

# Diagnostic Yield and Impact on Antimicrobial Management of 16s rRNA Testing on Clinical Specimens



**CONTACT INFORMATION**

Pruke Eamsakulrat, M.D.

Email: pruke.ea@gmail.com

Pruke Eamsakulrat, M.D.<sup>1</sup>, Pitak Santanirand, Ph.D.<sup>2</sup>, Angsana Phuphuakrat, M.D., Ph.D.<sup>1</sup>

<sup>1</sup>Department of Medicine, <sup>2</sup>Department of Pathology, Faculty of Medicine Ramathibodi Hospital, Mahidol University, Bangkok, Thailand

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## INTRODUCTION

- 16s rRNA gene sequencing has an advantage over traditional bacterial cultures in situations where bacteria are difficult to culture, unculturable, or have previously been exposed to an antimicrobial.
- Current studies on its applicability to direct clinical specimens are limited.

## AIM

- We studied the value of 16s rRNA gene sequencing from direct clinical specimens on antimicrobial management.

## METHODS

- A prospective study was conducted among inpatient adults during January to December 2021 in a university hospital in Bangkok, Thailand.
- Results of 16s rRNA gene sequencing and a corresponding bacterial culture from a direct clinical specimen were collected.
- There were no restrictions on ordering 16s rRNA gene sequencing at the time of the study.
- The diagnostic yield and the impact of 16s rRNA gene sequencing on antimicrobial management were investigated.
- The investigators were not involved in the clinical decisions or management.

## RESULTS

- A total of 434 specimens from 374 patients were requested.

Table 1. Clinical characteristics and demographic of the patients				
	All (n=434)	16s rRNA gene sequencing positive (n=108)	16s rRNA gene sequencing negative (n=326)	P-value
Median (IQR) age, years	62 (52-74)	66 (52-77)	61 (51-73)	0.059
Male, n (%)	208 (47.9)	63 (58.3)	145 (44.5)	0.012
Current on antibiotic, n (%) (regardless of susceptible)	294 (67.7)	81 (75.0)	213 (65.3)	0.063
Median (IQR) days current on antibiotic, days	8 (3-18)	10 (5-21)	7 (2-16)	0.027
<b>Specimen</b>				
Fluid, n (%)	284 (65.4)	77 (71.3)	207 (63.5)	0.140
Tissue, n (%)	150 (34.6)	31 (28.7)	119 (36.5)	
Gram stain positive for bacteria, n (%) (n=410)	60 (14.6)	47/106 (44.3)	13/304 (4.3)	<0.001
Culture positive, n (%)	131 (30.2)	92 (85.2)	39 (12.0)	<0.001
Median (IQR) turnaround time, days	3 (2-10)	11 (9-13)	2 (1-4)	<0.001
<b>Provisional diagnosis, n (%)</b>				
Skin and soft tissue infection	64 (14.7)	20 (18.5)	44 (13.5)	
Community-acquired pneumonia	50 (11.5)	19 (17.6)	31 (9.5)	
HAP/VAP	50 (11.5)	22 (20.4)	28 (8.6)	
Septic arthritis	47 (10.8)	10 (9.3)	37 (11.3)	
Meningitis	31 (7.1)	0 (0.0)	31 (9.5)	
Native vertebral osteomyelitis	28 (6.5)	3 (2.8)	25 (7.7)	
Eye infection	24 (5.5)	5 (4.6)	19 (5.8)	
Prosthetic joint infection	22 (5.1)	3 (2.8)	19 (5.8)	
Parapneumonic effusion	21 (4.8)	1 (0.9)	20 (6.1)	
Osteomyelitis	18 (4.1)	6 (5.6)	12 (3.7)	
Post-operative meningitis	14 (3.2)	1 (0.9)	13 (4.0)	
Intraabdominal collection	13 (3.0)	4 (3.7)	9 (2.8)	

- According to the final diagnosis,

- 253 (58.3%) specimens were collected from patients with bacterial infection.
- 181 (41.7%) specimens were collected from patients with non-bacterial infection.

**Table 2. Comparison of 16s rRNA sequencing results categorized by bacterial infection and non-bacterial infection (percentage among total cases)**

	Bacterial infection	Non-bacterial infection	Total
16s rRNA sequencing Positive	97 (22.4)	11 (2.5)	108 (24.9)
Negative	156 (35.9)	170 (39.2)	326
Total	253	181	434

16s rRNA gene sequencing  
Sensitivity 38.3% Specificity 93.9%

**Table 3. Comparison of bacterial culture and 16s rRNA gene sequencing among bacterial infection cases (percentage among total cases)**

	Culture-positive	Culture-negative	Total
16s rRNA sequencing Positive	82 (32.4)	15 (5.9)	97 (38.3)
Negative	26 (10.3)	130 (51.4)	156
Total	108	145	253

Additional yield from culture-negative = 15/145 (10.3%)

Agreement between bacterial culture and 16s rRNA gene sequencing 83.8% (Kappa coefficient 0.664, p<0.001)

## CONCLUSIONS

- The additional diagnostic yield of 16s rRNA gene sequencing in bacterial infection cases was 10.3%, highest in the skin and soft tissue infection, and pneumonia.
- Testing for 16s rRNA gene sequencing has an impact on clinical management in selected cases, 2.3% in this study.
- Testing on abscesses was the most likely to benefit from 16s rRNA sequencing, whereas testing on BAL fluid gave the lowest impact on antimicrobial management.

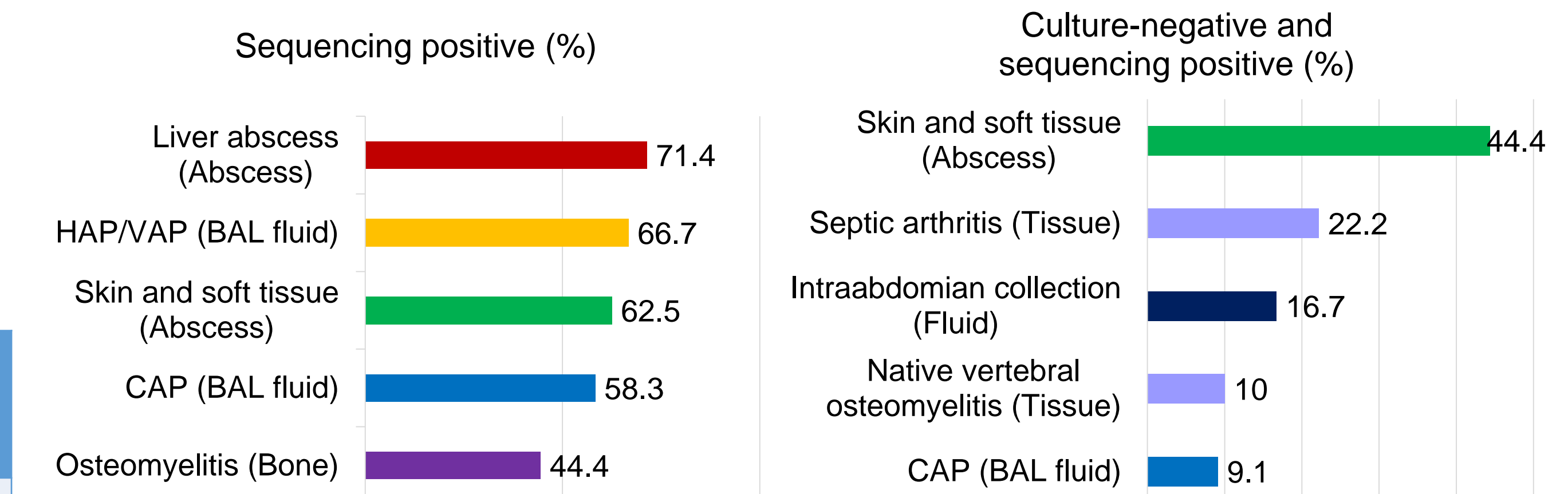
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## REFERENCES

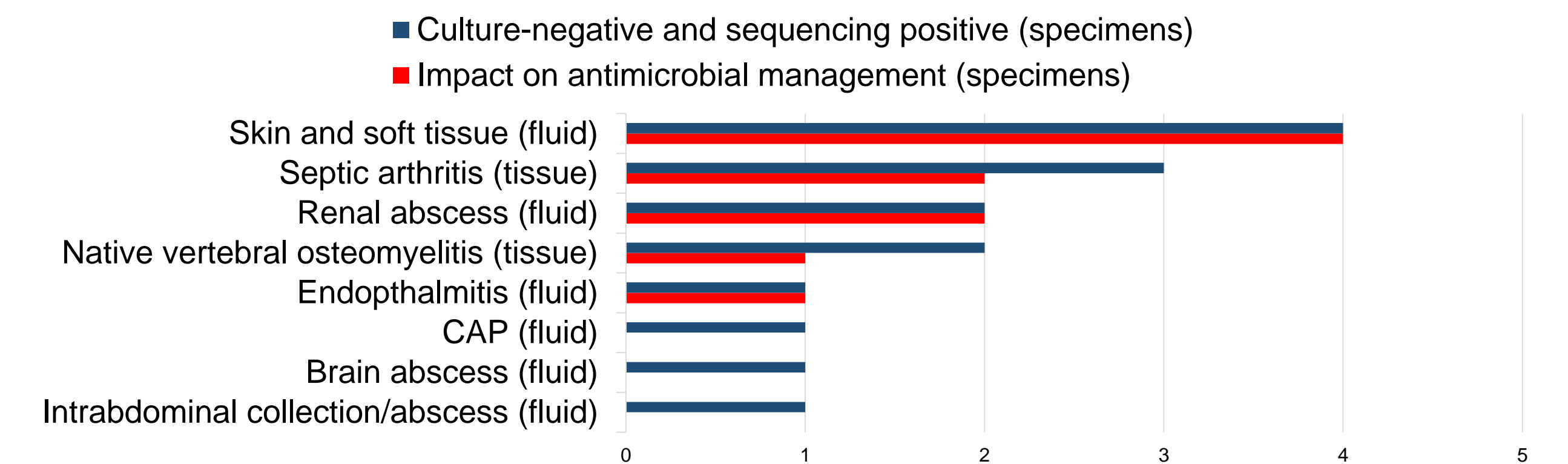
- Rampini SK, et al. Clin Infect Dis. 2011;53:1245-51.
- Harris KA, et al. J Med Microbiol. 2003;52:685-91.
- Tkadlek J, et al. Clin Microbiol Infect. 2019;25:747-52.
- Yoo IY, et al. Ann Lab Med. 2020;40:63-7.
- Bador J, et al. Med Mal Infect. 2020;50:63-73.
- Fida M, et al. Clin Infect Dis. 2021;73:961-8.



**Fig.1** Ranking proportion of bacterial culture and 16s rRNA gene sequencing results. (exclude N < 5)

## Impact on antimicrobial management

- 15/434 specimens had 16s rRNA gene sequencing positive/culture-negative.
  - 10/434 (2.3%) specimens had an impact on antimicrobial management or 10/145 (6.9%) among culture-negative bacterial infection cases.
- ==All these cases was the continuation of antibiotic==



**Fig.2** Comparison between the number of impacts on antimicrobial management and the number of culture-negative and sequencing positive specimens.