

Supplementary Materials:

Table S1. MIC analysis of citric acid against five representative strains.

Pathogens	MIC (µg/mL)
<i>E. coli</i> ATCC 25922	>512
<i>E. coli</i> B2	>512
<i>E. coli</i> O157:H7	>512
<i>S. aureus</i> ATCC 29213	>512
MRSA T144	>512

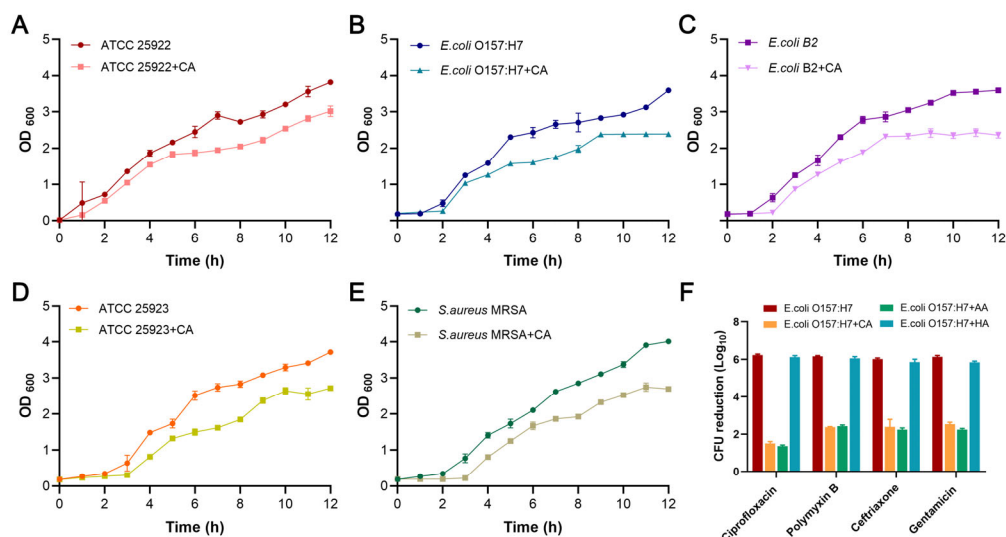


Figure S1 Growth curves of five representative strains grown in the presence of citric acid (final concentration 2%) for 12 hours. The optical density (OD₆₀₀) of citric acid and (A) *E. coli* ATCC 25922, (B) *E. coli* O157:H7, (C) *E. coli* B2, (D) *S. aureus* ATCC 25923, (E) MRSA T144 were monitored within 12 hours. (F) : Effect of adding different acidifiers on bactericidal activity of bactericidal antibiotics. CA: Citric acid, AA: Acetic acid, HA: Hydrochloric acid. After adding three acidifiers, the pH of the culture medium is about 2.2. Three biological replicates were used for the experiment.

Table S2 Co-culture of five representative strains with citric acid had no effect on MIC value of drugs

Antibiotic	Targets	$\mu\text{g/mL}$									
		<i>E. coli</i>		<i>E. coli</i>		<i>E. coli</i>		<i>S. aureus</i>		MRSA	
		ATCC 25922		O157:H7		B2		ATCC 29213		T144	
		MIC ^a	MIC ^b	MIC ^a	MIC ^b	MIC ^a	MIC ^b	MIC ^a	MIC ^b	MIC ^a	MIC ^b
CIP	DNA synthesis	0.03	0.03	<0.03	<0.03	32	32	0.5	0.5	8	16
CRO	Cell wall	0.03	0.03	<0.03	<0.03	256	256	4	4	>512	>512
PB	Cell membrane	0.5	1	0.5	0.5	2	2	-	-	-	-
GEN	Protein synthesis	0.5	0.5	0.5	0.5	64	64	0.5	0.5	128	128
KAN	Protein synthesis	2	2	2	2	512	512	2	2	512	512
TIG	Protein synthesis	0.125	0.125	0.03	0.03	0.5	0.5	0.125	0.125	0.125	0.125
VAN	Cell wall	-	-	-	-	-	-	0.5	1	0.5	0.5

^a Initial MIC of representative strains against antibiotics;

^b MIC of representative strains after co-culturing with citric acid (final concentration 2%) for 6 h.

Abbreviations: CIP, Ciprofloxacin; CRO, Ceftriaxone; PB, Polymyxin B; GEN, Gentamicin; KAN, Kanamycin; TIG, Tigecycline; VAN, Vancomycin.

Table S3 MIC analysis of five antibiotics before and after citric acid induced antibiotic tolerance in *E.coli* B2.

Antibiotic	MIC (µg/mL) ^a	MIC (µg/mL) ^b
Ceftriaxone	256	256
Ciprofloxacin	32	32
Polymyxin B	2	2
Gentamicin	64	64
Kanamycin	512	512

^a Initial MIC of *E.coli* B2 against antibiotics;

^b MIC of CA-*E. coli* B2 induced by citric acid.

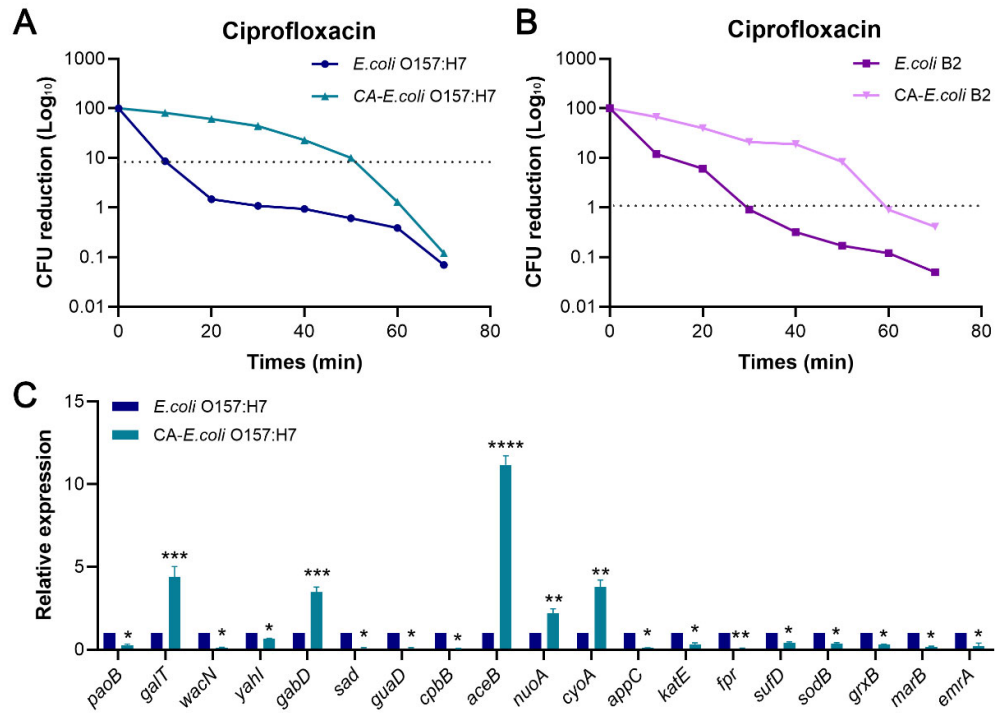


Figure S2: Growth status and mRNA expression of antibiotic tolerance strains induced by citric acid. (A and B): Determination of the growth rate of *E. coli* and CA-*E. coli* strains after stable inheritance of citric acid-induced antibiotic tolerance. Observe the absorbance value at OD₆₀₀ nm of different strains within 12 hours. Three biological replicates are used. (C): The transcriptome sequencing results of the strains before and after citric acid induction were verified by RT-qPCR. All data are presented as mean \pm SD and the significances determined by unpaired t test. All data from biological experiments performed in triplicate are presented as means \pm SD. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$.

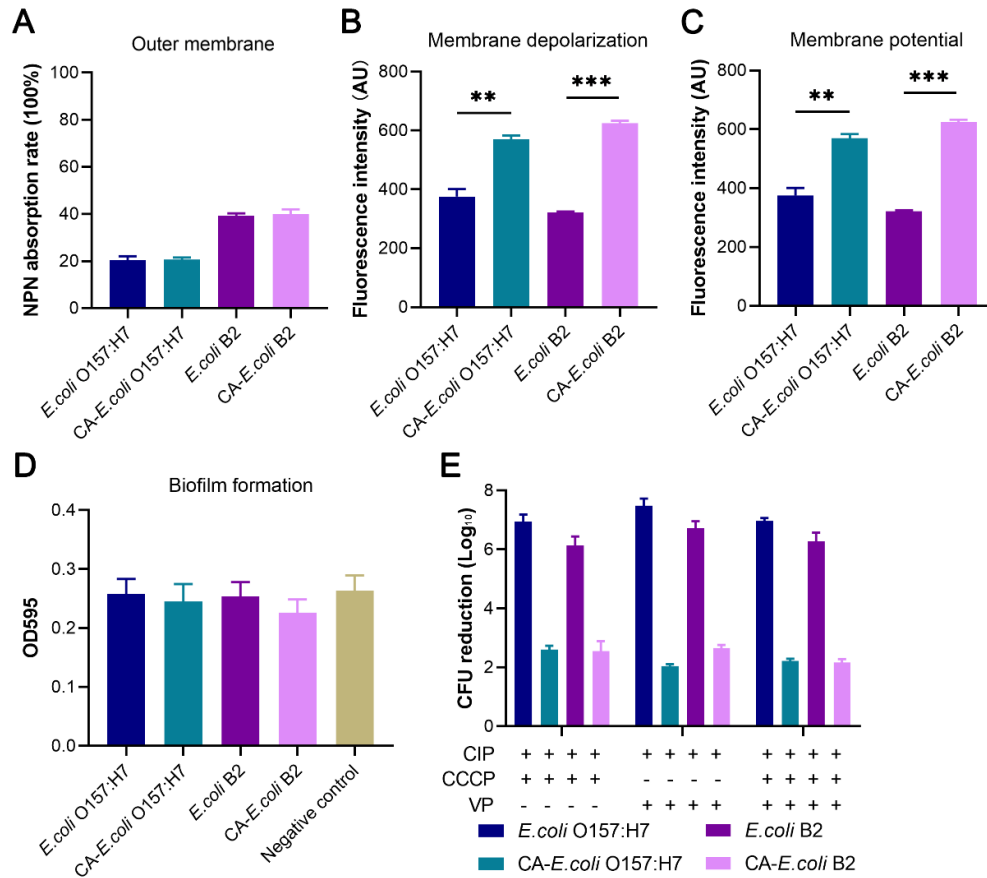


Figure S3: Effects of citric acid-induced antibiotic tolerance on outer membrane integrity, membrane permeability, membrane potential changes and biofilm formation of *E. coli* strain. (A and D): The outer membrane integrity and biofilm formation of the CA-*E. coli* strain did not change compared to the *E. coli* strain. (B and C): However, in the CA-*E. coli* strain, membrane depolarization and membrane potential dissipation occurred. (E): CCCP (efflux pump inhibitor, 100 μ M) and VP (calcium channel inhibitor, 100 μ M) alone or in combination did not affect the bactericidal activity of ciprofloxacin against CA-*E. coli*. All data from biological experiments performed in triplicate are presented as means \pm SD. ** $P < 0.01$, *** $P < 0.001$.

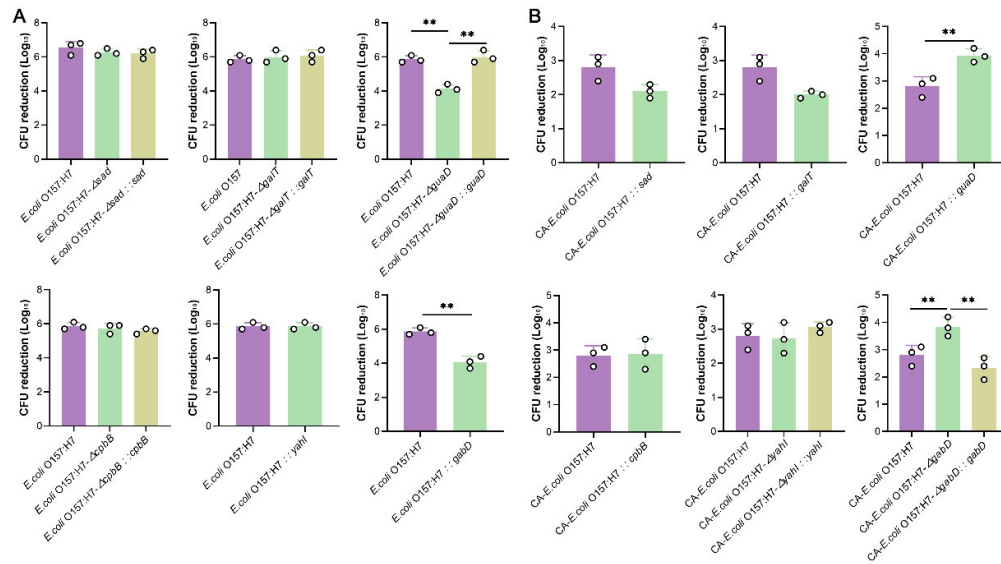


Figure S4: Effects of *guaD* gene and *gabD* gene on antibiotic tolerance in *E. coli*. A: Deletion and deletion-complemented of *guaD* gene and overexpression of *gabD* gene were constructed in *E. coli* O157:H7 strain. It was found that deletion of the *guaD* gene and overexpression of the *gabD* gene could improve antibiotic tolerance to some extent. B: Overexpression of the *guaD* gene, deletion and deletion-complemented of the *gabD* gene were constructed in CA-*E. coli* O157:H7 strain. It was also found that overexpression of the *guaD* gene and deletion of the *gabD* gene could restore the tolerance of the strain to ciprofloxacin to a certain extent. All data from biological experiments performed in triplicate are presented as means \pm SD. ** $P < 0.01$.

Table S4 Strains used in this study.

Strains	Source/Reference
Gram-negative bacteria	
<i>E. coli</i> ATCC 25922	ATCC
<i>E. coli</i> O157:H7	In this study
<i>E. coli</i> B2 (<i>mcr-1</i> + <i>bla</i> _{NDM-5})	In this study
<i>E. coli</i> O157:H7 $\Delta galT$	In this study
<i>E. coli</i> O157:H7 $\Delta galT :: galT$	In this study
<i>E. coli</i> O157:H7 $\Delta wcaN$	In this study
<i>E. coli</i> O157:H7 $\Delta wcaN :: wcaN$	In this study
<i>E. coli</i> O157:H7 Δsad	In this study
<i>E. coli</i> O157:H7 $\Delta sad :: sad$	In this study
<i>E. coli</i> O157:H7 $\Delta guaD$	In this study
<i>E. coli</i> O157:H7 $\Delta guaD :: guaD$	In this study
<i>E. coli</i> O157:H7 $\Delta cpbB$	In this study
<i>E. coli</i> O157:H7 $\Delta cpbB :: cpbB$	In this study
<i>E. coli</i> O157:H7 $:: yahl$	In this study
<i>E. coli</i> O157:H7 $:: gabD$	In this study
Gram-positive bacteria	
<i>S. aureus</i> ATCC 29213	ATCC
MRSA T144	In this study

ATCC, American Type Culture Collection.

Table S5 RT-qPCR primers used in this study.

Genes	Sequence (5'→3')	Product (bp)
<i>paoB</i>	AAGGTGTTTTTCAGCGGTGGGATG CTGGGCGGAGTAGCACATAAGC	122
<i>yahI</i>	CGGCATCGGCTATCTGATCCAAC TCCACTTCCACCTGAGTCACCAC	96
<i>wcaN</i>	GCAGCCACAATCTCGTCAACAATG GCAGTTATTCTGTAGCGGGTCTC	125
<i>sad</i>	ATTCAGCCAGCCATATACGCCTTG TTCCCATCATTCTTGACAGGTAACGG	128
<i>galT</i>	AGCTGCCAGTGTTGATTCTCTTCG GACAACCTCTTCCAGTGCTCCTTC	86
<i>cpdB</i>	AGCACGAAACCACAGTCACTCATC CCTGACGGTTGATCTTCGCT	102
<i>guaD</i>	TGCCTGGGTGAAATCGCTTTATCC AGATGGACGCAGTGAGCAAAGAC	105
<i>fixA</i>	GTATGGTCGGCGGCGGATATTG GCAAATGCGGCGATCTGTTCTTC	134
<i>fixX</i>	CAAGAAGCAGGATGACGGCAGTG CGTAACGGAACCTCCACACCAAAGG	140
<i>folA</i>	TGACGCATATCGACGCAGAAGTG CCGCCGCTCCAGAATCTCAAAG	143
<i>polB</i>	AGTTCACCCGCCATCAGTTTGTC GCCCAGCAGTTTCAGCAGGAG	101
<i>copA</i>	TACGCTCCGCCAGGTTTACCC ATGACGATGACAGCCAGCAGTTG	126
<i>degP</i>	CAACGGCGGCTGAGACTTCTTC GCTGACCACTGAAGGCATCACC	92
<i>rclA</i>	TCAATGCCCATGTGGAGCGAATC CTGGATGTAAACGAAGCGGTAGCC	132
<i>csgA</i>	CGGTGGTGGCGGTAATAATAGCG GTCAAGTCAGAGTTACGGGCATCAG	111
<i>ycdL</i>	CACCGAAATGAAAGAAGCGATAGCG GCCCCACGGAAAATCAGACTACG	81
<i>aceF</i>	AGAACGAAGAAGCGGCGAAACG AGCGAACTATTGAAGCGAGGCATC	112
<i>emrA</i>	CGTGCGTCTTCCTCGGTAATGTAG CACCTCTTCTATCGGCGTTGTCAC	117
<i>16S rRNA</i>	AACTGGAGGAAGGTGGGGATGAC CGGACTACGACGCACTTTATGAGG	135