## 10.1071/CP16435\_AC © CSIRO 2017

## Supplementary Material: Crop & Pasture Science, 2017, 68(5), 434-441.

Transcriptional expression of aminoacyl tRNA synthetase genes of *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) on rice-leaf extract treatment and crystal structure of *Xoo* glutamyl-tRNA synthetase

*Thien-Hoang Ho*<sup>A,F</sup>, *Myoung-ki Hong*<sup>A,F</sup>, *Seunghwan Kim*<sup>B</sup>, *Jeong-Gu Kim*<sup>B</sup>, *Jongha Lee*<sup>A</sup>, *Kyoungho Jung*<sup>A</sup>, *Inho Lee*<sup>A</sup>, *Munyoung Choi*<sup>A</sup>, *Hyunjae Park*<sup>A</sup>, *Sanghee Lee*<sup>C</sup>, *Yeh-Jin Ahn*<sup>D</sup> and Lin-Woo Kang<sup>A,E</sup>

<sup>A</sup>Department of Biological Sciences, Konkuk University, 1 Hwayang dong, Gwangjin-gu, Seoul, 05029, Republic of Korea.

<sup>B</sup>Genomics Division, National Institute of Agricultural Sciences, Rural Development Administration (RDA), Jeonju 03016, Republic of Korea.

<sup>c</sup>Department of Biological Sciences, Myongji University, 116 Myongjiro, Yongin, Gyeonggido 449-728, Republic of Korea.

<sup>D</sup>Department of Life Science, Sangmyung University, 7 Hongji-dong, Jongno-gu, Seoul 03016, Korea.

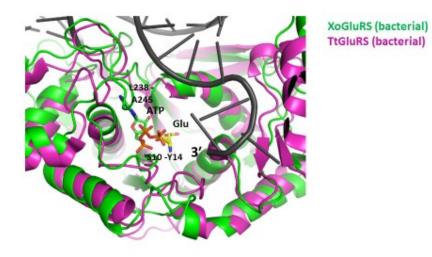
<sup>E</sup>Corresponding author. Email: lkang@konkuk.ac.kr

<sup>F</sup>These authors contributed equally to this work.

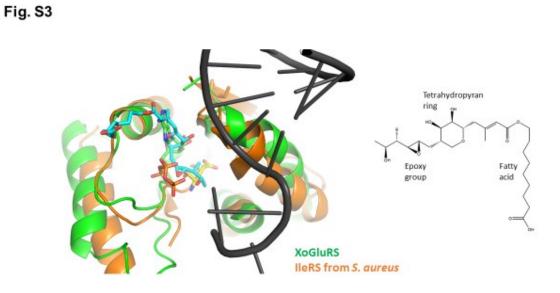


**Figure S1.** Sequence alignment of bacterial GluRSs. XoGluRS is GluRS from Xoo; TtGluRS (accession No.: WP\_011227935) from *Thermus thermophiles*; BbGluRS (accession No.: WP\_002665196) from *Borreliella burgdorferi*; TmGluRS (accession No.: WP\_010865423) from *Thermotoga maritima*; BtGluRS (accession No.: WP\_009890362) from *Burkholderia thailandensis*; MtGluRS' (accession No.: WP\_079066221) from *Mycobacterium tuberculosis*. The Rossmann-fold catalytic core domain is represented in purple box; the connective-peptide domain in orange box; the stem-contact domain in blue box; the anticodon-binding domain 1 in pink box; the anticodon-binding domain 2 in cyan box.





**Figure S2.** Superimposed ATP-binding site of XoGluRS (green) and TtGluRS (purple) in complex with tRNA<sup>Glu</sup>, ATP, and L-glutamol.



**Figure S3.** Superimposed Rossmann-fold domain of XoGluRS (green) and IleRS from *Staphylococcus aureus* (orange; PDB ID: 1FFY) and chemical structure of mupirocin. Mupirocin (cyan)-bound IleRS Rossmann-fold domain is superimposed onto the tRNA<sup>Glu</sup> (gray), ATP (green), and L-glutamol (yellow)-bound XoGluRS model (green).