

Supplemental material for

Title

High-resolution bacterial cytological profiling reveals intrapopulation morphological variations upon antibiotic exposure

Authors

Thanadon Samernate,¹ Htut Htut Htoo,¹ Joseph Sugie,² Warinthorn Chavasiri,³ Joe Pogliano,² Vorrapon Chaikeeratisak,⁴ Poochit Nonejuie^{1*}

¹ Institute of Molecular Biosciences, Mahidol University, Nakhon Pathom, Thailand

² Division of Biological Sciences, University of California, San Diego, La Jolla, California, USA

³ Center of Excellence in Natural Products Chemistry, Department of Chemistry, Chulalongkorn University, Bangkok, Thailand

⁴ Department of Biochemistry, Faculty of Science, Chulalongkorn University, Bangkok, Thailand

* Correspondence: poochit.non@mahidol.ac.th

This PDF file includes:

Figures S1 to S4

Tables S1 to S3

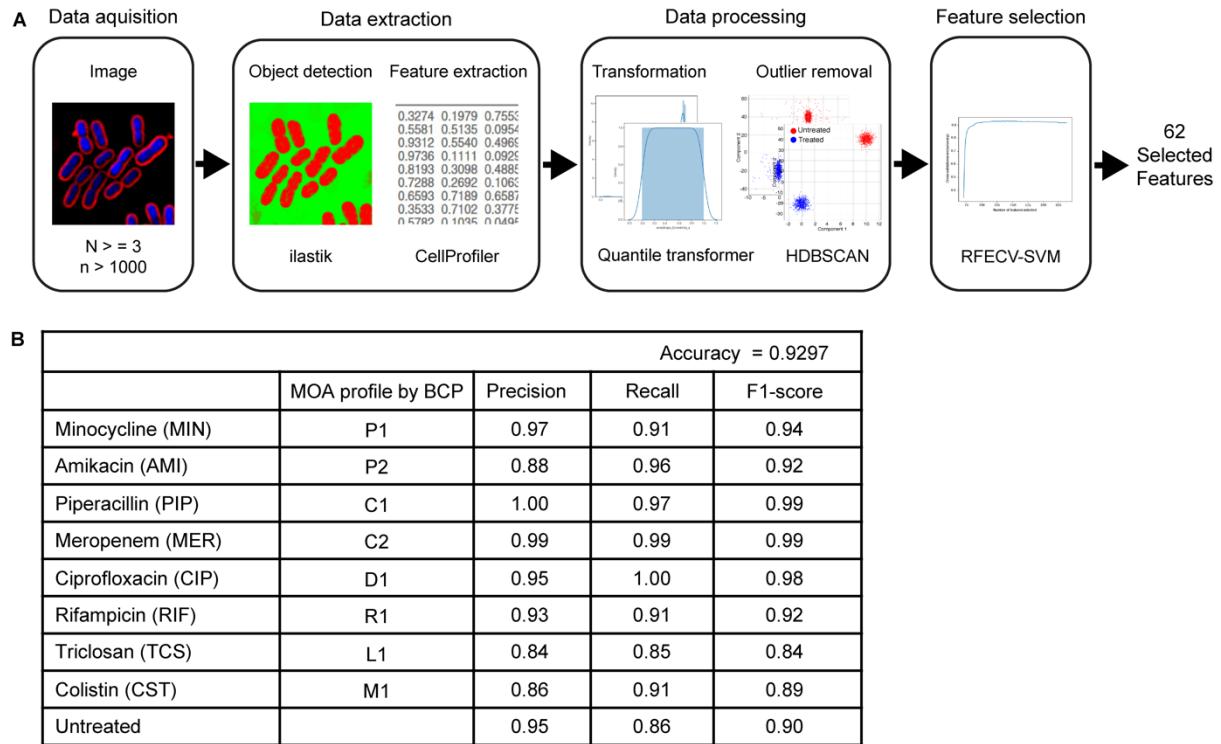
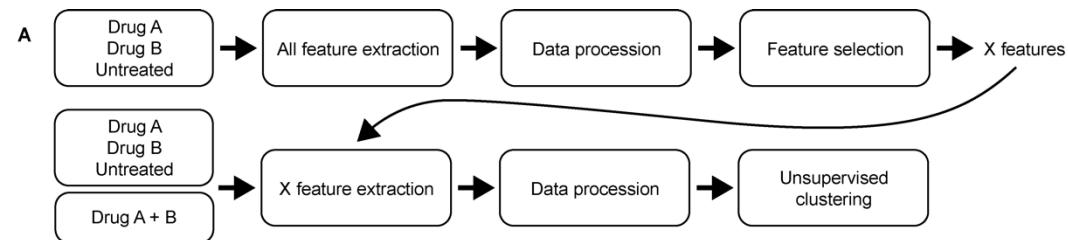


Figure S1. Feature selection pipeline for single antibiotic treatment and cell profile classification accuracy

(A) Data flow of cell feature selection starting from image acquisition, data extraction via ilastik and CellProfiler, data transformation and outlier removal, and feature selection via RFECE-SVM machine learning model. (B) Precision table of single cell profile classification using 62 features selected by RFECE-SVM.



B

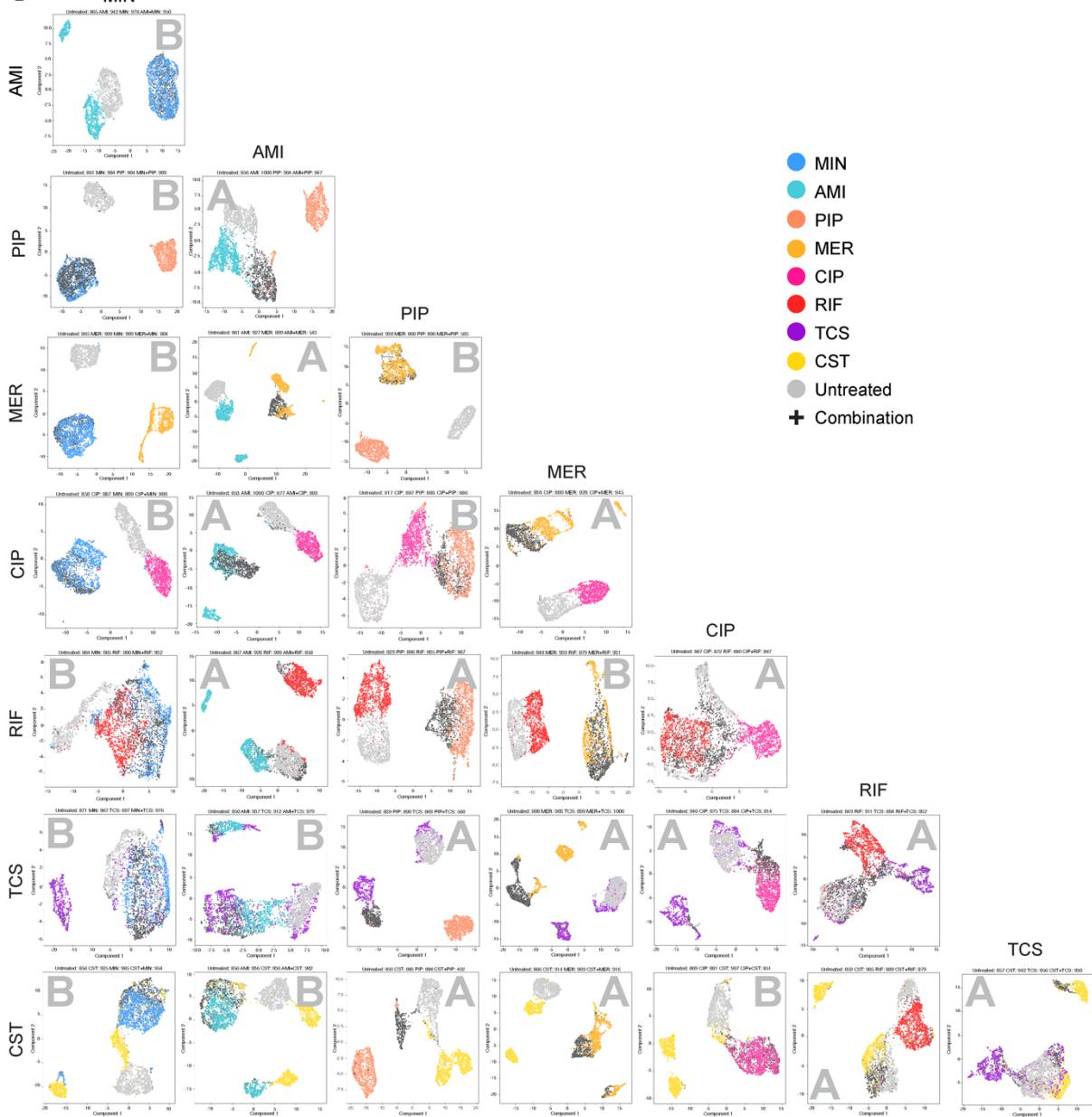


Figure S2. Feature selection pipeline for antibiotic combination treatment and the profiles of all combinations

(A) Data flow of cell feature selection from two antibiotics and unsupervised data analysis of antibiotic combination profiles. (B) PaCMAP plots of all 28 combination with designated combination type (Type A and B) indicated.

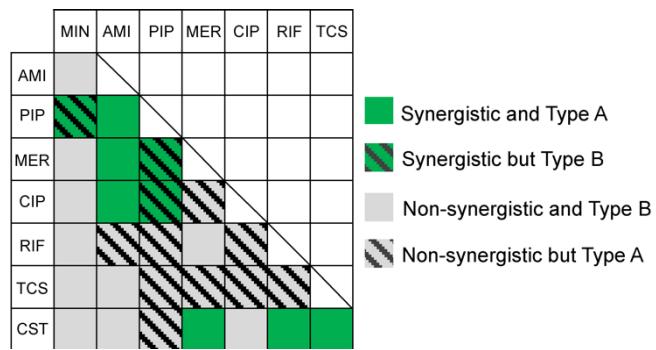


Figure S3. Combinatorial profile types and synergism of antibiotic pairs
 Drug interaction is synergistic when the Σ FICs is ≤ 0.5 , otherwise it is non-synergistic.

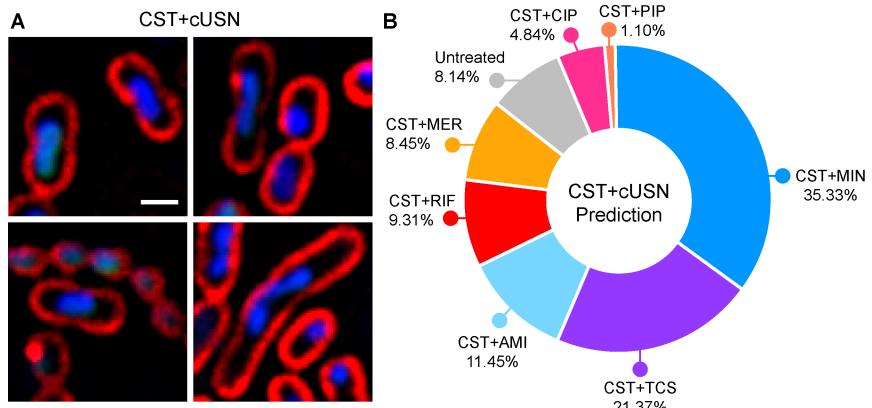


Figure S4. Cells treated with commercial usnic acid (cUSN) in combination with colistin (CST) resulted in multiple morphological changes and were classified into multiple antibiotic combinations

(A) Representative cell images of CST+cUSN-treated cells showing multiple morphological changes. *A. baumannii* cells treated with 0.25 x MIC of CST + 250 μ M cUSN for 1 hour. Scale bar represents 1 μ m. (B) CST+cUSN-treated cells were classified into different profiles by the predictive mode.

Table S1. Table showing the antibiotics used in this study, their MIC, their MOA profiles and cellular pathways inhibited.

Antibiotic name	MIC ($\mu\text{g/mL}$)	MOA profile by BCP	Cellular pathway
Minocycline (MIN)	0.50	P1	Protein translation
Amikacin (AMI)	4.00	P2	
Piperacillin (PIP)	40.00	C1	Cell wall synthesis
Meropenem (MER)	0.45	C2	
Ciprofloxacin (CIP)	0.45	D1	DNA replication
Rifampicin (RIF)	1.00	R1	RNA transcription
Triclosan (TCS)	0.05	L1	Lipid synthesis
Colistin (CST)	0.62	M1	Membrane integrity

Table S2. Table showing the selected features for each experiment.

Table S2 cont.

Table S3. Table showing the antibacterial activity of natural product-derived compounds against *B. subtilis* and *A. baumannii*.

Natural product-derived compounds	MIC (μM)		FIC (μM) (+ 0.25xMIC CST)
	<i>B. subtilis</i>	<i>A. baumannii</i>	<i>A. baumannii</i>
Anacardic acid	31.5	> 500	> 500
Chrysin	> 500	> 500	> 500
α -Mangostin	7.8	> 500	> 500
Mansonone G	15.6	> 500	> 500
Melodorinone B	> 500	> 500	> 500
Methyl 4-hydroxybenzoate	> 500	> 500	> 500
Phenoxyethanol	> 500	> 500	> 500
Pinostrobin	> 500	> 500	> 500
Piperic acid	> 500	> 500	> 500
Piperine	> 500	> 500	> 500
Usnic acid (USN)	1.5	> 500	250
Commercial usnic acid (cUSN)	1.5	> 500	250