 2 MALDI TOF systems

	Correct identification results at genus level	X^2	P	Correct identification results at species level	X^2	P
Bruker biotyper	92			84		
		0.505	0.477		0.068	0.794
Autof MS 1000	92			86		

Table 5. Difference analysis of Gram-positive isolates by 2 MALDI TOF systems

	Correct identification results at genus level	X^2	P	Correct identification results at genus level	X^2	P
Bruker biotyper	52			51		
		6.5625	0.0104		2.315	0.128
Autof MS 1000	60			57		

Conclusions: According to the statistical results show that the identification accuracy of Autof MS 1000 was higher than that of Bruker biotyper, and the identification accuracy at the genus level was significantly with Bruker biotyper, we can predict Autof MS 1000 will become a powerful tool for clinical identification of bacteria.