

Supplementary materials to RSC Advances

Effect of overexpression of endogenous and exogenous *Streptomyces* antibiotic regulatory proteins on tacrolimus (FK506) production in *Streptomyces* sp. KCCM 11116P

Chao Chen¹, Xinqing Zhao^{1, 2*}, Liangyu Chen¹, Yingyu Jin³, Zongbao K. Zhao⁴, Joo-Won Suh³

¹*School of Life Science and Biotechnology, Dalian University of Technology, Dalian 116024, China*

²*School of Life Science and Biotechnology, Shanghai Jiaotong University, Shanghai 200240, China*

³*Division of Bioscience and Bioinformatics, Myongji University, Yongin 449-728, South Korea*

⁴*Department of Biotechnology, Dalian Institute of Chemical Physics, Chinese Academy of Sciences, Dalian 116023, China*

*Corresponding author

Tel: +86-411-84706319, Fax: +86-411-84706329 (XQ Zhao)

E-mails: xqzhao@dlut.edu.cn (XQ Zhao).

Supplementary tables

Table S1 Strains and plasmids used in this study.

| | Description | Source and references |
|--|---|-----------------------|
| Strains | | |
| <i>E. coli</i> DH5 α | Cloning host | Laboratory stock |
| <i>E. coli</i> ET12567 | <i>dam dcm hsdS cat tet</i> | [1] |
| <i>E. coli</i> ET12567/ pWHM3 | Strain to obtain non-methylated pWHM3 | This study |
| <i>E. coli</i> ET12567/ pWHM3- <i>Sx5140</i> | Strain to obtain non-methylated pWHM3- <i>Sx5140</i> | This study |
| <i>E. coli</i> ET12567/ pWHM3- <i>bulZ</i> | Strain to obtain non-methylated pWHM3- <i>bulZ</i> | This study |
| <i>E. coli</i> ET12567/ pWHM3- <i>bulY</i> | Strain to obtain non-methylated pWHM3- <i>bulY</i> | This study |
| <i>Streptomyces</i> sp. KCCM 11116P | Wild-type FK506 producer | Laboratory stock |
| <i>S. xinghaiensis</i> S187 ^T | Source to obtain <i>Sx5140</i> | [2] |
| <i>Streptomyces</i> sp. CC01 | <i>Streptomyces</i> sp. KCCM 11116P transformed with the empty plasmid pWHM3 which was used as control strain, Tsr ^r | This study |

Table S1 Cont.

| | Description | Source |
|-------------------------------|--|---------------|
| <i>Streptomyces</i> sp. CC02 | <i>Streptomyces</i> sp. KCCM 11116P transformed with plasmid pWHM3- <i>bulZ</i> , Tsr ^r | This study |
| <i>Streptomyces</i> sp. CC03 | <i>Streptomyces</i> sp. KCCM 11116P transformed with plasmid pWHM3- <i>bulY</i> , Tsr ^r | This study |
| <i>Streptomyces</i> sp. C5140 | <i>Streptomyces</i> sp. KCCM 11116P transformed with plasmid pWHM3- <i>Sx5140</i> , Tsr ^r | This study |
| Plasmids | | |
| pMD-19T | Cloning vector, Amp ^r | Takara |
| pMD-19T- <i>bulZ</i> | pMD-19T carrying <i>bulZ</i> , Amp ^r | This study |
| pMD-19T- <i>bulY</i> | pMD-19T carrying <i>bulY</i> , Amp ^r | This study |
| pMD-19T- <i>Sx5140</i> | pMD-19T carrying <i>Sx5140</i> , Amp ^r | This study |

Table S1 Cont.

| | Description | Source |
|----------------------|--|---------------|
| pWHM3 | Cloning vector, colE1 replicon, pSG5 replicon, Tsr ^r , Amp ^r | [3] |
| pWHM3- <i>bulZ</i> | pWHM3 carrying <i>bulZ</i> in <i>Bam</i> HI- <i>Hind</i> III sites, Amp ^r , Tsr ^r | This study |
| pWHM3- <i>bulY</i> | pWHM3 carrying <i>bulY</i> in <i>Bam</i> HI- <i>Hind</i> III sites, Amp ^r , Tsr ^r | This study |
| pWHM3- <i>Sx5140</i> | pWHM3 carrying <i>Sx5140</i> in <i>Bam</i> HI- <i>Hind</i> III sites, Amp ^r , Tsr ^r | This study |

Table S2 Primers used in this study*.

| Primers | 5' to 3' primer sequences | Product size | Purpose |
|--------------------------------|---------------------------------------|--------------|-----------------------------|
| <i>bulZ</i> -FP ^a | GCTCTAGAATGAGAATTCAGGTTCTGGG | 822 bp | To amplify |
| <i>bulZ</i> -RP ^b | AAAAAGCTTTCAGGCGGCGAAGAGGTC GA | | <i>bulZ</i> |
| <i>bulY</i> -FP ^a | GCTCTAGAATGGATATTGATGTGCTGGG | 867 bp | To amplify |
| <i>bulY</i> -RP ^b | AAAAAGCTTTCACACCTGCGCCATGCGG C | | <i>bulY</i> |
| <i>Sx5140</i> -FP ^c | AAAGGATCCATGGACATCAAGGTATTG GGCCCG | 795 bp | To amplify <i>Sx5140</i> |
| <i>Sx5140</i> -RP ^b | AAAAAGCTTTCAGCCCGCGGCGGGCAC | | |
| <i>hrdB</i> -FP | AGCCGTTTCCATCGTTCC | 126 bp | Control for |
| <i>hrdB</i> -RP | GATCTGCCCATCAGCCTTTC | | qRT-PCR |
| <i>tsuR1</i> -FP | TGCTTCTGTGTTTCGACGAGTG | 105 bp | qRT-PCR |
| <i>tsuR1</i> -RP | TTGGACGGGAAGTGAAAGTAGAG | | of <i>tsuR</i> |
| <i>tsuS1</i> -FP | ATGTCGTCCTCGCCGAAA | 95 bp | qRT-PCR |
| <i>tsuS1</i> -RP | GTAGTGGTCGCTGGTGTGCT | | of <i>tsuS1</i> |
| <i>tsuS2</i> -FP | TGGAAGGCGACCACTTCA | 98 bp | qRT-PCR |
| <i>tsuS2</i> -RP | CGTTTCTGCGGCAATCAG | | of <i>tsuS2</i> |
| <i>fkbN</i> -FP | ATCACCTCACTGACGGAGTCG | 80 bp | qRT-PCR |
| <i>fkbN</i> -RP | TGGTCGGCTATCTCCCTGTT | | of <i>fkbN</i> |
| <i>fkbG</i> -FP | GGGTCGTTTCGATGTCGTGT | | |

Table S2 Cont.

| Primers | 5' to 3' primer sequences | Product size | Purpose |
|-----------------|---------------------------|--------------|---------------------------|
| <i>fkbG</i> -RP | GCTTCCGCAACAAGGTGA | 256 bp | qRT-PCR of <i>fkbG</i> |
| <i>fkbH</i> -FP | CTGGGATCTGGACAACACCTT | 143 bp | qRT-PCR |
| <i>fkbH</i> -RP | GGTCGTGGTCGTTCTTGCT | | of <i>fkbH</i> |
| <i>fkbI</i> -FP | ATGACATCGCAGGGAATGG | 85 bp | qRT-PCR |
| <i>fkbI</i> -RP | TGGTCAGCTCCTTCAGATAGGTC | | of <i>fkbI</i> |
| <i>fkbQ</i> -FP | CACGCCGATCACCGTATGTA | 121 bp | qRT-PCR |
| <i>fkbQ</i> -RP | GAAATGCCACCCGAGAA | | of <i>fkbQ</i> |
| <i>tcsA</i> -FP | GCTTCTTCTACTCCCACGGTCT | 81 bp | qRT-PCR |
| <i>tcsA</i> -RP | GGGTCATGTCGTTACCATC | | of <i>tcsA</i> |
| <i>tcsB</i> -FP | CGGACTGTTACCCGACGACT | 178 bp | qRT-PCR |
| <i>tcsB</i> -RP | CCCGTGCAGTTTGGAGAA | | of <i>tcsB</i> |
| <i>tcsD</i> -FP | CAGGTGTCGTTCTCCGACTG | 96 bp | qRT-PCR |
| <i>tcsD</i> -RP | GATTCTGCTGGCGTTGAGG | | of <i>tcsD</i> |

*FP and RP stand for forward primer and reverse primer in each primer pairs, respectively, the purpose of PCR using these primers was indicated in the table.

Underlined: a. *Xba*I site TCTAGA; b. *Hind*III site AAGCTT; c. *Bam*HI site GGATCC.

Supplementary figures

Figure S1. Effect of precursor addition on FK506 production in the transformants. Disodium malonate⁴ was selected as a precursor and was added at 4th day during fermentation of *Streptomyces* sp. CC01 and *Streptomyces* sp. C5140 at a final concentration of 5 mM. Samples were collected from the 5th day of fermentation, and the fermentation and detection procedures were described in Materials and methods in section 2.5 and 2.6.

Figure S2. Quantitative real-time RT-PCR analysis of *tsuS2* in *Streptomyces* sp. CC01, *Streptomyces* sp. CC02, *Streptomyces* sp. CC03 and *Streptomyces* sp. C5140. *tsuS2* expression levels at 24 h and 48 h were compared with that of the control strain *Streptomyces* sp. CC01, and was quantified by the fold change. The expression level of *tsuS2* at 72 h was undetectable and thus the result was not included in this manuscript.

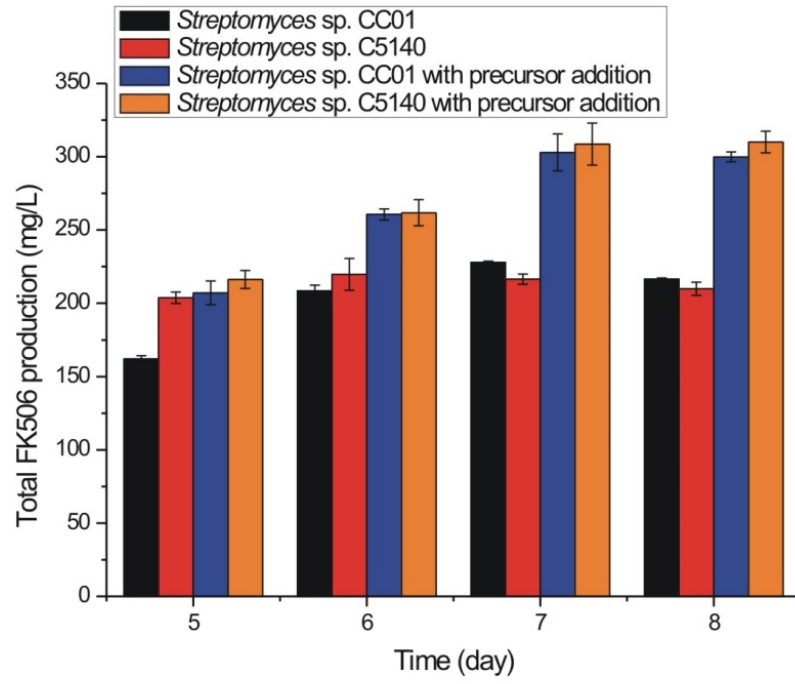


Figure S1

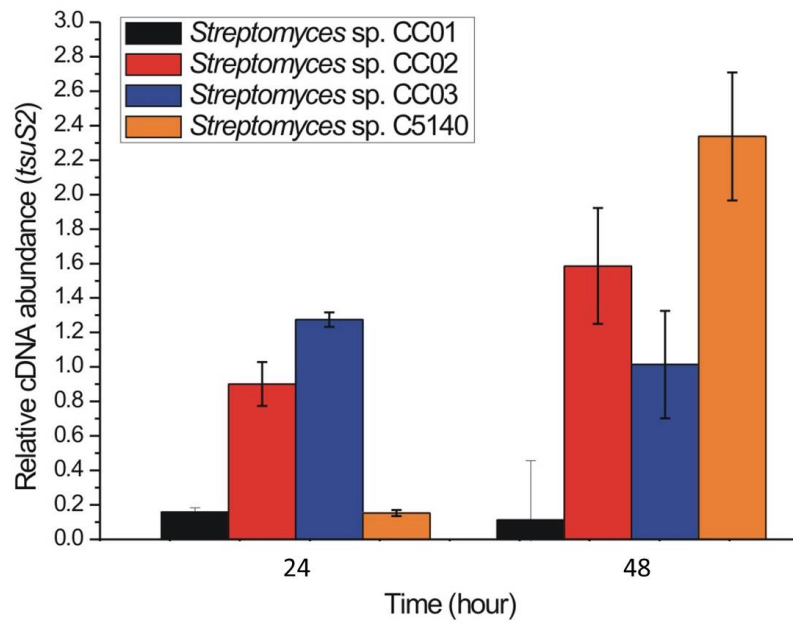


Figure S2

References

- [1] D. J. MacNeil, K. M. Gewain, C. L. Ruby, G. Dezeny, P. H. Gibbons and T. MacNeil, *Gene*, 1992, **111**, 61-68.
- [2] X. Q. Zhao, W. J. Li, W. C. Jiao, Y. Li, W. J. Yuan, Y. Q. Zhang, H. P. Klenk, J. W. Suh and F. W. Bai, *Int. J. Syst. Evol. Microbiol.*, 2009, **59**, 2870-2874.
- [3] J. Vara, M. Lewandowska-Skarbek, Y. G. Wang, S. Donadio and C. Hutchinson, *J. Bacteriol.*, 1989, **171**, 5872-5881.
- [4] W. J. Du, D. Huang, M. L. Xia, J. P. Wen and M. Huang, *J. Ind. Microbiol. Biotechnol.*, 2014, **41**, 1131-1143.