**Supplementary material**

Type of the Paper (Article)

Lipopeptides Produced by Bacillus spp.: Detection of Genes and Meta-analysis of Their Activity Against Phytopathogenic Fungi

Nubia Noemi Cob-Calan1, Marcos Enrique Cua-Basulto2, Wilber Hernández-Montiel3, Rosa Yazmin Us- Camas1, Arturo Reyes-Ramírez2, Dany Alejandro Dzib Cauich1, Jairo Cristóbal-Alejo2, Esaú Ruiz-Sánchez2\*, and Emanuel Hernández-Núñez1\*

1 Departamento de Posgrado e Investigación, Instituto Tecnológico Superior de Calkiní. Av. Ah Canul S/N por carretera Federal, 24930 Calkiní, Campeche, México. ncalan@itescam.edu.mx, ryuscamas@itescam.edu.mx, dadzib@itescam.edu.mx. ehernandez@itescam.edu.mx

2 Tecnológico Nacional de México, Instituto Tecnológico de Conkal, Avenida Tecnológico s/n, C.P. 97345, Conkal, Yucatán, México. marcos.cua@itconkal.edu.mx, arturo.rr@conkal.tecnm.mx, jairoca54@hotmail.com, esau.ruiz@itconkal.edu.mx

3 Instituto de Agroingeniería, Universidad del Papaloapan, Av. Ferrocarril s/n, Ciudad Universitaria, Campus Loma Bonita, Oaxaca 68400, Oaxaca, México. wilber.montiel11@gmail.com

**\*** Correspondence: E.H.-N. ehernandez@itescam.edu.mx, and E.R. -S. esau.ruiz@itconkal.edu.mx Tel.: (+52 (999) 1055211

**Table S2.** Oligonucleotides used for detection of lipopeptide biosynthesis genes.[1]

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Lipopeptides** | **gene** | **First** | **Sequence (5’—3’)** | **Tm (°C)** | **Size (pb)** |
| Iturin A | *ituA* | ITUD1FITUD1R | GATGCGATCTCCTTGGATGTATCGTCATGTGCTGCTTGAG | 60 | 647 |
| Fengicine | *fenD* | FENDIFFEND1R | TTTGGCAGCAGGAGAAGTTTGCTGTCCGTTCTGCTTTTTC | 62 | 964 |
| Surfactin | *srfA* | SUR3FSUR3F | ACAGTATGGAGGCATGGTCTTCCGCCACTTTTTCAGTTT | 57 | 441 |

Tm: Melting Temperature; pb: Base pairs.

**Table S1.** General summary of data sources for Meta-analysis.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Species** | **Lipopeptide** | **Variable** | **Dose** | **Reference** |
| *F. graminearum* | Iturin | ICM (%) | 5, 10, 25, 50 μg/mL | [2] |
| *B. maydis* | Iturin | Severity | 50, 100, 300,500 μg/mL | [3] |
| *F. moniliforme* | Surfactin | ICM (%) | 6.25, 12.5, 25, 50, 100, 200 μg/mL | [4] |
| *R. stolonifer* | Fengicine | ICM (%) | 25, 50, 100, 200, 400, 600 μg/mL | [5] |
| *F. oxysporum* | Fengicine | ICM (%) | 12.5, 25, 50 μg/mL | [6] |
| *C. gloeosporioides* | Iturin | Severity | 10.50μg/mL | [7] |
| *C. gloeosporioides* | Surfactin | Severity | 10.50μg/mL | [7] |
| *Z. tritici* | Surfactin | Severity | 100 μg/mL | [8] |
| *Z. tritici* | Fengicine | Severity | 100 μg/mL | [8] |
| *A. flavus* | Surfactin | ICM (%) | 20, 40, 80 μg/mL | [9] |
| *A. alternata* | Iturin | ICM (%) | 60 μg/mL | [10] |
| *B. cinerea* | Iturin | ICM (%) | 60 μg/mL | [10] |
| *C. gloeosporioides* | Iturin | ICM (%) | 60 μg/mL | [10] |
| *F. oxysporum* | Iturin | ICM (%) | 60 μg/mL | [10] |
| *R. solani* | Iturin | ICM (%) | 60 μg/mL | [10] |
| *P. oryzae* | Iturin | Severity | 500 μg/mL | [11] |
| *P. oryzae* | Surfactin | Severity | 500 μg/mL | [11] |
| *S. oryzae* | Iturin | Severity | 500 μg/mL | [11] |
| *S. oryzae* | Surfactin | Severity | 500 μg/mL | [11] |
| *B. cinerea* | Iturin | Severity | 250, 500 μg/mL | [11] |
| *B. cinerea* | Surfactin | Severity | 250 μg/mL | [11] |
| *P. infestans* | Iturin | Severity | 500 μg/mL | [11] |
| *P. infestans* | Surfactin | Severity | 500 μg/mL | [11] |
| *P. trichina* | Iturin | Severity | 500 μg/mL | [11] |
| *C. gloeosporioides* | Iturin | Severity | 250, 500 μg/mL | [11] |
| *C. gloeosporioides* | Surfactin | Severity | 250, 500 μg/mL | [11] |

**Phylogenetic analysis**

The phylogenetic tree was constructed using the deduced amino acid sequence of iturin A, fengycin, and surfactin and their homologous protein sequences retrieved from the NBCI and UniProt database. The phylogenetic tree was constructed using the Maximum Likelihood method based on Jones-Taylor-Thornton (JTT) substitution using 1000 bootstrap through MEGA X software.[12,13] Sites with less than 95% coverage such as gaps, missing data, and ambiguous bases were partially eliminated. Amino acid sequences were aligned using MUSCLE with default MEGA X parameters. The substitution model was estimated using the best-fit substitution model (ML) function in the MEGA X software.



**Figure S1.** Phylogenetic tree of the deduced amino acid sequence of iturin A (ituA), surfactin (srfA), and fengycin (FenD) from Bacillus strains (CBRF5, CBRF6, CBRM9 CBRF15) and their homologous protein sequences. The accession number of the proteins used is indicated. Protein sequences were retrieved from the NCBI and UniProt database.

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