Distinguishing between susceptible and resistant *Neisseria gonorrhoeae* by image recognition Al Tsubasa Inagaki, Reiichi Ariizumi, Hiroaki Ozaki, Mitsutaka Nakada, Shogo Maeta, Masakazu Nakajima, Makoto Taketani

Background

Gonorrhea is a major public health concern because it causes complications that can seriously affect maternal and newborn health, including infertility and neonatal eye infections leading to blindness. Antimicrobial resistance (AMR) of the causative pathogen, Neisseria gonorrhoeae (Ng), emerged shortly after antimicrobial agents started to be used. AMR of Ng has continued to grow over the past 80 years, culminating in the current outbreak of the gonorrhea superbugs, a broad spectrum of drugresistant strains of Ng. Gonorrhea superbugs can be a major challenge inducing prolonged complications of gonococcal infection and increasing the number of patients with complications. Here, we demonstrated whether resistant Ng can be morphologically distinguished from susceptible Ng using our artificial intelligence (AI) assisted image recognition of Gram stained specimens, which are inexpensive and can be diagnosed in the clinical field.

Method

Gram-stained images of ATCC 49226, a susceptible strain of Ng, and NCTC 13480 (WHO L), a strain resistant to penicillin G and ciprofloxacin (high-lev of Ng, were prepared. The parts of the images containing bacteria were cropped and used to bu an AI model. The number of images for susceptib and resistant Ng was 196 and 203, respectively. E bacteria were cropped from those images and th number of cropped images for susceptible and resistant Ng was about 2,500 and 6,000, respective Of these, 60% of the images were used as training data, 20% as validation data and 20% as test data confirm the accuracy of the AI model. As a final test, 20 images were taken for both strains from samples not used in the training data to check the accuracy.

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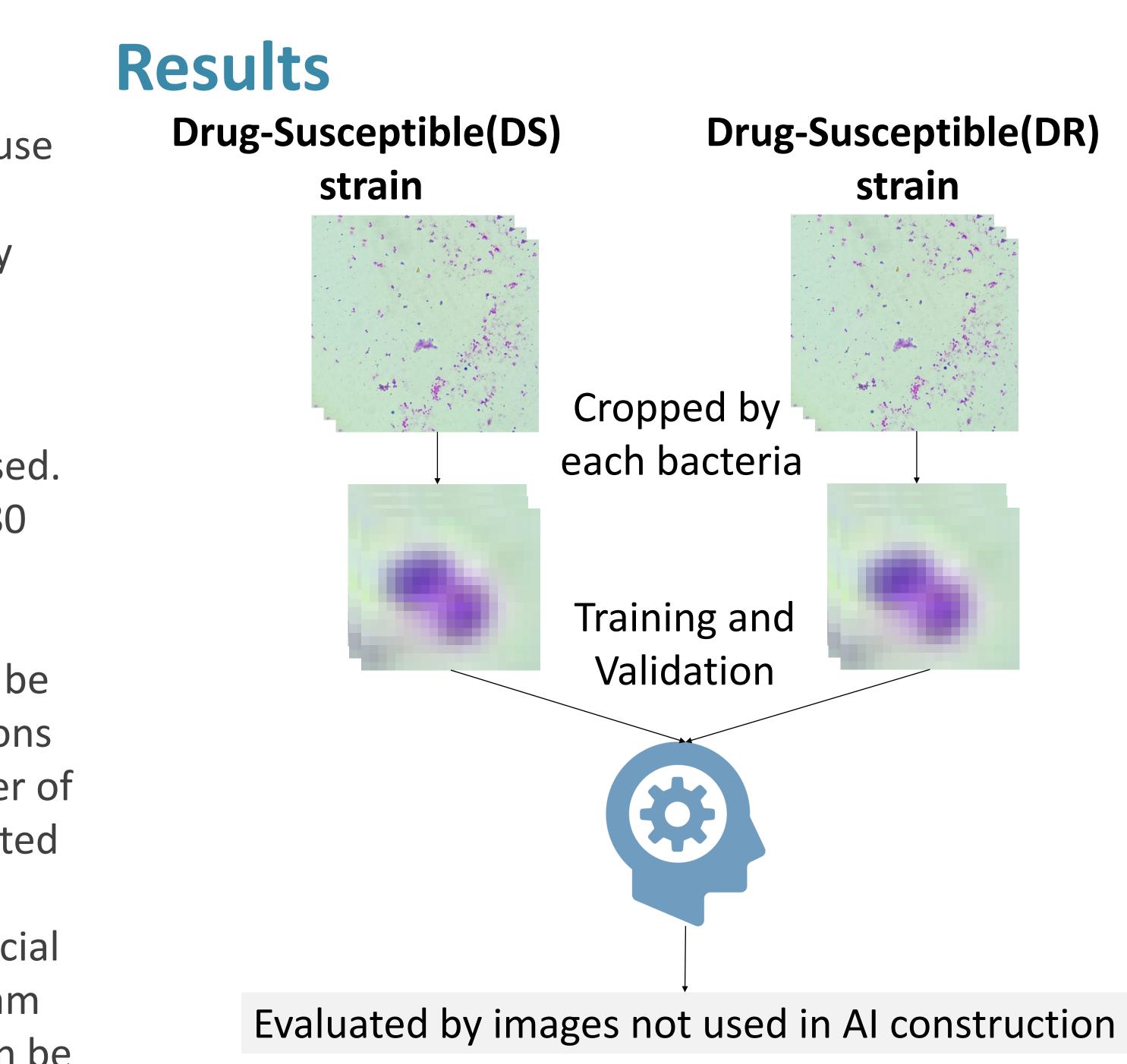


Figure 1. Scheme of AI construction and evaluation

evel)		DR	598 (TD)	30 (гр	
uild	Prediction label		(TP)	(FP	
ble Each he		DS	187 (FN)	200 (TN	
tively.			DR	DS	
ng	True label				
a to	Table1. Classification result of constructed				

d Al for test image data: 20 images not used in AI model construction were used and cropped bacteria from those 20 images were classified.



Sensitivity	Specificit
76%	87%

Table2. Sensitivity, specificity, precision, and accuracy of our AI model for distinguishing DR Ng (Positive) from DS Ng (Negative) : Sensitivity = TP / (TP + FN) Specificity = TN / (TN + FP) Precision = TP / (TP + FP)Accuracy = (TP + TN) / (TP + FN + TN + FN)where TP = True Positive, TN = True Negative, FP = False Positive, FN = False Negative

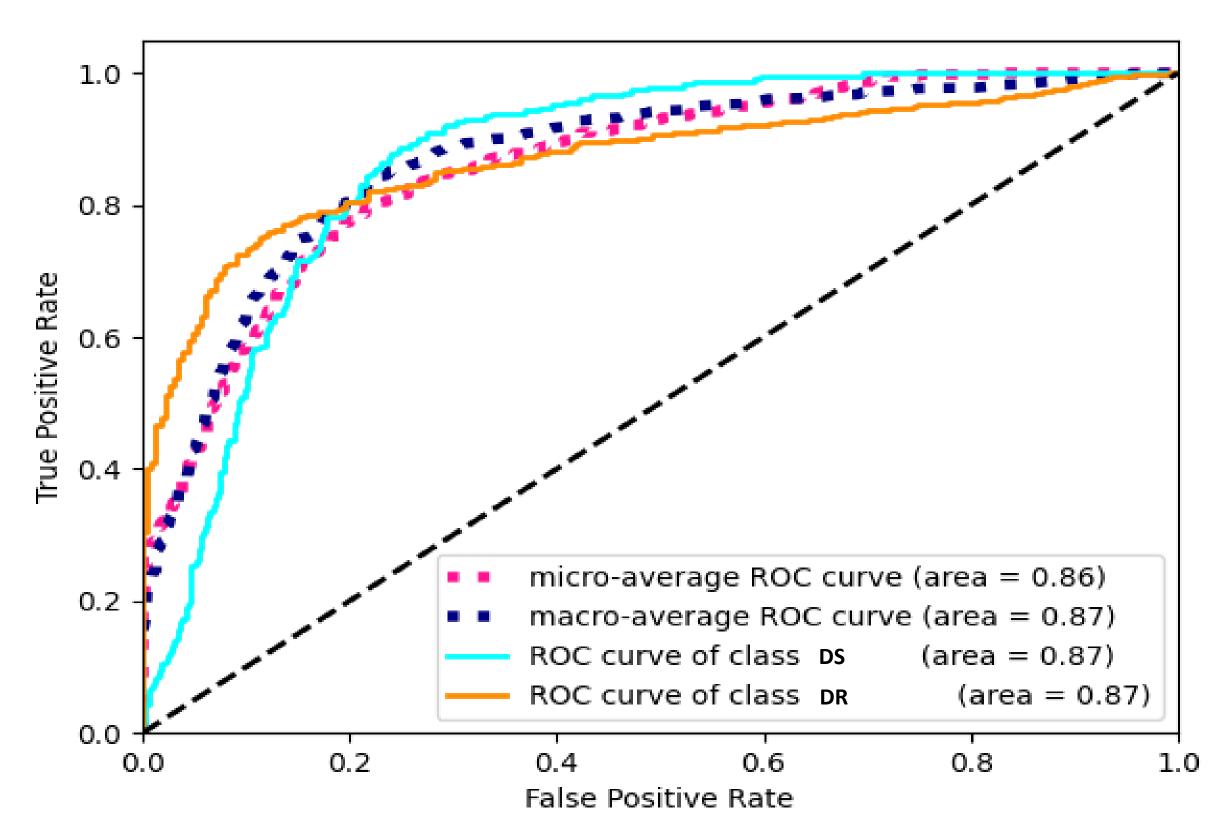


Figure2. ROC curve of our AI model for distinguishing DR Ng (Positive) from DS Ng (Negative) : The AUC (Area under the curve) of this ROC curve was 0.87.

Conclusion

Our preliminary AI model was able to distinguish drug-resistance Ng from drug-susceptible Ng on Gram stained specimens, demonstrating the potential for low-cost point-of-care diagnosis of Ng. We only used only one strain for AI model construction respectively, and so we should collect more Ng strains for improving the accuracy and preventing the deep learning overfitting. However, such a diagnosis will promote the proper use of antimicrobial agents, which can help to prevent the spread of drug-resistant Ng.



