

SUPPLEMENTARY MATERIAL FOR

Biofilm Inhibitory Abscisic Acid Derivatives from the Plant-Associated Dothideomycete Fungus, *Roussoella* sp.

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S1. Morphological features and molecular phylogenetic

S1.1 Identification of *Roussoella* sp. MFLUCC 17-2059

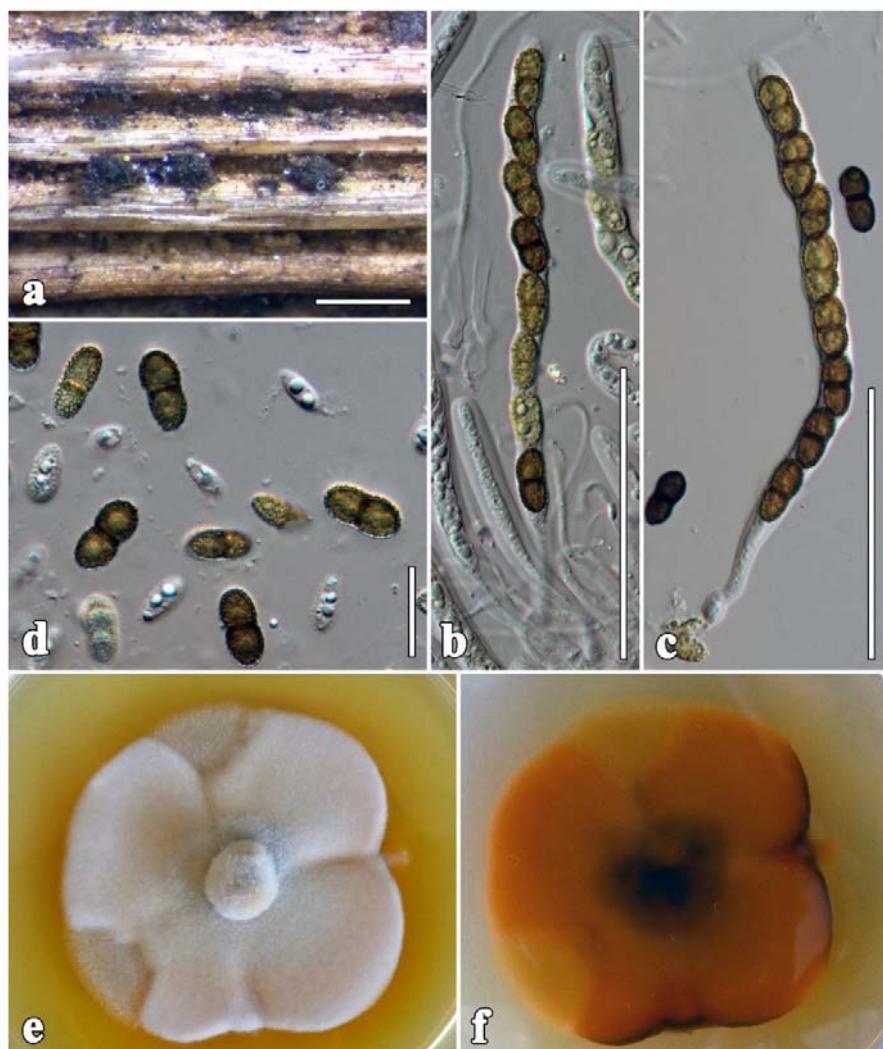


Figure S1.1 *Roussoella* sp. MFLUCC 17-2059 **a** Appearance of ascomata on host surface **b-c** Ascospores **d** Ascospores **e-f** Culture characters on YMG agar. **Scale bars:** a = 500 μ m, b-c = 50 μ m, d = 10 μ m.

Material examined: Dried branched *Clematis subumbellata* (Ranunculaceae), Thailand, living culture = MFLUCC 17-2059.

S1.2 Phylogenetic study

The aligned ITS and TEF-1 α sequences were concatenated to generate multigenes alignment phylogenetic tree. Maximum Likelihood were constructed by using CIPRES webportal online tools (Miller et al. 2010), including 1,000 bootstrap replicates. According to the data set combining the morphological features and phylogenetic analysis, the fungus was identified as *Roussoellaceae* member.

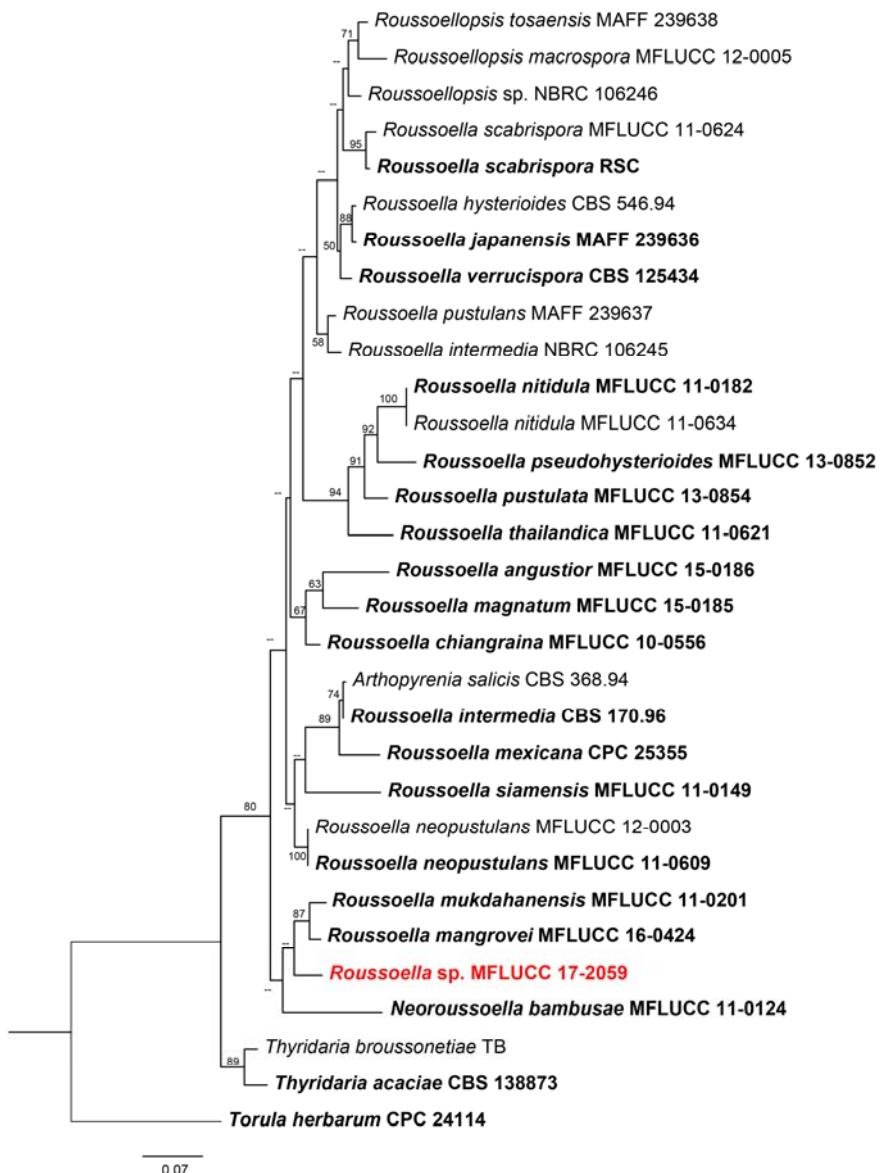
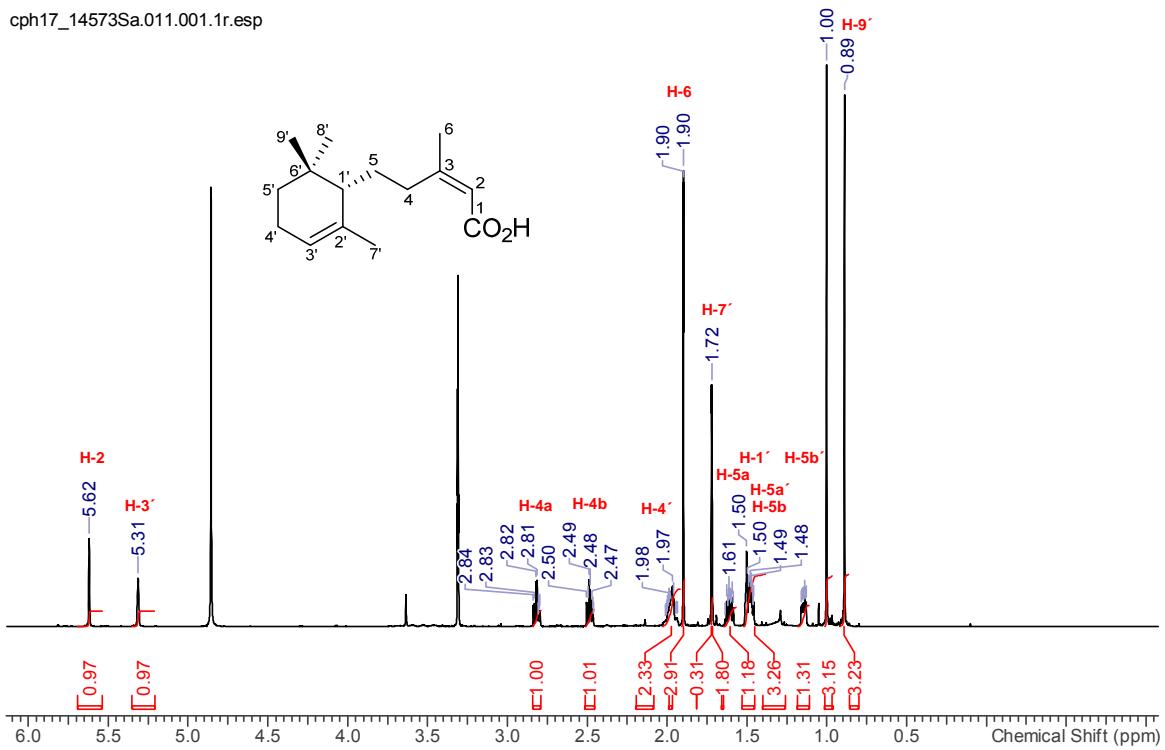
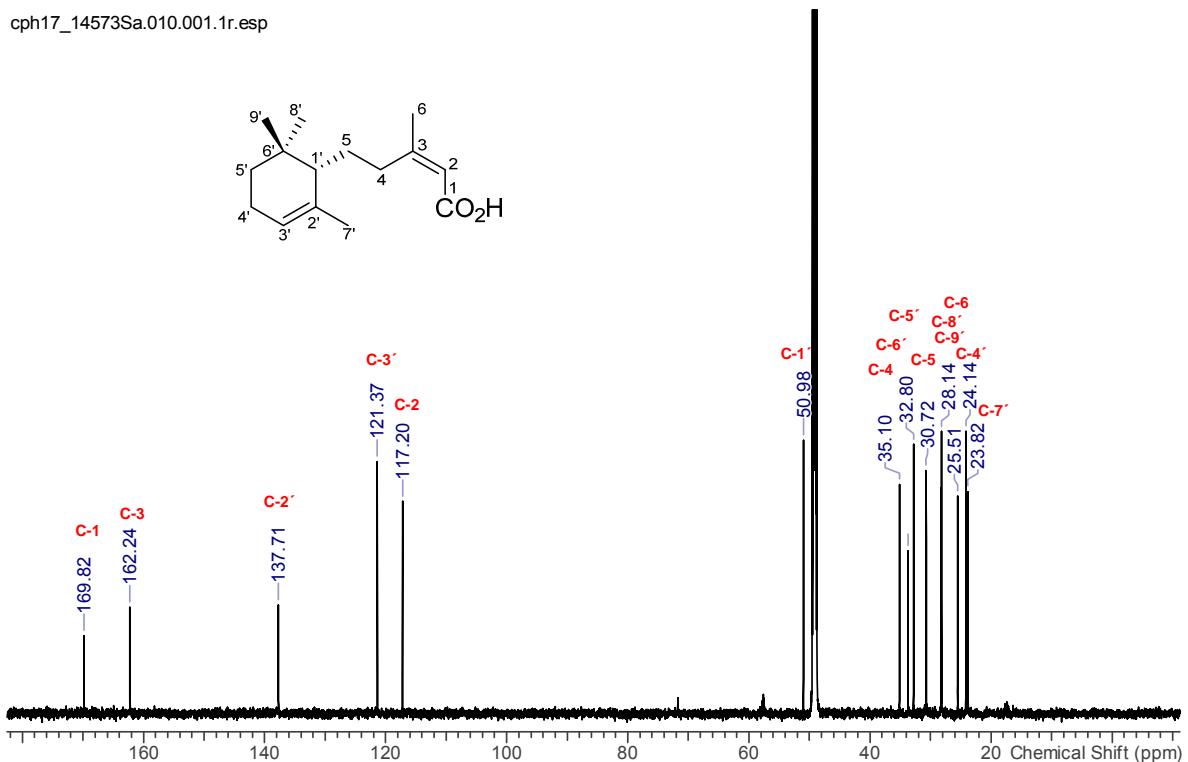


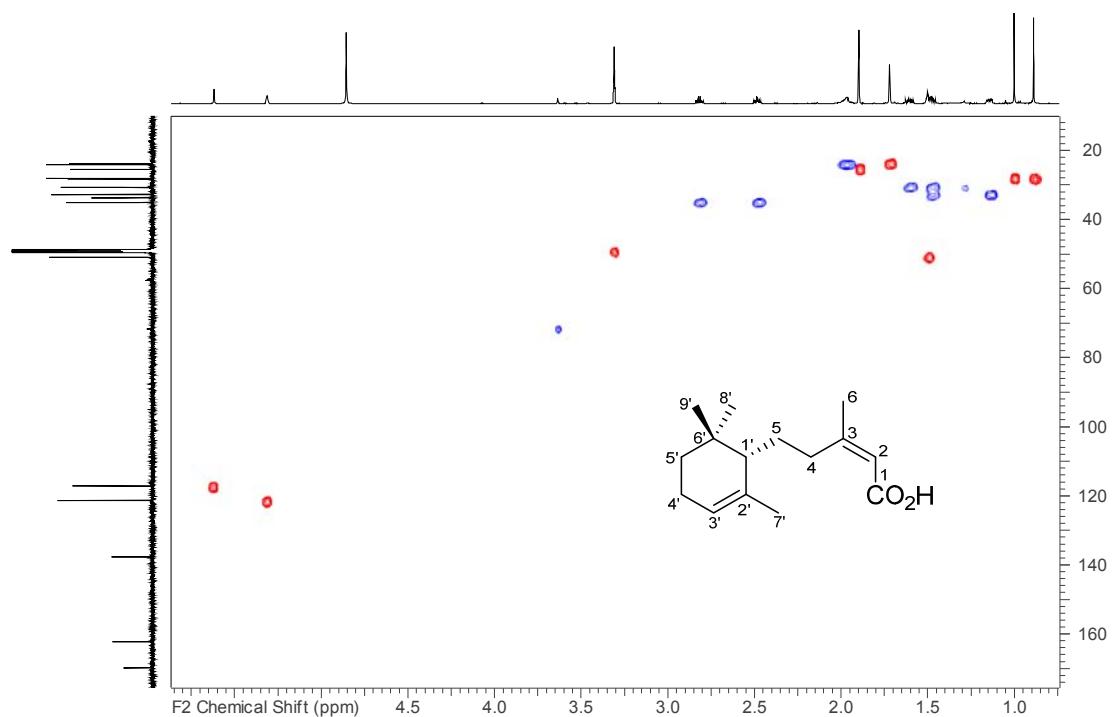
Fig S1.2. Phylogenetic tree of the combined data set of two markers, RAxML (ITS and TEF-1 α). The strain produced secondary metabolites in this study is marked in red.



S2. ^1H NMR spectrum ($\text{MeOH}-d_4$, 700 MHz) of roussoellenic acid (**1**).

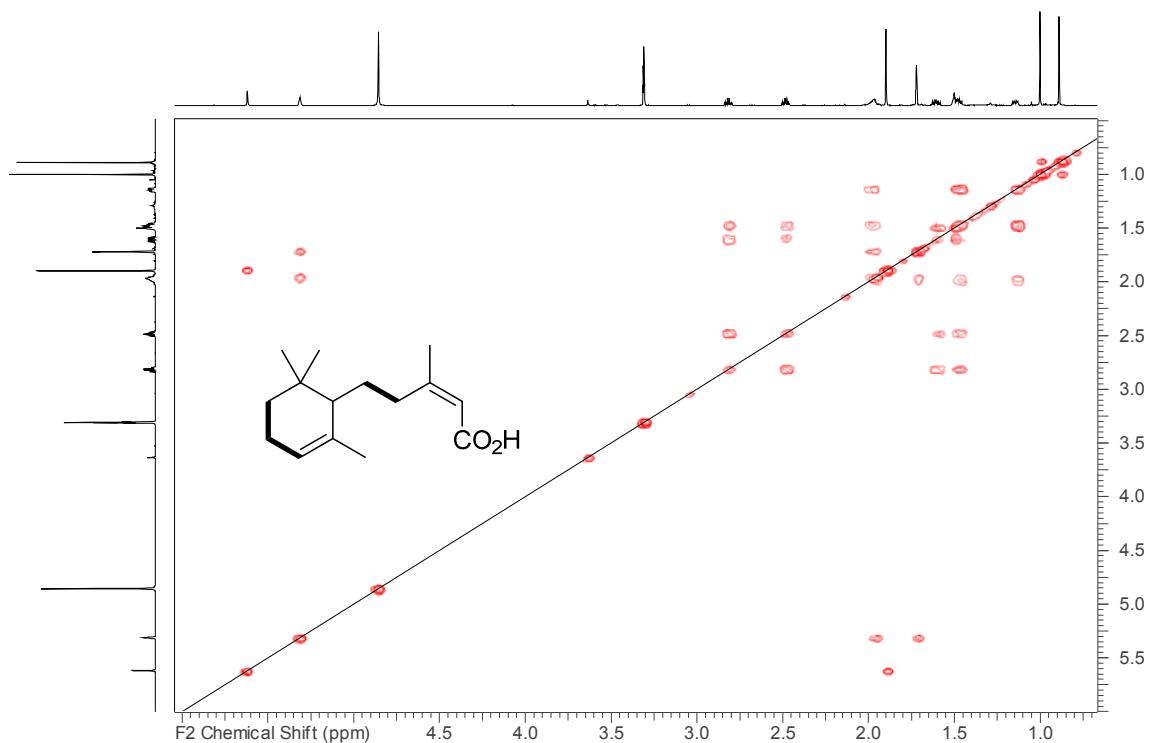


S3. ^{13}C NMR spectrum ($\text{MeOH}-d_4$, 175 MHz) of roussoellenic acid (**1**).

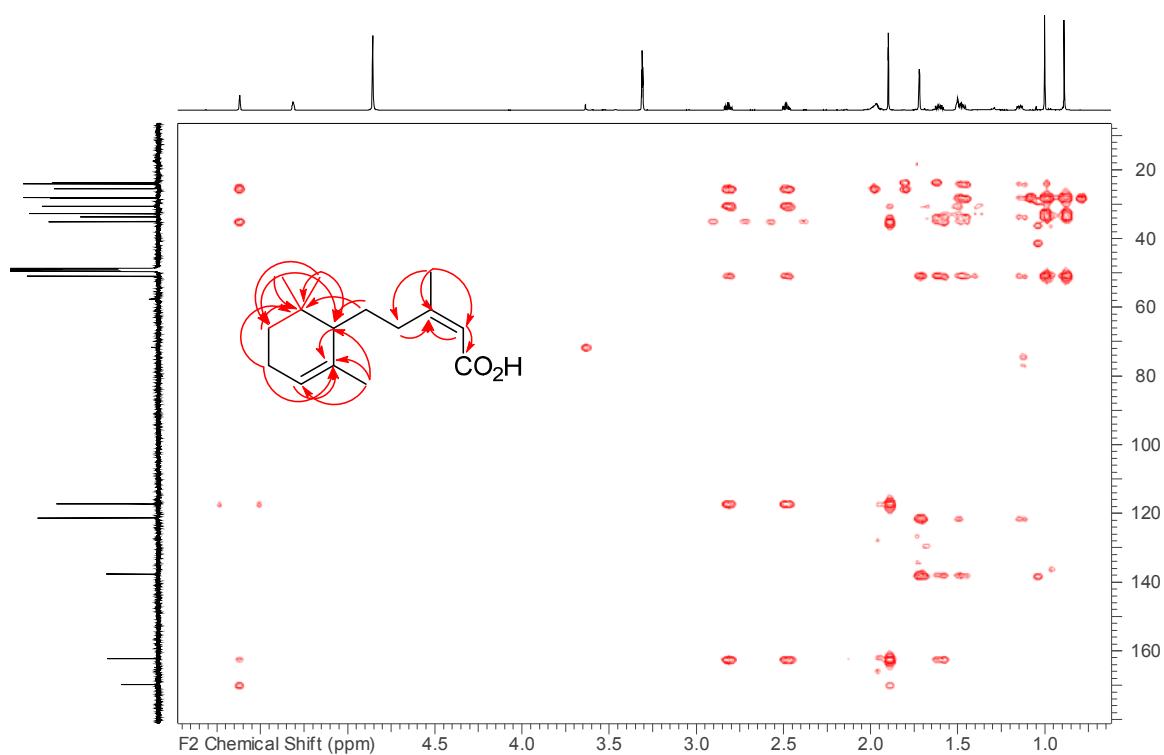


S4. HSQC-DEPT* edited spectrum of roussoellenic acid (**1**).

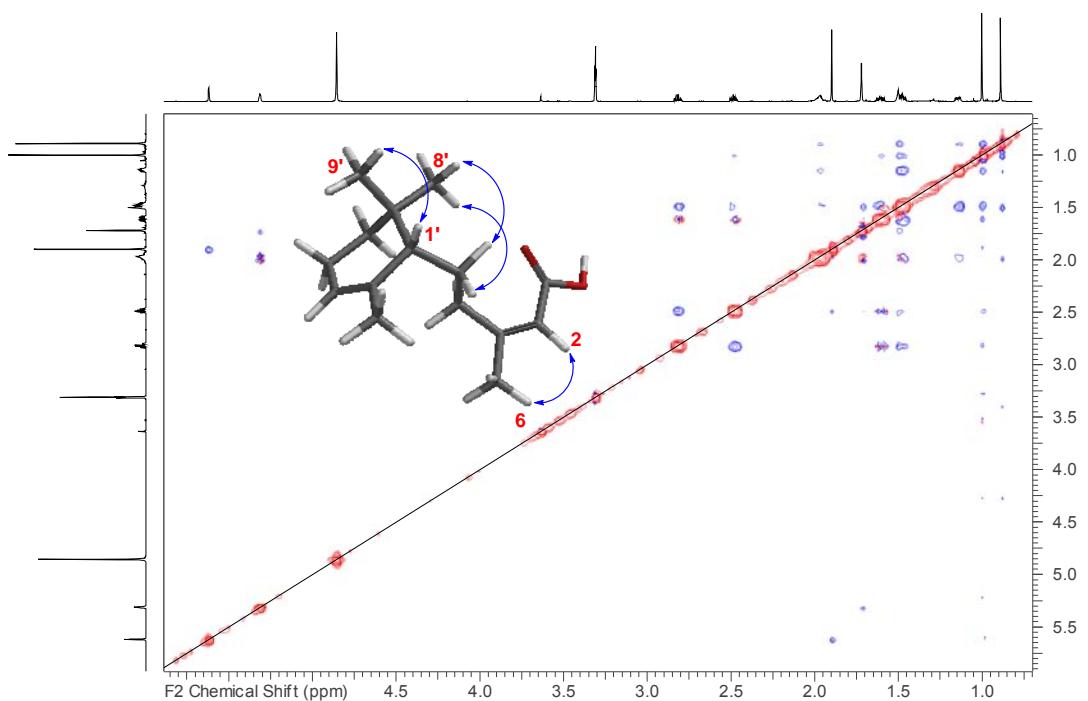
* blue crosspeak – CH_2 ; red crosspeak – CH/CH_3



S5. COSY spectrum of I roussoellenic acid (**1**).

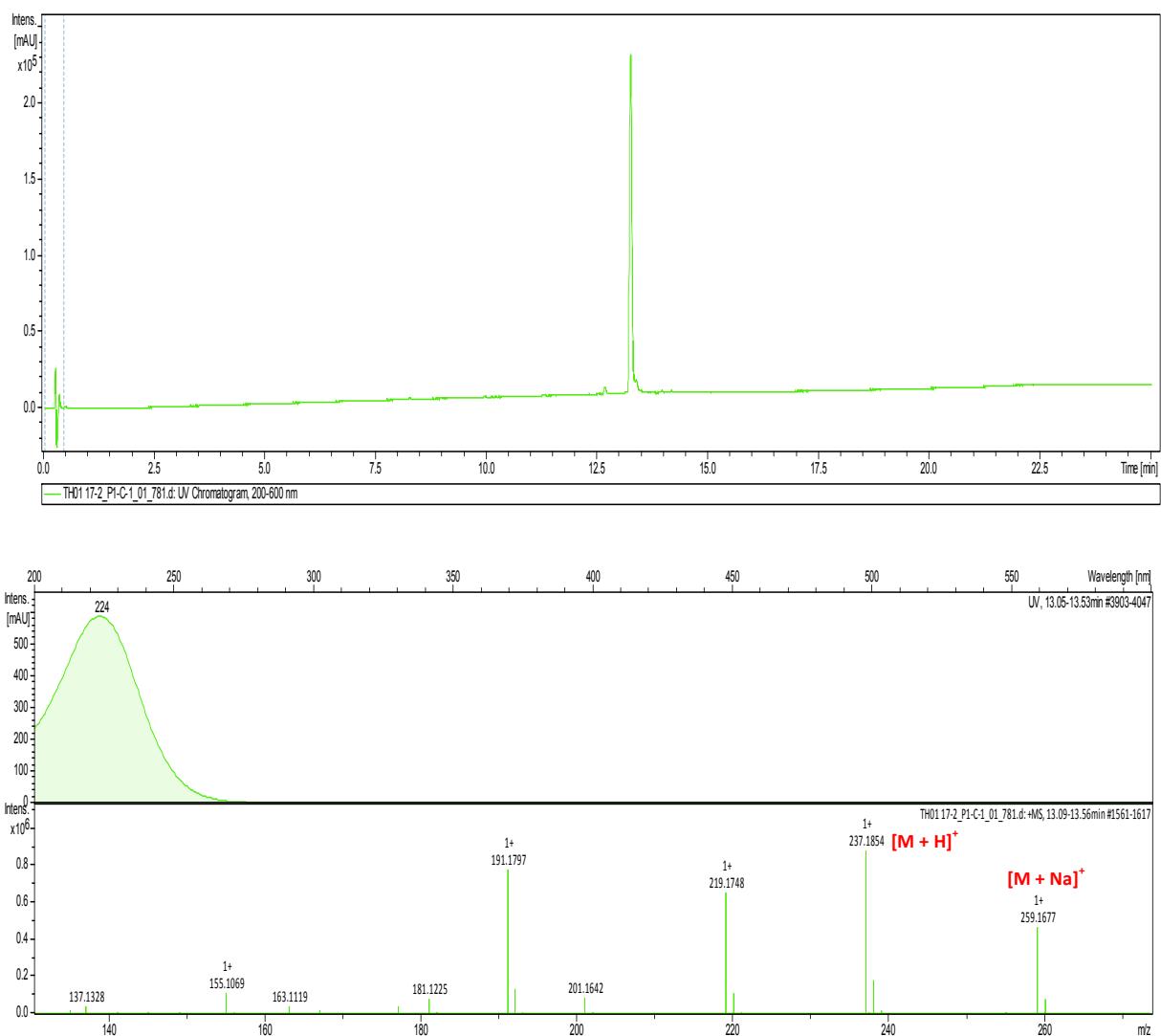


S6. HMBC spectrum of roussoellenic acid (**1**).

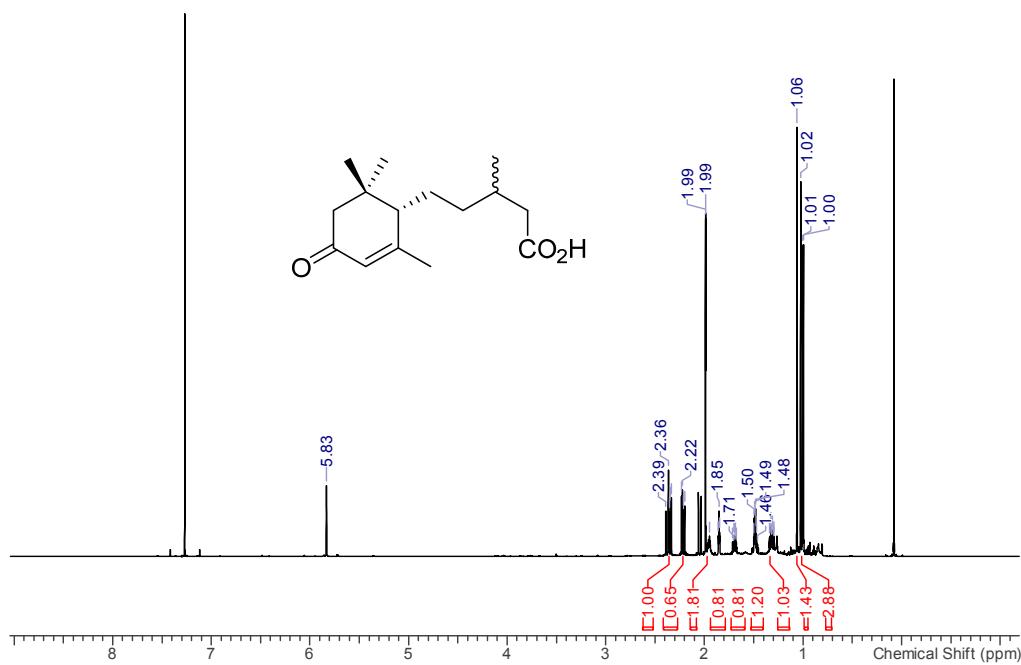


S7. NOESY spectrum of roussoellenic acid (**1**).

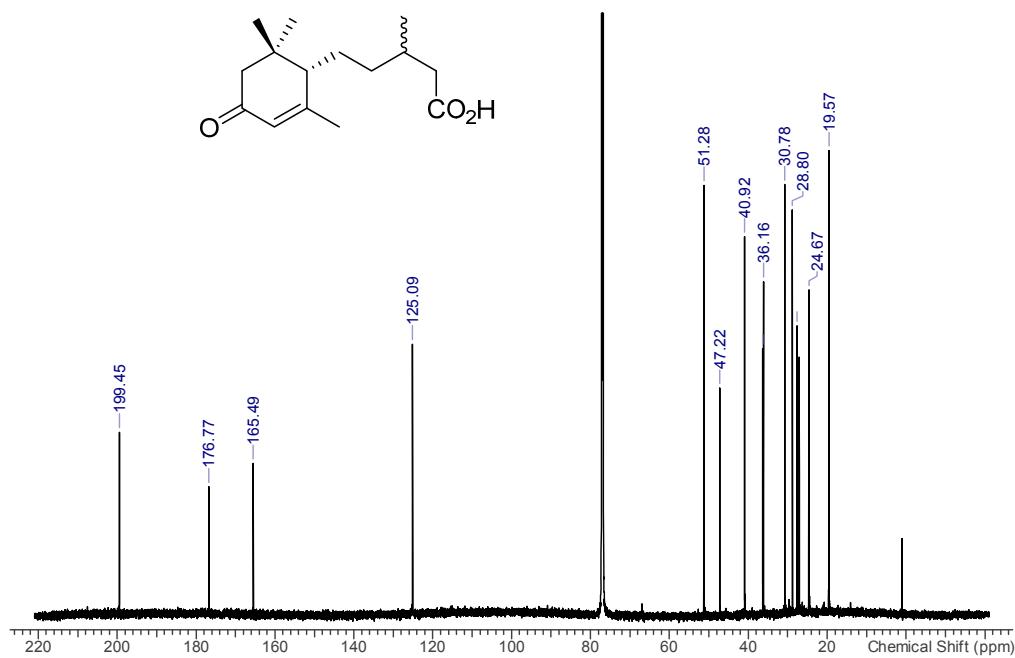
* NOE correlations are indicated by blue off-diagonal peaks.



S8. LC-DAD-HR-ESIMS spectrum of roussoellenic acid (**1**).

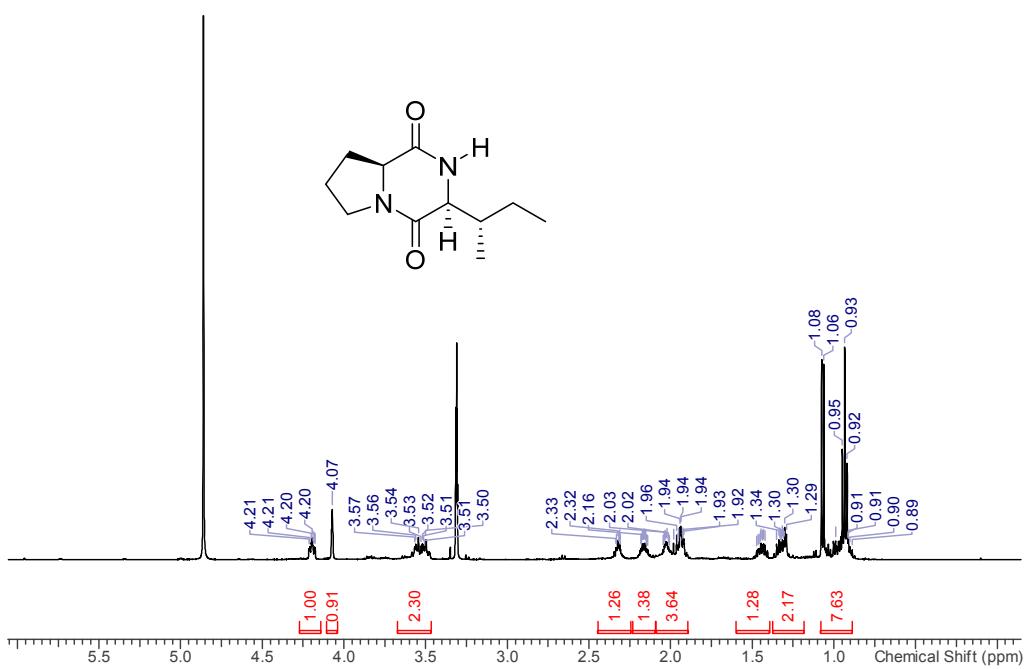


S9. ¹H NMR spectrum (CDCl₃, 700 MHz) of pestabacillin B (**2**).

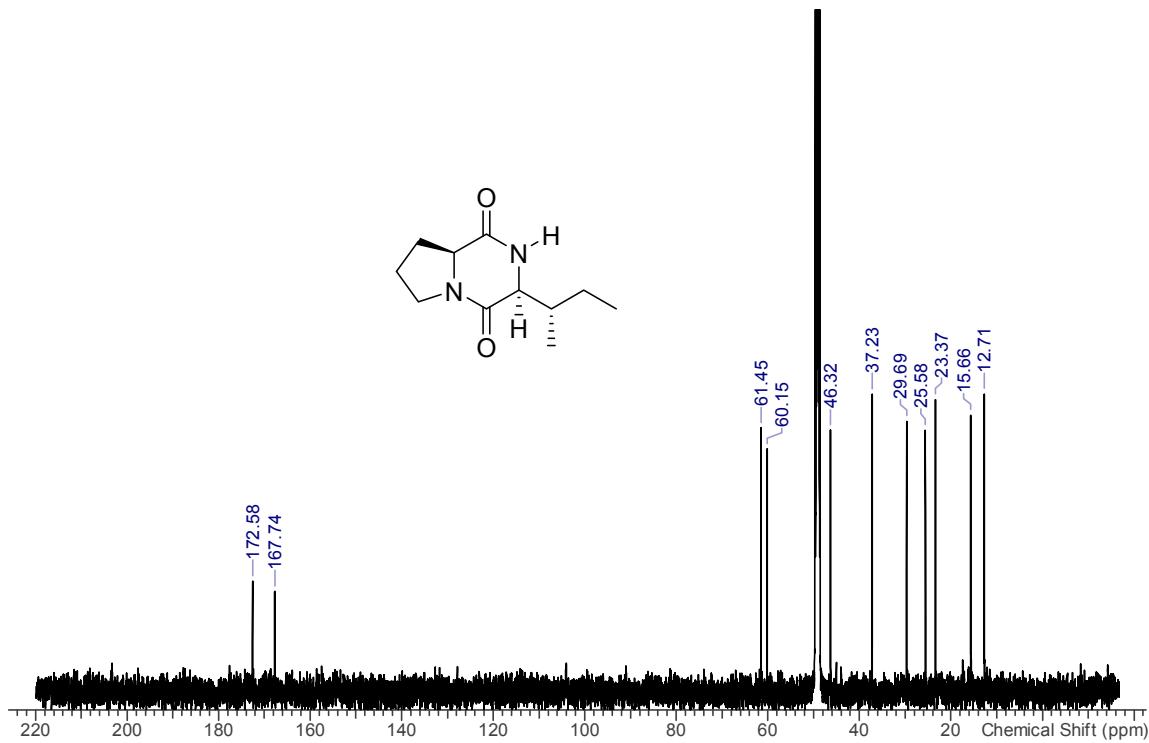


S10. ¹³C NMR spectrum (CDCl₃, 175 MHz) of pestabacillin B (**2**).

Liu, S.; Dai, H.; Heering, C.; Jania, C.; Lin, W.; Liu, Z.; Proksch, P. *Tetrahedron Lett.* **2017**, *58*, 257-261.



S11. ¹H NMR spectrum (MeOH-d₄, 700 MHz) of cyclo(S-Pro-S-Ile) (**3**).



S12. ¹³C NMR spectrum (MeOH-d₄, 175 MHz) of cyclo(S-Pro-S-Ile) (**3**).

Pedras, M.; Soledade C.; Yu, Y.; Liu, J.; Tandron-Moya, Y.A. *Zeitschrift fuer Naturforschung, C: J. Biosci.* **2005**, *60*, 717–722.

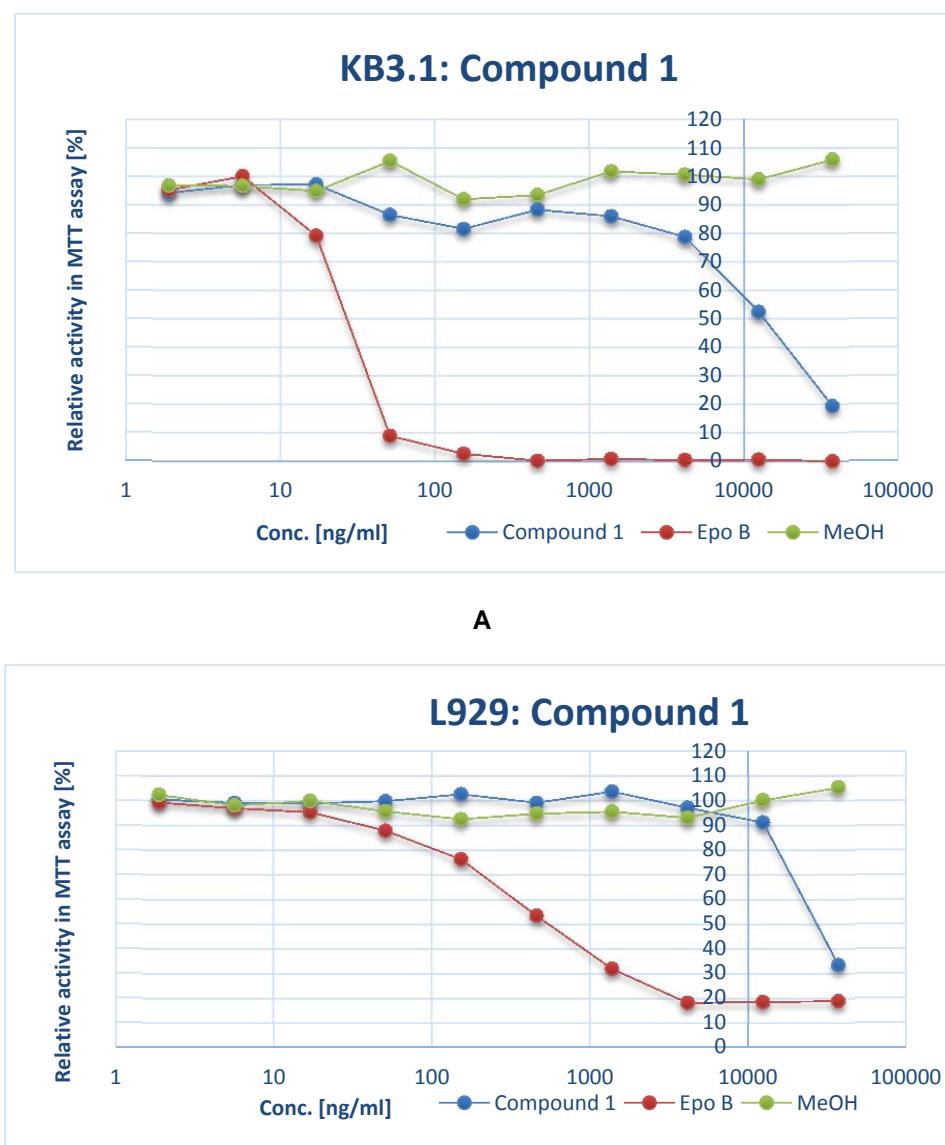
S13. Antimicrobial assay results of compounds 1-3.

Table S13. Antimicrobial activities of compounds 1-3.

Strain	Compound 1	Compound 2	Compound 3	Positive control ($\mu\text{g/mL}$)
Bacteria	MIC ($\mu\text{g/mL}$)			
<i>Bacillus subtilis</i> DSM 10	66.7	-	-	4.1
<i>Chromobacterium violaceum</i> DSM 30191	-	-	-	0.4
<i>Escherichia coli</i> DSM 1116	-	-	-	3.3
<i>Micrococcus luteus</i> DSM 1790	66.7	-	-	0.2
<i>Mycobacterium smegmatis</i> ATCC 700084	-	-	-	3.3
<i>Pseudomonas aeruginosa</i> PA14	-	-	-	1.7
<i>Staphylococcus aureus</i> DSM 346	66.7	-	-	3.3
Fungi				
<i>Candida albicans</i> DSM 1665	-	-	-	66.7
<i>Mucor hiemalis</i> DSM 2656	66.7	-	-	33.3
<i>Pichia anomala</i> DSM 6766	-	-	-	33.3
<i>Rhodoturula glutinis</i> DSM 10134	-	-	-	33.3
<i>Schizosaccharomyces pombe</i> DSM 70572	-	-	-	33.3
Cell lines	Cytotoxicity IC ₅₀ ($\mu\text{g/mL}$)			
KB 3.1	14	-		5×10^{-4}
L929	27	-		1.1×10^{-3}

(-) no activity

S14. Cytotoxicity assay results of compounds **1**.



A

L929: Compound 1

B

Figure S14. Proliferation assay. Graph of MTT assay after 5 days of incubation. *In vitro* cytotoxicity (IC_{50}) of compounds **1** was determined against HeLa (KB-3.1) (A) and mouse fibroblast L929 (B) cell lines. Epothilone B was used as the positive control while methanol was used as the negative control.

S15. Biofilm inhibitory activity of compounds 1-3.

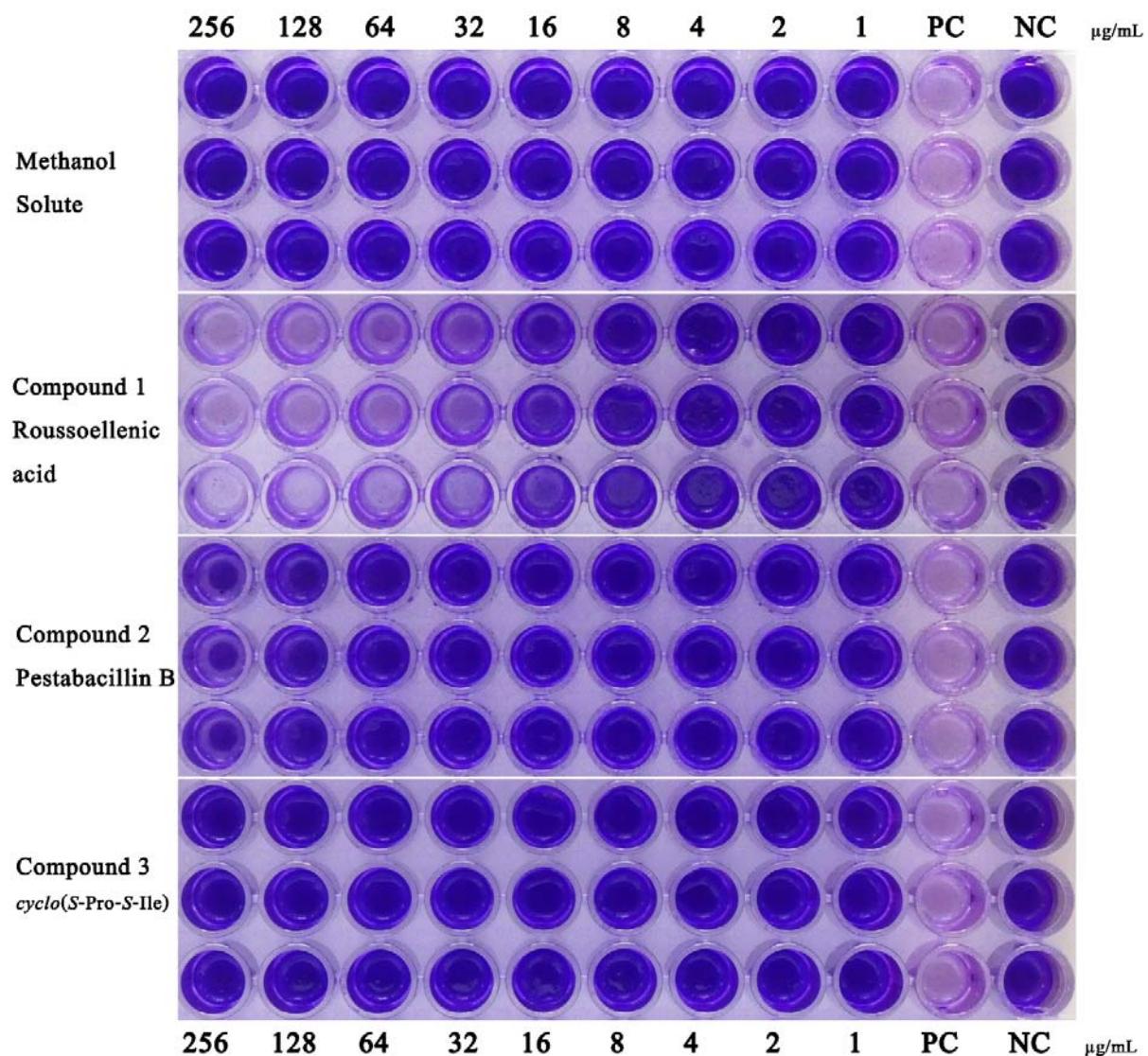


Figure S15. Inhibition of the biofilm formation from *Staphylococcus aureus*. CASO medium containing 4% glucose was used as the negative control and tetracycline (100 µg/mL) was used as the positive control.