

Additional file 1

Journal name: AMB Express

Article title: The two-component system CepRS regulates the cephamycin C biosynthesis in

Streptomyces clavuligerus F613-1

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Captions

1. Table S1 Plasmids and strains used in this study.
2. Table S2 Primers used in this study.
3. Figure S1. (A) Polymerase chain reaction-based verification of the $\Delta cepS$ and $\Delta cepR$ strains. M: DNA marker. (B) Phenotype of F613-1, $\Delta cepRS$, $\Delta cepR$, $\Delta cepS$ and $\Delta cepRS$ on BSCA solid media. (C) Ceph C (cephamycin C) obtained in F613-1, $\Delta cepRS$, $\Delta cepR$ and $\Delta cepS$ strains on TSA solid medium. *, statistically significant difference ($P < 0.05$) between $\Delta cepRS$, $\Delta cepR$, $\Delta cepS$ and F613-1 at the same time point.
4. Figure S2. Biomass and clavulanic acid (CA) concentration of F613-1, $\Delta cepRS$ and the complemented strain. A: Growth curves of F613-1, $\Delta cepRS$ and $\Delta cepRScom$ in SCF fermentation medium. Samples for growth curve analysis were harvested at five time points (1, 3, 5, 7 and 9 d). Data are the mean \pm SD of three independent experiments. B: Analysis of the change of CA concentration during fermentation. Data are the mean \pm SD of three independent biological experiments.
5. Figure S3. Expression of genes in the CA biosynthetic gene cluster were examined by RT-qPCR between F613-1 (black bars), $\Delta cepRS$ (grey bars) and $\Delta cepRScom$ (dark grey bars). Results were normalized for 16S rRNA gene content and are shown as fold change over the F613-1 control. Data are the mean \pm SD of three independent biological experiments.
6. Figure S4. A: Phenotype of F613-1, $\Delta cepRS$, $\Delta cepRScom$ and $\Delta cepRS-cepRS$ (over-expression strain) on BSCA solid media. B: Cephamycin C obtained in F613-1, $\Delta cepRS$ and $\Delta cepRS-cepRS$ (over-expression strain) strains on TSA solid medium. *, compared with F 613-1, $P < 0.05$. Data are the mean \pm SD of three independent biological experiments. C: Expression of genes in the cephamycin C biosynthetic gene cluster were examined by RT-qPCR between F613-1 (black bars), $\Delta cepRS$ (grey bars) and $\Delta cepRS-cepRS$ (over-expression strain) (dark grey bars). Results were normalized for 16S rRNA gene content and are shown as fold change over the F613-1 control. *, compared with F613-1, $P < 0.05$. Data are the mean \pm SD of three independent biological experiments.

Table S1 Plasmids and strains used in this study.

| Strains or plasmids | Description | Source/Reference |
|---|--|----------------------|
| <i>Streptomyces clavuligerus</i> strains | | |
| F613-1 | Industrial clavulanic acid producer | (Qin 2017) |
| $\Delta cepRS$ | F613-1 mutant with <i>cepRS</i> double-gene deletion | This study |
| $\Delta cepR$ | F613-1 mutant with <i>cepR</i> gene deletion | This study |
| $\Delta cepS$ | F613-1 mutant with <i>cepS</i> gene deletion | This study |
| $\Delta cepRScom$ | $\Delta cepRS$ complemented with <i>cepRS</i> | This study |
| $\Delta cepRS-cepRS$ | $\Delta cepRS$ overexpressed with <i>cepRS</i> | This study |
| $\Delta cepRScom$ -pSET152 | $\Delta cepRS$ complemented with the empty vector pSET152 | This study |
| <i>E. coli</i> strains | | |
| DH5 α | General cloning host | Trans (China) |
| BL21 (DE3) | Strain used for protein expression | Trans (China) |
| <i>E. coli</i> ESS 2235 | a supersensitive organism to beta-lactam antibiotics | (Leite et al. 2016) |
| ET12567/pUZ8002 | Strain used for conjugation between <i>E. coli</i> and <i>Streptomyces</i> spp | (Kieser et al. 2000) |
| Plasmids | | |
| pJTU1278 | <i>E. coli</i> - <i>Streptomyces</i> shuttle vector, <i>tsr</i> ^a <i>bla</i> ^a <i>oriT</i> | (He et al. 2010) |
| pHLY12 | <i>Streptomyces</i> overexpression vector with the strong promoter ermEp | Preserved in our lab |
| pHLY-cepRS | pHLY12 containing the coding sequence of <i>cepRS</i> | This study |
| pSET152 | <i>Streptomyces</i> integrated vector | BioVector (China) |
| pET-15b | Expression vector containing the T7 promoter and 6 \times His-thrombin | Novagene (USA) |
| pSET-cepRS | pSET152 containing the coding sequence of <i>cepRS</i> plus <i>cepR</i> upstream intergenic sequence | This study |
| pET-cepR | pET15b containing the coding sequence of <i>cepR</i> | This study |
| pEasy-Blunt-Simple | General cloning vector | Trans (China) |
| pJTU-cepR | pJTU1278 containing the <i>cepR</i> -disrupted cassette | This study |
| pJTU-cepS | pJTU1278 containing the <i>cepS</i> -disrupted cassette | This study |
| pJTU-cepRS | pJTU1278 containing the <i>cepRS</i> -disrupted cassette | This study |

^a *tsr*, thiostrepton-resistance gene; *bla*, ampicillin-resistance gene.

Table S2 Primers used in this study.

| Oligonucleotides | DNA Sequence (5'→3')* |
|--|--|
| Recombinant plasmid pJTU-cepRS, pJTU-cepS, pJTU-cepR construction | |
| <i>cepRS</i> L-F | GG <u>ACTAGT</u> ACCACATAGGAACGGGTA |
| <i>cepRS</i> L-R | CCTCTAGAAATGCA <u>AAGCTT</u> GTGAAGACCTATGTGAGCC |
| <i>cepRS</i> R-F | GGA <u>AAGCTT</u> GATCTCCACGAGGATCATGC |
| <i>cepRS</i> R-R | CGTCTAGAGGAAACAGCCGAAACAG |
| <i>cepR</i> R-F | GG <u>ACTAGT</u> AGTCACCCTCACTCAGCC |
| <i>cepR</i> R-R | CCTCTAGAAATGCA <u>AAGCTT</u> TGCACGCCCTTCAGGAGC |
| <i>cepS</i> L-F | GG <u>ACTAGT</u> TTCCCCACTGCTTCGGC |
| <i>cepS</i> L-R | CCTCTAGAAATGCA <u>AAGCTT</u> AGGTGGAGGGCTGATCCG |
| Validation of ΔcepRS, ΔcepS, ΔcepR and ΔcepRScom strain | |
| <i>cepRS</i> V-F | CTGCACCCGGTTCTCGCA |
| <i>cepRS</i> V-R | GTGAAGCTCTCATCCTCGA |
| Recombinant plasmid pSET-cepRS construction | |
| <i>cepRScom</i> -F | GGCTGCAGGTCGACTCTAGACCTCGTCGTCCGCCCCGCTC |
| <i>cepRScom</i> -R | TCGCGCGCGGCCGCGGATCCCCATGCATCGCCGGGGTCCA |
| Recombinant plasmid pHLY-cepRS construction | |
| <i>cepRS</i> -F | GGAATTCCATATGCGGATCGGCGCCCCGTCAT |
| <i>cepRS</i> -R | CTAGTCTAGACCGCCGAGACCGGGGTGTGA |
| Recombinant plasmid pET-cepR construction | |
| <i>cepRHis</i> -F | <u>CATATG</u> ACGGGGGCGCCGATCCGGGTGGTCATCGCC |
| <i>cepRHis</i> -R | <u>CTCGAGT</u> CAGCCCACGCCAGACCCGCGTCCCGCGC |
| EMSAs | |
| cmcI-cefD p1 For | TCGTTCAATTGCCCTCTTCCTTGAGTG |
| cmcI-cefD p1 Rev | ATGGTCGTCCGATCGCCGCA |
| cmcI-cefD p2 For | CGCCGTTGTGCACCCATGGG |
| cmcI-cefD p2 Rev | CCCAGTCGGCTACCGCCATGTC |
| cmcI-cefD p3 For | TGCGGCGATCGGACGACCAT |
| cmcI-cefD p3 Rev | CCCATGGGTGCACAACGGCG |
| lat p For1 | GCCCATGGGTGAGAACTCCTGGG |
| lat p Rev1 | CGGTCCCAGGCTTCGATGGC |
| lat p For2 | GCCATCGAAGCCTGGGACCG |
| lat p Rev2 | CAACTGCCCTGAAGCGGGCC |
| ccaR For1 | TGGCTTCGGCGTAATCCTTG |

| | |
|----------------|-----------------------|
| ccaR Rev1 | CTGTCCCAAATCGTCCATGC |
| ccaR For2 | TCGGTGAACCCGGAAGAACC |
| ccaR Rev2 | TTTGCCGAGGATTTCCGGAC |
| orf10 For1 | TTTGAGTACCGTCCGCCGCC |
| orf10 Rev1 | TTCCTCACACAGAGCAGACC |
| orf10 For2 | GGTCTGCTCTGTGTGAGGAA |
| orf10 Rev2 | GTTTCCCTGAACCAACGCTG |
| pcbAB For | CATCATTCGTGGGCTCTCCG |
| pcbAB Rev | TGGCGAGCAGTGTACGGCG |
| cmcT For | GCATGCCGCACGGATGACGC |
| cmcT Rev | CAGCGGAACTCCCTCGCATG |
| pbpA For | TACCAGCGGAAGGAGGCACC |
| pbpA Rev | CTGTCTCCTTCATACGCCGC |
| RT-qPCR | |
| 16S-RT For | GAGATCCGCCTTCGCCACCG |
| 16S-RT Rev | CTGCATTCGATACGGGCAGGC |
| pcbR-F | CCAACCTCAAGCCGACGAAG |
| pcbR-R | ACGCGACCTTCCACTCCTTG |
| pcbC-F | TGACCGACCAGGAGAAGCAC |
| pcbC-R | GACCGCCTTGTAGTAGCCGT |
| pcbAB-F | GCCTATCTCACCTACACCTC |
| pcbAB-R | AGCGTCTGCCCCGTTGATGAG |
| lat-F | AGGCACTTGAGCAGCATATG |
| lat-R | ATGCTGGGCGGGTTGATTCC |
| blp-F | ATGGTGAAGAAGACATGGAG |
| blp-R | TGGTCGGCACCGGCGAGCTG |
| orf10-F | CCGATGTCCCGCAGTTGTTG |
| orf10-R | CCTGGATGACGTCGTCGATC |
| ccaR-F | TTCGCGGATGTGACCTCCAG |
| ccaR-R | TCATCAGGCTCACATACAGG |
| cmcH-F | GTTCTTCACCTCCACGCACG |
| cmcH-R | CCGAAGAGGAAGGAGTAGCG |
| cefF-F | TCTTCAACCTCGCCGCACTG |
| cefF-R | AAGAAGTCCATCGCCGTGTC |
| cmcJ-F | ACGCGGTGGAGTTCTTCGAC |

| | |
|---------------|-----------------------|
| cmcJ-R | TCGACGTGCACCCGCAGATG |
| cmcI-F | CCCACGCCAACACCTTCAAC |
| cmcI-R | CGATGATGAAGTAGTCGCCC |
| cefD-F | CCACCGTCGTCAACCTCAAC |
| cefD-R | AGCAGGAAGTCCATCGGCTC |
| cefE-F | CACCCTCATCCAGCAGACAC |
| cefE-R | TGCCCGCTATCTGGTCCCTG |
| pcd-F | TCACCGAGCACAAACAGGAC |
| pcd-R | TCGCAGATGTCGATCATCTC |
| cmcT-F | AGGTGCCGCTCTGGTACTTC |
| cmcT-R | AGCGAGACCAGCAGCATGAC |
| pbp74-F | AGAGGGGTTCGAAAAGGCTG |
| Pbp74-R | GCTCCGGCTTCGGCTCCTTG |
| bla-F | TCGCCTTCTGCTCCACGTTC |
| bla-R | GGTGAGATCGAGTCGACGTC |
| gcas-RT For | CACCCCTGGCCGACTATGCC |
| gcas-RT Rev | GCCCGTGGGTGTACCAGGAC |
| orf16-RT For | CACCGTCTGCTTCCCGCACG |
| orf16-RT Rev | GCGGTGCTTGGTCATGTCCG |
| oppA2-RT For | ACGTCTGGGTGTGGCTGCTC |
| oppA2-RT Rev | GCAGCCGGTAGGTCCAGGTC |
| orf14-RT For | CGGCCAACGACGACGAAACG |
| orf14-RT Rev | CCAGTCGTCGAGGGCGGTC |
| orf13-RT For | TCCTCTCCGCGATGCGGTTC |
| orf13-RT Rev | GCATGCCGATGTCGATGGCG |
| orf12-RT For | AGGGCCGACAAGGAGCGATG |
| orf12-RT Rev | GTCCGGACGAGGTCAGCAGC |
| fd-RT For | GCCCCGAGATCTTCGACCAG |
| fd-RT Rev | TAGCCCTCGGTGACCGTGAT |
| cyp450-RT For | AGCCAGGTGTGGCTGGTGAC |
| cyp450-RT Rev | GCGGATGAACGACGCCGACT |
| cad-RT For | CCGACTGGACCCGGATGATCG |
| cad-RT Rev | TTCGTGGCCTGGTAGACGGC |
| claR-RT For | TGCTGTCGCTGGTCTCCACG |
| claR-RT Rev | TAGGCCGCGTCCACCTGGTA |

| | |
|--------------|------------------------|
| oppA2-RT For | ACGTCTGGGTGTGGCTGCTC |
| oppA2-RT Rev | GCAGCCGGTAGGTCCAGGTC |
| oat2-RT For | CGACTTCACCGTCCTCGCCT |
| oat2-RT Rev | GGTCGCGACATTCGCGTTGC |
| cas2-RT For | CTCCGAGCTTCCCGAGGTGC |
| cas2-RT Rev | CGCGCAGCAGCAGATAACCG |
| pah2-RT For | ACGGCGCAGAGCCATCTGTC |
| pah2-RT Rev | TTGGTGTCCGGAGTGC GCGTC |
| bls2-RT For | TGCCGCTGTACACCTGTGTGG |
| bls2-RT Rev | CGCGGGCACCTGGTAGACAC |
| ceaS2-RT For | AGGCCGCGTCGATTCTCTTCG |
| ceaS2-RT Rev | AGAGGTTGGTCATACCGGGGC |
| cas1-RT For | GAGGACCGCTCCCTGCTGAC |
| cas1-RT Rev | CTCCGAGGACAGGTGGTGCG |

* Restriction enzyme sites are underlined and were used for cloning purposes.

Figure S1

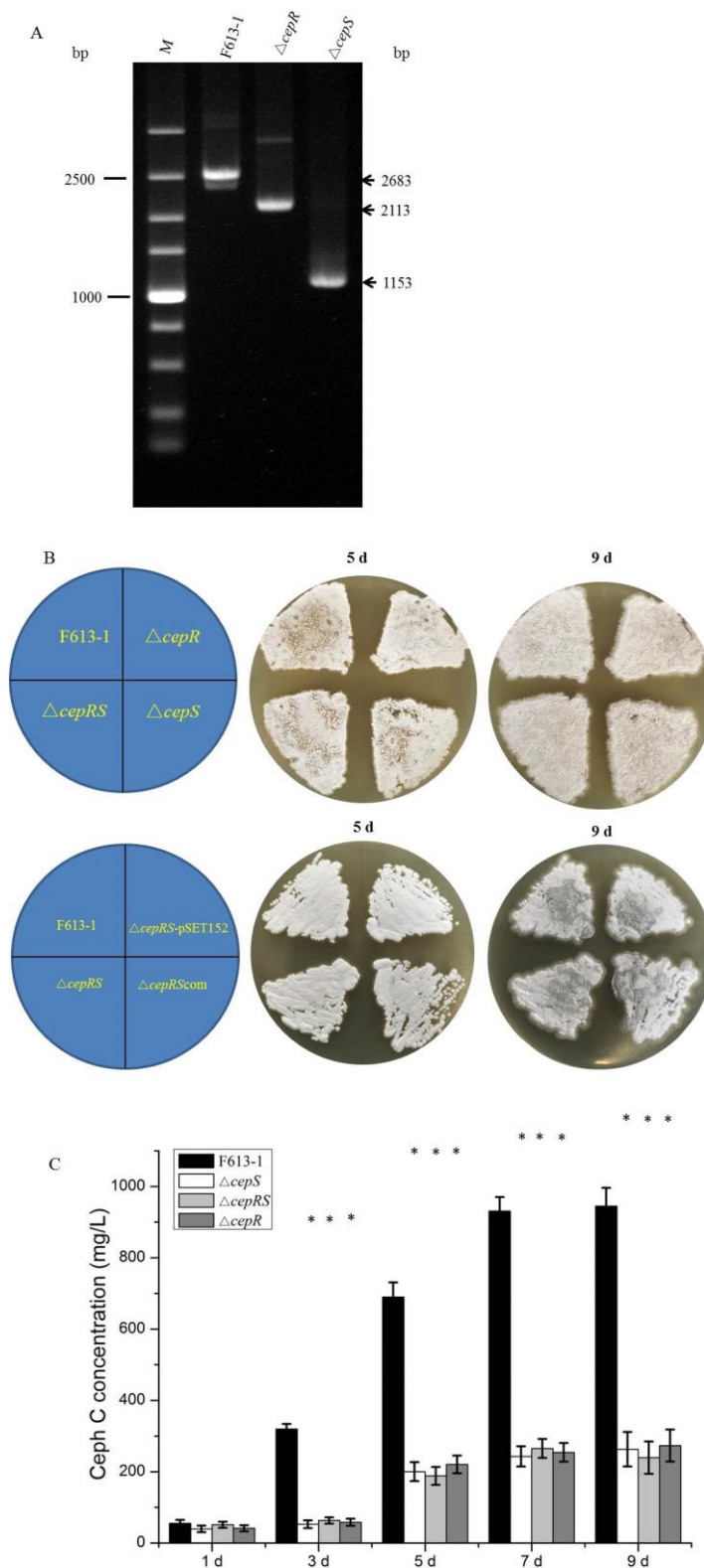


Figure S1. (A) Polymerase chain reaction-based verification of the $\Delta cepS$ and $\Delta cepR$ strains. M: DNA marker. (B) Phenotype of F613-1, $\Delta cepRS$, $\Delta cepR$, $\Delta cepS$ and $\Delta cepRS$ on BSCA solid media. (C) Ceph C (cephamycin C) obtained in F613-1, $\Delta cepRS$, $\Delta cepR$ and $\Delta cepS$ strains on TSA solid medium. *, statistically significant difference ($P < 0.05$) between $\Delta cepRS$, $\Delta cepR$, $\Delta cepS$ and F613-1 at the same time point.

Figure S2

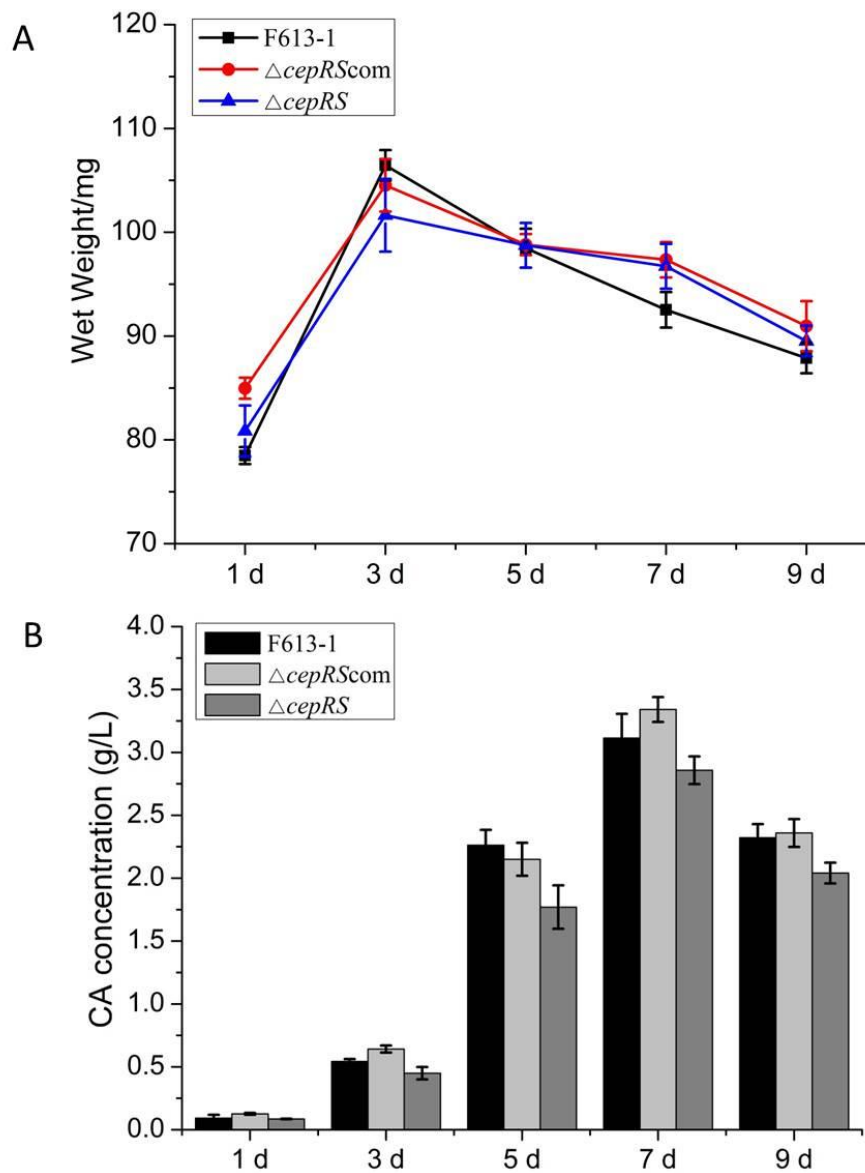


Figure S2. Biomass and clavulanic acid (CA) concentration of F613-1, $\Delta cepRS$ and the complemented strain. **A:** Growth curves of F613-1, $\Delta cepRS$ and $\Delta cepRScom$ in SCF fermentation medium. Samples for growth curve analysis were harvested at five time points (1, 3, 5, 7 and 9 d). Data are the mean \pm SD of three independent experiments. **B:** Analysis of the change of CA concentration during fermentation. Data are the mean \pm SD of three independent biological experiments.

Figure S3

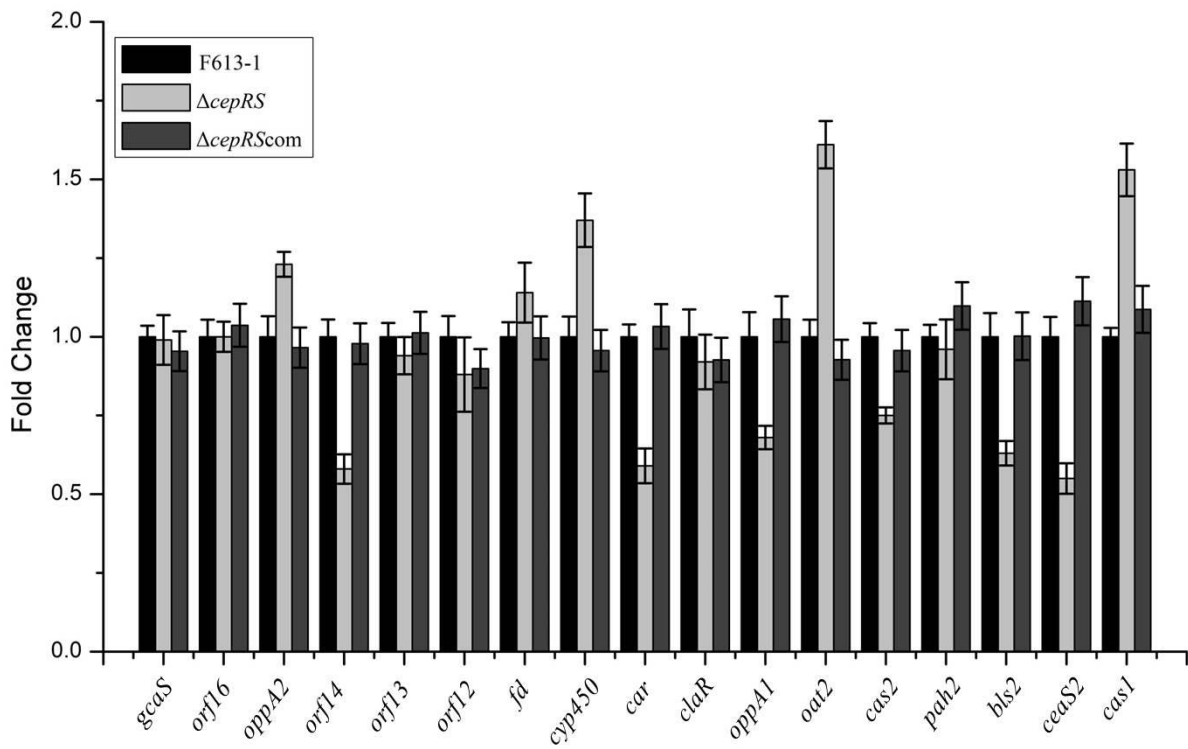


Figure S3. Expression of genes in the CA biosynthetic gene cluster were examined by RT-qPCR between F613-1 (black bars), $\Delta cepRS$ (grey bars) and $\Delta cepRScom$ (dark grey bars). Results were normalized for 16S rRNA gene content and are shown as fold change over the F613-1 control. Data are the mean \pm SD of three independent biological experiments.

Figure S4

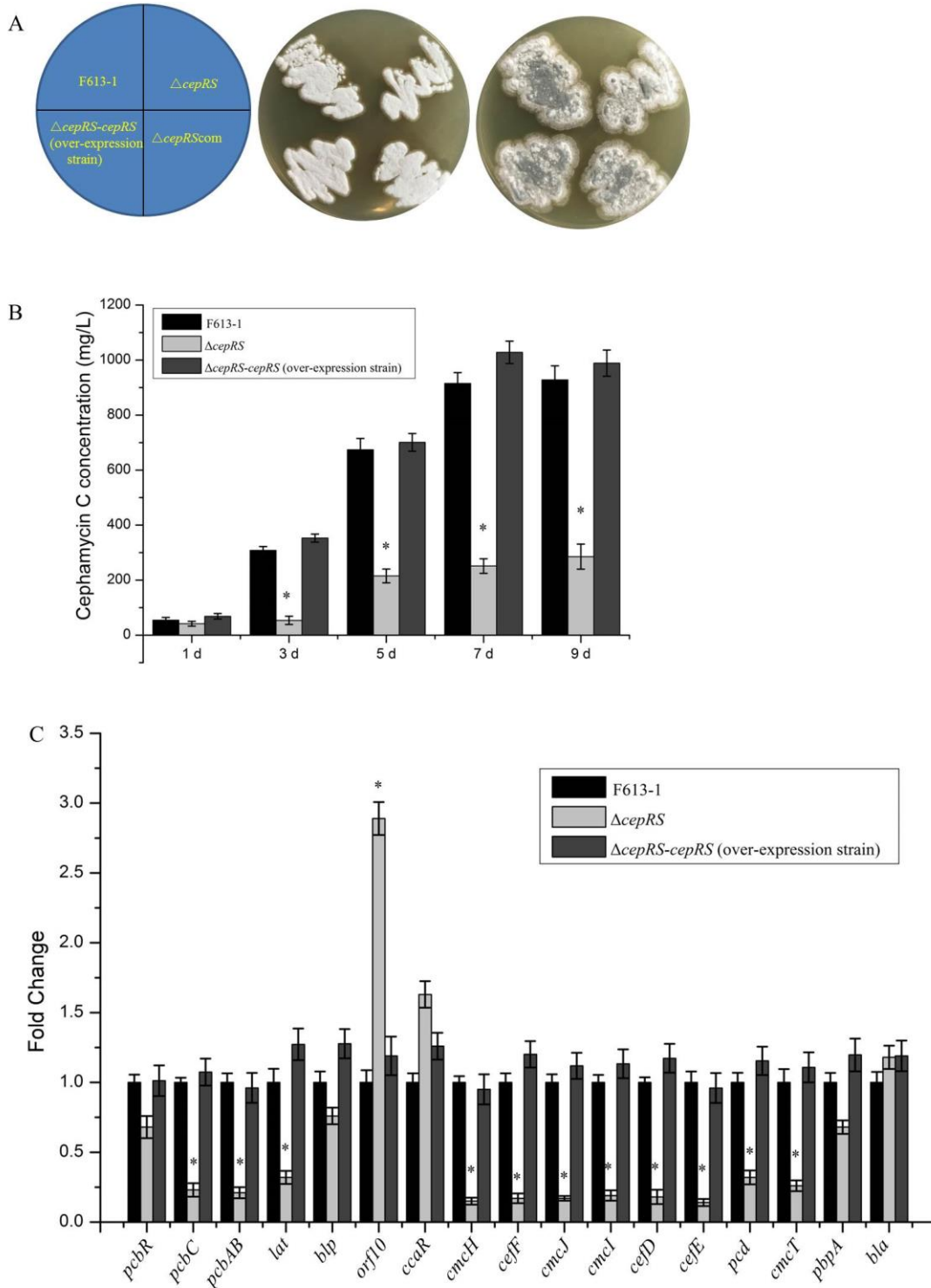


Figure S4. A: Phenotype of F613-1, $\Delta cepRS$, $\Delta cepRScom$ and $\Delta cepRS-cepRS$ (over-expression strain) on BSCA solid media. B: Cephamycin C obtained in F613-1, $\Delta cepRS$ and $\Delta cepRS-cepRS$ (over-expression strain) strains on TSA solid medium. *, compared with F 613-1, $P < 0.05$. Data are the mean \pm SD of three independent biological experiments. C: Expression of genes in the cephamycin C biosynthetic gene cluster were examined by RT-qPCR between F613-1 (black bars), $\Delta cepRS$ (grey bars) and $\Delta cepRS-cepRS$ (over-expression strain) (dark grey bars). Results were normalized for 16S rRNA gene content and are shown as fold change over the F613-1 control. *, compared with F613-1, $P < 0.05$. Data are the mean \pm SD of three independent biological experiments.

References:

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