



# 새로운 MALDI-TOF질량분석기 ASTA MicroIDSys의 *Acinetobacter* 종 동정에 관한 성능 평가: Bruker Biotyper와의 비교

## Performance of the ASTA MicroIDSys, a Novel MALDI-TOF MS Platform for Identifying Various *Acinetobacter* Species: Comparison with the Bruker Biotyper

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**Background:** Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) is a rapid and reliable method for microorganism identification. Herein, we compared the performance of the recently developed ASTA MicroIDSys (ASTA, South Korea) with that of the Bruker Biotyper (Bruker Daltonics, Germany) for identifying various *Acinetobacter* species.

**Methods:** A total of 207 specimens comprising 22 *Acinetobacter* type or reference strains and 185 clinical isolates previously identified using molecular methods were tested per the manufacturers' recommendation, and the obtained results were compared.

**Results:** The overall correct identification rates at the species level using the Bruker Biotyper and the ASTA MicroIDSys systems were significantly different ( $P < 0.001$ ) at 89.4% (185/207) and 96.6% (200/207), respectively. The correct identification rates within the *Acinetobacter baumannii* (Ab) group were similar ( $P = 0.094$ ) at 94.9% (166/175) and 97.1% (170/175), respectively. However, the correct identification rates within the non-Ab group were significantly different ( $P < 0.05$ ), at 59.4% (19/32) and 93.8% (30/32), respectively. When the twelve strains were excluded as the species were absent from the Bruker database, the overall identification results did not differ significantly ( $P = 0.289$ ).

**Conclusions:** Both instruments were suitable for identifying commonly isolated *Acinetobacter* species in clinical microbiology laboratories, showing equivalent performance for the Ab group, while the ASTA MicroIDSys identified the non-Ab group with higher accuracy than the Bruker Biotyper.

**Key Words:** Comparative Study, Database, Routine Diagnostic Tests, Mass spectrometry, Matrix-Assisted Laser Desorption-Ionization, *Acinetobacter*

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Received: December 8, 2021

Revision received: March 7, 2022

Accepted: March 30, 2022

This article is available from <https://www.labmedonline.org>

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## INTRODUCTION

There has been increasing global concern regarding the clinical importance of nosocomial infections caused by *Acinetobacter* species, including ventilator-associated pneumonia, catheter-related sepsis, meningitis, and urinary tract infections [1, 2]. Using conventional phenotypic assays alone, it is difficult to accurately identify *Acinetobacter* at the species level [3]. Four *Acinetobacter* species, namely, *Acinetobacter baumannii*, *A. calcoaceticus*, *A. nosocomialis*, and *A. pittii*, are collectively called the *Acinetobacter baumannii* group (Ab group) because they share biochemical

and genetic similarities [2]. However, differences in clinical progression and pathogenicity have been observed among *Acinetobacter* species. *A. baumannii* is the most frequently isolated [4] and most clinically significant *Acinetobacter* species owing to its association with severe nosocomial infections, high incidence of multidrug resistance, and high mortality [5]. Advances in molecular techniques have allowed the identification of various *Acinetobacter* species belonging to the non-Ab group from clinical samples, some of which are associated with human infections [6]. *Acinetobacter junii* is a rare pathogen that causes bacteremia, pneumonia, and neonatal sepsis [7-9]. *Acinetobacter soli* also causes bloodstream infections in newborns, and carbapenem-resistant *A. soli* reportedly causes bloodstream infections [10-12]. Bloodstream infections caused by *A. lwoffii*, *A. ursingii*, and *A. radioresistens* have also been reported [13]. Accordingly, the need for reliable identification techniques at the species level is rapidly increasing to ensure rapid and accurate diagnosis.

In the past, to classify *Acinetobacter* at the species level, it was essential to use molecular genetic methods, such as sequencing housekeeping genes, including *rpoB* and *gyrB*, which are both labor-intensive and time-consuming. These methods are difficult to perform routinely in many clinical microbiology laboratories [2]. However, as microbial identification using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) can be performed more rapidly and inexpensively, this method is preferably used to identify *Acinetobacter* species.

The Bruker Biotyper (Bruker Daltonik GmbH, Bremen, Germany) and VITEK MS (bioMérieux S.A., Marcy l'Etoile, France) are two MALDI-TOF MS systems used worldwide for microbial identification [14]. The ASTA MicroIDSys (ASTA Inc., Suwon, South Korea) is a relatively new MALDI-TOF MS instrument that was introduced in 2016. Some studies have compared the performance of ASTA MicroIDSys with existing MALDI-TOF MS instruments for identifying commonly isolated microorganisms [14, 15]. While previous studies analyzed most species requested for culture and strain identification in clinical microbiology laboratories, our study included clinically isolated strains and type or reference strains of *Acinetobacter* consisting of various species previously identified using molecular methods [16, 17]. The aim of our study was to compare the performance of ASTA MicroIDSys with the Bruker Biotyper for identifying various *Acinetobacter* species.

## MATERIALS AND METHODS

### 1. Bacterial isolates

A total of 207 *Acinetobacter* strains, consisting of 22 type or reference strains and 185 clinical isolates, were analyzed in this study. The 22 *Acinetobacter* type or reference strains used in this study were obtained from the Korean Collection for Type Cultures (KCTC), the National Culture Collection for Pathogens (NCCP), and the German Collection of Microorganisms and Cell Cultures (DSM). The 185 *Acinetobacter* clinical isolates were randomly chosen from previously identified and stored *Acinetobacter* strains at Chonnam National University Hospital (collected between January 2010 and December 2012) and from Chosun University Hospital (collected between September 2005 and May 2012). These clinical *Acinetobacter* strains were first identified by routine biochemical methods using the VITEK 2 system and then by molecular methods using *rpoB* gene sequencing. Based on the studies performed at Chonnam National University Hospital [16] and at Chosun University Hospital [17], a 450-base pair (bp) sequence (variable zone 2) and a 350 bp sequence (variable zone 1) were selected as the target regions of the *rpoB* gene. Based on molecular identification using *rpoB* gene sequencing, reference identification of the strain was established.

Of the 207 strains used in this study, 175 strains (84.5%) belonged to the Ab group, which consisted of 79 strains of *A. baumannii*, 70 strains of *A. nosocomialis*, 25 strains of *A. pittii*, and one strain of *A. calcoaceticus*. The other 32 strains belonged to the non-Ab group and consisted of eight strains of *A. soli*, six strains of *A. berzeziniae*, two strains of *A. ursingii*, and one strain each of the following: *A. baylyi*, *A. bouvetii*, *A. gernerii*, *A. guillouiae*, *A. baemolyticus*, *A. indicus*, *A. johnsonii*, *A. junii*, *A. lwoffii*, *A. marinus*, *A. oleivorans*, *A. parvus*, *A. qingfengensis*, *A. radioresistens*, *A. schindleri*, and *A. tandonii*.

This study was approved by the Institutional Review Board of Chosun University Hospital (CHOSUN NON2018-003). Informed consent was waived.

### 2. MALDI-TOF MS analysis

Identification of the bacterial isolates was conducted simultaneously at both institutions using the MALDI-TOF MS system per the manufacturer's instructions. For the Bruker Biotyper, one colony was selected per strain, smeared on a target plate, and over-

laid with 1 µL of saturated MALDI matrix solution containing  $\alpha$ -cyano-4-hydroxycinnamic acid (CHCA) (Bruker Daltonik GmbH) in 50% acetonitrile and 2.5% trifluoroacetic acid. Peptide mass spectra were acquired using a Bruker Microflex LT system, Biotyper software 3.1, and the MALDI Biotyper reference library version 4.0.0, which included 945 species of gram-negative bacteria and 20 *Acinetobacter* species. For the ASTA MicroIDSys, one colony was isolated per strain and smeared on the spot. Subsequently, 1.5 µL of 70% formic acid was added and dried for 2 minutes, 1.5 µL of CHCA matrix solution was added and dried for 2 minutes, and the MALDI-TOF MS analysis was performed. The ASTA MicroIDSys CoreDB 1.27-build001, which included 715 species of gram-negative bacteria and 26 *Acinetobacter* species, was used for the spectrum analysis.

According to the manufacturer's instructions, an identification score of <1.7 on the Bruker Biotyper system or a value of <140 on the ASTA MicroIDSys system was considered an unreliable identification score. The samples reported as unreliable were re-

tested up to two times with the most favorable identification results used for comparative analysis.

### 3. Results interpretation

The identification results obtained using each MALDI-TOF MS system were classified into three categories based on their consistency with the reference identification determined by molecular identification results of previous studies [16, 17]: (a) correct identification to the species level when the MALDI-TOF result was consistent with that of the reference identification, (b) misidentification when the MALDI-TOF result was inconsistent with that of the reference identification, and (c) invalid identification when the instrument failed to identify the isolate.

### 4. Statistical analysis

The McNemar test was used to compare the correct identification rates of the two systems using IBM SPSS Statistics version 23 (SPSS Inc., Chicago, IL, USA). Statistical significance was set at *P*

**Table 1.** Identification results for 22 type or reference strains of *Acinetobacter* using the Bruker MALDI Biotyper versus ASTA MicroIDSys compared to reference identifications\*

Reference Strain	Bruker MALDI Biotyper		ASTA MicroIDSys	
	Result	Score	Result	Score
<i>A. baumannii</i> NCCP 14654	<i>A. baumannii</i>	2.427	<i>A. baumannii</i>	272.8
<i>A. calcoaceticus</i> KCTC 2357 <sup>†</sup>	<i>A. calcoaceticus</i>	2.487	<i>A. calcoaceticus</i>	177.1
<i>A. nosocomialis</i> NCCP 15916	<i>A. nosocomialis</i>	2.418	<i>A. nosocomialis</i>	214.7
<i>A. pittii</i> DSM 25618 <sup>†</sup>	<i>A. pittii</i>	2.13	<i>A. pittii</i>	218.2
<i>A. baylyi</i> KCTC 12413 <sup>†</sup>	<i>A. baylyi</i>	2.249	<i>A. baylyi</i>	202.2
<i>A. bereziniae</i> KCTC 42001 <sup>†</sup>	<i>A. bereziniae</i>	2.454	<i>A. bereziniae</i>	208
<i>A. bouvetii</i> KCTC 12414 <sup>†</sup>	<i>A. bouvetii</i>	2.274	<i>A. bouvetii</i>	215.3
<i>A. gernerii</i> KCTC 12415 <sup>†</sup>	<i>A. gernerii</i>	2.252	<i>A. gernerii</i>	228.9
<i>A. guillouiae</i> KCTC 23200 <sup>†</sup>	<i>A. guillouiae</i>	2.287	<i>A. guillouiae</i>	228.1
<i>A. haemolyticus</i> KCTC 12404 <sup>†</sup>	<i>A. haemolyticus</i>	2.406	<i>A. haemolyticus</i>	193.1
<i>A. indicus</i> KCTC 42000 <sup>†</sup>	<b>No identification<sup>‡</sup></b>	1.545	<i>A. indicus</i>	166.4
<i>A. johnsonii</i> KCTC 12045 <sup>†</sup>	<i>A. johnsonii</i>	2.293	<i>A. johnsonii</i>	242.2
<i>A. junii</i> KCTC 12416 <sup>†</sup>	<i>A. junii</i>	2.326	<i>A. junii</i>	241.3
<i>A. lwoffii</i> KCTC 12407 <sup>†</sup>	<i>A. lwoffii</i>	2.278	<i>A. lwoffii</i>	210.7
<i>A. marinus</i> KCTC 12259 <sup>†</sup>	<b>No identification<sup>‡</sup></b>	1.652	<i>A. marinus</i>	187.4
<i>A. oleivorans</i> KCTC 23045 <sup>†</sup>	<b><i>A. calcoaceticus</i><sup>‡</sup></b>	2.292	<b><i>A. calcoaceticus</i></b>	164.9
<i>A. parvus</i> KCTC 12408 <sup>†</sup>	<i>A. parvus</i>	2.395	<i>A. parvus</i>	251.7
<i>A. qingfengensis</i> KCTC 32225 <sup>†</sup>	<b>No identification<sup>‡</sup></b>	1.624	<i>A. qingfengensis</i>	212.2
<i>A. radioresistens</i> KCTC 12411 <sup>†</sup>	<i>A. radioresistens</i>	2.119	<i>A. radioresistens</i>	211.8
<i>A. schindleri</i> KCTC 12409 <sup>†</sup>	<i>A. schindleri</i>	2.288	<i>A. schindleri</i>	264.8
<i>A. tandonii</i> KCTC 12417 <sup>†</sup>	<i>A. tandonii</i>	2.299	<i>A. tandonii</i>	200.7
<i>A. ursingii</i> KCTC 12410 <sup>†</sup>	<i>A. ursingii</i>	2.401	<i>A. ursingii</i>	211.7

\*Reference identifications were carried out by *rpoB* sequencing; <sup>†</sup>Species of the type strain was not included in the Bruker MALDI Biotyper database; <sup>‡</sup>Type strains. Misidentifications or no identifications are highlighted in bold.

Abbreviations: KCTC, Korean Collection for Type Cultures; DSM, German Collection of Microorganisms and Cell Cultures; NCCP, National Culture Collection for Pathogens.

<0.05. For *Acinetobacter* species identified from more than five isolates, sensitivity, specificity, positive predictive value (PPV), and negative predictive value (NPV) were calculated with 95% confidence intervals (CIs) and compared between the systems.

## RESULTS

The identification results for the 22 type or reference strains, consisting of 20 type strains and two reference strains, are shown in Table 1. The Bruker Biotyper correctly identified 18 (81.8%) strains, but misidentified *A. oleivorans* KCTC 23045 and failed to identify *A. marinus* KCTC 12259, *A. qingfengensis* KCTC 32225, and *A. indicus* KCTC 42000. These four species were absent from the Bruker database. In contrast, the ASTA MicroIDSys correctly identified 21 (95.5%) strains but misidentified *A. oleivorans* KCTC 23045, despite this species being registered in the ASTA database.

The identification results of the 185 clinical isolates are presented in Table 2. Incorrectly identified strains were as follows. The most misidentified species in the Ab group were *A. nosocomialis* (six strains for the Bruker Biotyper, three for the ASTA MicroIDSys). Among the non-Ab group, the Bruker Biotyper misidentified eight

strains of *A. soli* and one strain of *A. ursingii*, whereas the ASTA MicroIDSys misidentified one strain of *A. bereziniae*.

The identification results of all 207 strains using the two systems are compared in Table 3. The correct identification rates of MALDI-TOF MS for all *Acinetobacter* were 89.4% (185/207) and 96.6% (200/207) using the Bruker Biotyper and ASTA MicroIDSys, respectively, showing a statistically significant difference ( $P<0.001$ ). For the Ab group, the Bruker Biotyper and ASTA MicroIDSys demonstrated similar performances of 94.9% (166/175) and 97.1% (170/175), respectively ( $P=0.219$ ). For the non-Ab group, however, the correct identification rates at the species level were significantly different ( $P<0.01$ ) at 59.4% (19/32) and 93.8% (30/32), respectively. We reanalyzed the data after excluding *A. indicus*, *A. marinus*, *A. oleivorans*, *A. qingfengensis*, and *A. soli*, which were absent from the Bruker database. Consequently, the correct identification rates of the Bruker Biotyper and ASTA MicroIDSys were 94.9% (185/195) and 96.9% (189/195), respectively ( $P=0.289$ , data not shown).

The sensitivity, specificity, PPV, and NPV of the systems are listed in Table 4. Both instruments provided similar sensitivity, specificity, PPV, and NPV for the Ab group. With respect to the non-Ab

**Table 2.** Identification results for 185 clinical *Acinetobacter* strains using the Bruker MALDI Biotyper versus ASTA MicroIDSys compared to reference identifications\*

Species	N	Bruker MALDI Biotyper		ASTA MicroIDSys	
		Result	Average score	Result	Average score
<i>A. baumannii</i> complex	171				
<i>A. baumannii</i> (78)	75	<i>A. baumannii</i>	2.333	<i>A. baumannii</i>	250.4
	1	<i>A. baumannii</i>	2.362	<i>A. nosocomialis</i>	193.7
	1	<i>A. calcoaceticus</i>	2.170	<i>A. baumannii</i>	215.9
	1	<i>A. nosocomialis</i>	2.034	<i>A. baumannii</i>	241.5
<i>A. nosocomialis</i> (69)	63	<i>A. nosocomialis</i>	2.383	<i>A. nosocomialis</i>	203.1
	3	<i>A. baumannii</i>	2.244	<i>A. nosocomialis</i>	181.4
	2	<i>A. haemolyticus</i>	2.037	<i>A. baumannii</i>	165.5
	1	<i>A. junii</i>	1.901	<i>A. baumannii</i>	196.3
<i>A. pittii</i> (24)	23	<i>A. pittii</i>	2.253	<i>A. pittii</i>	231.2
	1	<i>A. baumannii</i>	2.404	<i>A. baumannii</i>	273.9
Non- <i>A. baumannii</i> complex	14				
<i>A. bereziniae</i> (5)	4	<i>A. bereziniae</i>	2.161	<i>A. bereziniae</i>	188.2
	1	<i>A. bereziniae</i>	2.391	<i>A. baumannii</i>	274.4
<i>A. soli</i> * (8)	5	No identification	1.488	<i>A. soli</i>	192.2
	3	<i>A. baylyi</i>	1.818	<i>A. soli</i>	200.9
<i>A. ursingii</i> (1)	1	<i>A. baumannii</i>	2.404	<i>A. ursingii</i>	245.5
Total	185				

\*Reference identifications were carried out by *rpoB* sequencing; †Species not included in the Bruker MALDI Biotyper database.

**Table 3.** Performance of two MALDI-TOF MS systems in identifying 207 *Acinetobacter* strains compared to reference identifications\*

Species	N	Bruker MALDI Biotyper			ASTA MicroIDSys		
		Correct ID	Mis-ID	No ID	Correct ID	Mis-ID	No ID
		N (%)	N (%)	N (%)	N (%)	N (%)	N (%)
<i>A. baumannii</i> complex	175	166 (94.9)	9 (5.1)	0 (0.0)	170 (97.1)	5 (2.9)	0 (0.0)
<i>A. baumannii</i>	79	77 (97.5)	2 (2.5)		78 (98.7)	1 (1.3)	
<i>A. calcoaceticus</i>	1	1 (100.0)			1 (100.0)		
<i>A. nosocomialis</i>	70	64 (91.4)	6 (8.6)		67 (95.7)	3 (4.3)	
<i>A. pittii</i>	25	24 (96.0)	1 (4.0)		24 (96.0)	1 (4.0)	
Non- <i>A. baumannii</i> complex	32	19 (59.4)	5 (15.6)	8 (25.0)	30 (93.8)	2 (6.3)	0 (0.0)
<i>A. baylyi</i>	1	1 (100.0)			1 (100.0)		
<i>A. bereziniae</i>	6	6 (100.0)			5 (83.3)	1 (16.7)	
<i>A. bouvetii</i>	1	1 (100.0)			1 (100.0)		
<i>A. gernerii</i>	1	1 (100.0)			1 (100.0)		
<i>A. guillouiae</i>	1	1 (100.0)			1 (100.0)		
<i>A. haemolyticus</i>	1	1 (100.0)			1 (100.0)		
<i>A. indicus</i> <sup>†</sup>	1			1 (100.0)	1 (100.0)		
<i>A. johnsonii</i>	1	1 (100.0)			1 (100.0)		
<i>A. junii</i>	1	1 (100.0)			1 (100.0)		
<i>A. lwoffii</i>	1	1 (100.0)			1 (100.0)		
<i>A. marinus</i> <sup>†</sup>	1			1 (100.0)	1 (100.0)		
<i>A. oleivorans</i> <sup>†</sup>	1		1 (100.0)			1 (100.0)	
<i>A. parvus</i>	1	1 (100.0)			1 (100.0)		
<i>A. qingfengensis</i> <sup>†</sup>	1			1 (100.0)	1 (100.0)		
<i>A. radioresistens</i>	1	1 (100.0)			1 (100.0)		
<i>A. schindleri</i>	1	1 (100.0)			1 (100.0)		
<i>A. soli</i> <sup>†</sup>	8		3 (37.5)	5 (62.5)	8 (100.0)		
<i>A. tandoii</i>	1	1 (100.0)			1 (100.0)		
<i>A. ursingii</i>	2	1 (50.0)	1 (50.0)		2 (100.0)		
Total	207	185 (89.4)	14 (6.8)	8 (3.9)	200 (96.6)	7 (3.4)	0 (0.0)

\*Reference identifications were carried out by *rpoB* sequencing; <sup>†</sup>Species not included in the Bruker MALDI Biotyper database.

Abbreviations: Correct ID, correct identification at the species level; Mis-ID, misidentification; No ID, failed identification, or failure to identify the isolate.

group, the sensitivities for identification of *A. bereziniae* of the Bruker Biotyper and ASTA MicroIDSys were 100.0% (95% CI, 51.7–100.0) and 83.3% (95% CI, 36.5–99.1), respectively.

## DISCUSSION

The results of our study indicate that the ASTA MicroIDSys identified *Acinetobacter* species more accurately than the Bruker Biotyper. For the Ab group, the systems showed similar identification performance. However, the ASTA MicroIDSys demonstrated superior identification ability for the non-Ab group. This result may be attributable to the ASTA database, which included more *Acinetobacter* species within the non-Ab group.

Our study showed that the ASTA MicroIDSys identified the Ab group with high accuracy comparable to that of the Bruker Bio-

typer. This finding is consistent with earlier studies showing that the ASTA MicroIDSys, Bruker Biotyper, and VITEK MS have equivalent identification performances [14, 15, 18]. Lee et al. [14] reported agreement rates of 99.8% and 100% for *A. baumannii* (N=436) and *A. nosocomialis* (N=18) using the Bruker Biotyper and the ASTA MicroIDSys systems, respectively. In a study by Jung et al. [18], the correct identification rates using the VITEK MS and the ASTA MicroIDSys systems were 99.3% and 100.0% for *A. baumannii* (N=138), respectively. Liu et al. [15] showed that within the Ab group, *A. baumannii* (N=47), *A. nosocomialis* (N=28), and *A. pittii* (N=13) had correct identification rates at the species level of 100.0%, 100.0%, and 100.0% for the Bruker Biotyper system and 100.0%, 78.6%, and 100.0% for the ASTA MicroIDSys system, respectively. Regarding the non-Ab group, 31 strains consisting of 14 species were evaluated in the same study. ASTA MicroIDSys



**Table 4.** Sensitivity, specificity, positive predictive value, and negative predictive value of the identification performance of the Bruker MALDI Biotyper versus ASTA MicroIDSys systems for each *Acinetobacter* species, in comparison to reference identifications\*

Species <sup>†</sup>	N	Bruker MALDI Biotyper				ASTA MicroIDSys			
		Sensitivity (%) (95% CI)	Specificity (%) (95% CI)	PPV (%) (95% CI)	NPV (%) (95% CI)	Sensitivity (%) (95% CI)	Specificity (%) (95% CI)	PPV (%) (95% CI)	NPV (%) (95% CI)
<i>A. baumannii</i> group	174								
<i>A. baumannii</i>	79	97.5 (90.3–99.6)	96.1 (90.7–98.6)	93.9 (85.7–97.7)	98.4 (93.8–99.7)	98.7 (92.2–99.9)	98.4 (93.9–99.7)	97.5 (90.4–99.6)	99.2 (95.0–100.0)
<i>A. nosocomialis</i>	70	91.4 (81.7–96.5)	99.3 (95.4–100.0)	98.5 (90.6–99.9)	95.8 (90.6–98.3)	95.7 (87.2–98.9)	99.3 (95.4–100.0)	98.5 (91.0–99.9)	97.8 (93.3–99.4)
<i>A. pittii</i>	25	96.0 (77.7–99.8)	100.0 (97.4–100.0)	100.0 (82.8–100.0)	99.5 (96.5–100.0)	96.0 (77.7–99.8)	98.4 (94.9–99.6)	88.9 (69.7–97.1)	99.4 (96.5–100.0)
Non- <i>A. baumannii</i> group	14								
<i>A. bereziniae</i>	6	100.0 (51.7–100.0)	100.0 (97.7–100.0)	100.0 (51.7–100.0)	100.0 (97.7–100.0)	83.3 (36.5–99.1)	100.0 (97.7–100.0)	100.0 (46.3–100.0)	99.5 (96.8–100.0)
<i>A. soli</i> <sup>‡</sup>	8	0.0 (0–40.2)	100.0 (97.6–100.0)	IC	96.1 (92.3–98.2)	100.0 (59.8–100.0)	100.0 (97.6–100.0)	100.0 (59.8–100.0)	100.0 (97.6–100.0)
				IC					

\*Reference identifications were carried out by *rpoB* sequencing; <sup>†</sup>Species that were identified from more than five isolates were included in the analysis; <sup>‡</sup>Species not included in the Bruker MALDI Biotyper database. Abbreviations: CI, confidence interval; PPV, positive predictive value; NPV, negative predictive value; IC, incalculable.

correctly identified *A. bereziniae* (N=8), *A. baemolyticus* (N=4), *A. ursingii* (N=4), *A. radioresistens* (N=2), *A. baylyi* (N=1), and *A. johnsonii* (N=1) at the species level. One strain of *A. oleivorans* was not identified correctly at the species level. These findings were generally consistent with our results, differing only for *A. soli*. Two strains of *A. soli* could not be correctly identified by ASTA MicroIDSys with CoreDB 1.26.02 [15]. Conversely, in our study eight strains of *A. soli* were correctly identified at the species level using the ASTA MicroIDSys with CoreDB 1.27-build001. Hence, the discrepancy between our results and those of Liu et al. [15] can be explained by the updated ASTA database.

Our study is another example demonstrating that database expansion leads to improved identification performance of MALDI-TOF MS systems. The statistically significant difference in identification rates in our study was primarily caused by *Acinetobacter* species whose protein spectra were only included in the ASTA database, such as *A. indicus*, *A. marinus*, *A. oleivorans*, *A. qingfengensis*, and *A. soli*. A study by Jeong et al. [19] showed that when representative mass spectra of 63 *Acinetobacter* strains were added to the default Bruker database, the agreement rate between the Bruker Biotyper system and *rpoB* sequencing increased from 69.8% to 100.0%. This strengthened the notion that constant updating of the database will improve MALDI-TOF MS-based microbial identification, leading to timely management of infection and better clinical outcomes. *A. oleivorans* and *A. soli*, which are becoming increasingly common etiologic agents of nosocomial infections, can carry antimicrobial resistance genes to various antibiotics such as  $\beta$ -lactams, aminoglycosides, tetracyclines, and macrolides [20]. This greatly impacts the selection of antibiotics and effective treatment strategies. MALDI-TOF MS would allow rapid identification and, consequently, antibiotic susceptibility testing. Although *A. indicus*, *A. marinus*, and *A. qingfengensis* are currently rare bacteria isolated from the natural environment [6], MALDI-TOF MS systems could be utilized to identify these bacteria rapidly and accurately, allowing the evaluation of their clinical significance.

In conclusion, we expect the identification capability of MALDI-TOF MS systems will continue to improve with continuous database enhancements. Such improvements may enhance our understanding of the clinical implications of rarely isolated species. Additional comparative studies following database upgrades are needed to evaluate performance improvements.

## 요약

**배경:** MALDI-TOF 질량분석법은 신속하고 정확하여 현재 널리 이용되고 있는 미생물 동정법이다. 저자들은 다양한 *Acinetobacter* 종의 동정에 최근 개발된 ASTA MicroIDSys (ASTA, South Korea)와 Bruker Biotyper (Bruker Daltonics, Germany)의 성능을 비교평가하였다.

**방법:** 표준 또는 참조균주 22주와 이전에 분자진단검사로 동정된 185주의 임상분리주로 이루어진 총 207주의 *Acinetobacter* 균주를 제조업체의 권장 사항에 따라 검사하여 그 동정 결과를 서로 비교하였다.

**결과:** 전체 균주에 대하여 정확한 균종 수준 동정률은 Bruker Biotyper와 ASTA MicroIDSys 장비에서 각각 89.4% (185/207)와 96.6% (200/207)로 유의한 차이를 보였다( $P < 0.001$ ). *Acinetobacter baumannii* group에 속하는 균주의 정확한 균종 수준 동정률은 각각 94.9% (166/175)와 97.1% (170/175)로 유사하였다( $P = 0.094$ ). 그러나, Non-Ab group에 속하는 균주의 정확한 균종 수준 동정률은 각각 59.4% (19/32)와 93.8% (30/32)로 유의한 차이를 보였다( $P < 0.05$ ). 하지만 Bruker MALDI 데이터베이스에 등록되지 않은 12주를 제외하고 분석을 시행하였을 때, Ab group과 non-Ab group을 통틀어 정확한 균종 수준 동정률은 두 장비에서 유의한 차이를 보이지 않았다( $P = 0.289$ ).

**결론:** ASTA MicroIDSys가 Bruker Biotyper보다 더 높은 정확도로 non-Ab group을 동정하였으나, Ab group에 대해서는 동등한 동정 성능을 보여주어 임상미생물 검사실에서 자주 분리되는 *Acinetobacter* 균종을 동정하는 용도에 있어서는 두 장비 모두 적합한 것으로 사료된다.

## Conflict of Interest

None declared.

## Acknowledgments

The present study was supported by grants from the Clinical Medicine Research Institute at Chosun University Hospital (2021).

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