presentation number : 4804 **Poster Presentation: 16, 17** 10:30 am - 11:30 am, 4:00 pm – 5:00 pm **Poster Presentation: 18** 10:30 am - 11:30 am, 3:00 pm - 4:00 pm

### **Revised Abstract**

### Due to improvements in the model, the accuracy has changed since the abstract submission.

**Background**: In the treatment of bacterial infections, proper administration of antimicrobial agents is very important, not only because it improves patient prognosis, but also because it reduces the development of bacterial resistance. Urine gram stain is a useful test for initial antimicrobial selection, but it requires a certain degree of skill to decipher. Therefore, we developed an image analysis system for Gram stain images of urinary and verified whether it is possible to estimate the species of bacteria in order to facilitate the initial selection of antimicrobial agents, regardless of the level of proficiency.

**Methods**: Slides and bacterial species identification information from an anonymized Gram stain registry at two medical institutions, National Center for Global Health and Medicine (NCGM) and Kobe University Hospital (KUH), were used for the study. Urine culture specimens of 1290 cases were included. Mock-specimens were used for rare bacteria. A total of 12,321 images were generated by capturing the observation field of view of an optical microscope with a smartphone. A total of 17 categories of bacteria were used for classification: 15 categories that frequently occur in urine samples + no bacteria + multiple bacteria. The data were divided into training data and test data at a ratio of 8 to 2 for each category, and a deep learning algorithm was trained using the training data.

**<u>Results</u>**: The macro-average recall (sensitivity) and accuracy for the test data were 74% and 77%, respectively. The results showed the possibility of performing bacterial species classification with an accuracy of over 70% using only Gram stained images via image recognition AI. In particular, the seven categories of GNR, GNC, GPR, GPC, yeast bacteria, non-bacteria, and multiple bacteria are predicted to have 94% accuracy, 95% for the macro average recall.

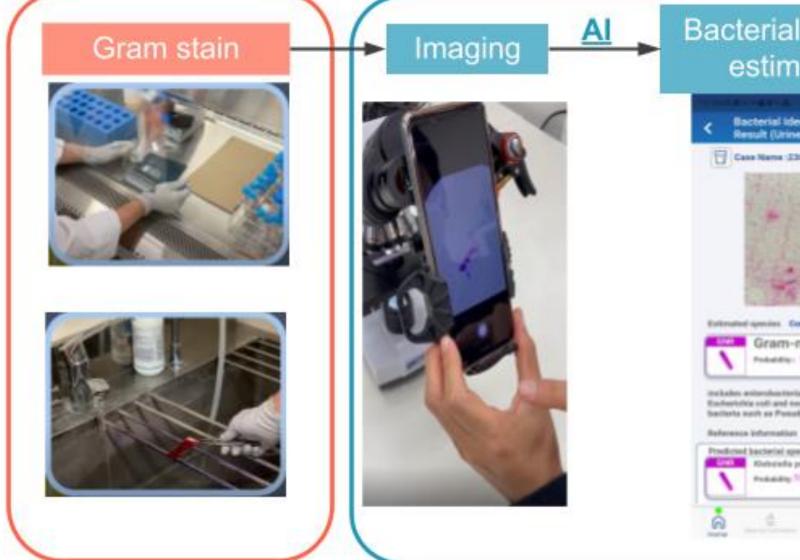
**Conclusion**: The research has shown that it is possible to classify bacterial species to a certain extent only by observing the Gram stain images. Since the accuracy varies by bacterial species, we aim to improve the accuracy of classification by adding more cases, and also by devising learning methods for the species with lower accuracy. We are planning to make comparisons with specialists in the future, and are currently working to achieve an accuracy that will allow us to show that AI is non-inferior to specialists.

# **Research and Development of Image Recognition AI to Estimate Bacterial Species Using Gram Stain Findings in Urine Specimens**

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## **Bacterial species estimation procedure by Al**



Bacterial species estimation proced	lure by Al	Bacterial	species	sestima	ation p	ertorm	ance
Gram stain Imaging <u>AI</u> Bacterial species S	<section-header></section-header>	GNC GNR GPC GPR Multiple None yeast macro average	speciesprecision100.00%95.19%85.69%90.20%93.52%99.72%97.46%94.54%	Sensitivity   95.24%   98.93%   95.86%   96.84%   99.16%   100.00%   94.73%	f1-score   97.56%   97.02%   90.49%   93.40%   99.44%   98.71%   94.45%	ertorm specificity 100.00% 96.85% 96.58% 99.67% 99.96% 99.96% 99.83% 98.77%	ance support 42 1219 556 95 693 359 192 192 3156 93.57%
		Table 2. Res	ults of Al e	estimation	for test o	lata in 7-c	
Figure 1. Assumed flow for estimating bacterial   After Gram staining of urine specimen, the slide   under a microscope with a 100x objective lens a   Classification category   UGC_01 Candida spp.   UGC_02 GPC cluster   UGC_03 Enterococcus faecalis	is observed	ON 40 0 0   Image: Second s	0 0 12 1   1 0 22 0   92 0 3 0   0 192 0 0	-1000 tes -800 ma -600 GN ba ba ba	st data. Ve ade within NC, GPR. ( cteria are cteria (GI	onfusion n ery few m n GNR, GF Often, mu e mistaker NR, GPC), e mistaker cteria.	istakes an PC, Yeast, Itiple for singl and singl
UGC_04 Enterococcus faecium	GPC	Predict	ion label				
UGC_05 Streptococcus agalactiae	GPC		precision	sensitivity	f1-score	specificity	support
UGC_06 other GPC	GPC	UGC_01	97.46%	100.00%	98.71%	99.83%	192
UGC_07 Corynebacterium spp.	GPR	UGC_02	77.95%	96.12%	86.09%	98.10%	206
UGC_08 Enterobacter cloacae	GNR	UGC_03	67.90%	50.46%	57.89%	99.15%	109
UGC_09 Escherichia coli	GNR	UGC_04	75.00%	68.97%	71.86%	99.35%	87
UGC_10 Klebsiella oxytoca	GNR	UGC_05	54.23%	85.56%	66.38%	97.88%	90
UGC_11 Klebsiella pneumoniae	GNR	UGC_06	69.23%	70.31%	69.77%	99.35%	64 05
UGC_12 Pseudomonas aeruginosa	GNR	UGC_07 UGC 08	90.20%	96.84%	93.40%	99.67%	95 102
UGC_13 other GNR Enterobacteriaceae	GNR	UGC_08	59.34% 64.85%	52.94% 81.06%	55.96% 72.05%	98.79%	102 528
UGC_14 other GNR Glucose non-fermenting bacteria	GNR	UGC_09	70.24%	67.82%	69.01%	91.17% 99.19%	87
UGC_15 GNC	GNC	UGC_10 UGC_11	46.11%	49.11%	47.56%	99.19% 96.75%	169
Multiple There are more than two types of		UGC_11	66.00%	75.86%	70.59%	98.89%	87
bacteria in broad category.NoneNo bacteria.	- -	UGC_12	26.09%	13.87%	18.11%	97.72%	173
		UGC_14	96.67%	79.45%	87.22%	99.94%	73
Tabel 1. Classification Category Table. 15 categories that		UGC_15	100.00%	95.24%	97.56%	100.00%	42
frequently occur in urine samples + no bacteria + multiple		Multiple	93.52%	77.06%	84.49%	98.50%	693
bacteria. Initially, the seven broad categories (Yeast, GPC, GPR,		None	99.72%	99.16%	99.44%	99.96%	359
GNR, GPC, Multiple, None) are classified using AI.		macro	73.79%	74.11%	73.30%	98.48%	3156
If the AI's prediction result is GPC or GNR, it is fu	average accuracy					76.71%	
into a detailed category using a dedicated AI.		Table 2 Po		octimatia	n for toot	data in 1	

**Conclusion** : Our image identification AI can classify test data from Gram-stained images into seven categories with an average sensitivity of over 90%. In addition, an average sensitivity of more than 70% was achieved in 17 categorical classifications. This classification results indicate that AI may be able to identify Gram-stained images, which may also facilitate initial antimicrobial selection. Future tests comparing specialists and AI are planned.

**Table 3**. Results of AI estimation for test data in 17-category.

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### **Bacterial species estimation performance**