

## Molecular Genetic Mining of the *Aspergillus*

### Secondary Metabolome: Discovery

### of the Emericellamide Biosynthetic Pathway

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#### Supplemental Results

#### Detailed structural Characterization of Emericellamide C-F

Emericellamide C (**2**) was isolated as a white powder. The molecular formula  $C_{30}H_{53}N_5O_7$  was established by its  $^{13}C$  NMR, DEPT and HRFABMS data, representing seven indices of hydrogen deficiency (IHD). The  $^1H$  NMR spectrum in DMSO- $d_6$  (Table S3) exhibited five typical amide NH signals ( $\delta_H$  8.20, 8.11, 7.82, 7.61, and 7.53), one ester carbinol proton ( $\delta_H$  4.81), and six  $\alpha$ -amino protons [ $\delta_H$  4.38 (1H), 4.01-4.09 (3H), 3.91 (1H), and 3.58 (1H)].  $^{13}C$  NMR and DEPT spectral (Table S4) data exhibited six amide or ester carbonyl groups ( $\delta_C$  172.9, 171.6, 171.4, 171.2, 170.9, and 169.4) and one oxygenated carbon [ $\delta_C$  75.0 (d)], which correlated with  $\delta_H$  4.81 in the gHMQC spectrum. These results, together with the IR absorption band at  $3307\text{ cm}^{-1}$  (amide N-H stretching),  $1758\text{ cm}^{-1}$  (ester C=O stretching), and  $1636\text{ cm}^{-1}$  (amide C=O stretching), suggested that emericellamide C (**2**) is a monocyclic depsipeptide containing five amino acids and one ester functional group. Emericellamide A (**1**), a known compound isolated from marine-derived *Emericella* sp. [1] and also found in this study, exhibited similar  $^1H$  and  $^{13}C$  NMR spectral features with emericellamide C (**2**), as it also contained two alanines (Ala-1 and Ala-2), one leucine (Leu), one valine (Val), and one glycine (Gly). The spectral differences between emericellamide A and C are that emericellamide A (**1**) has an additional methyl group [ $\delta_H$  0.82;  $\delta_C$  12.9, CH<sub>3</sub>-31] and the carbinol proton in emericellamide A (**1**) [ $\delta_H$  4.93 (br d,  $J$  = 9.6 Hz, H-22)] is shifted upfield to  $\delta_H$  4.81 (ddd,  $J$  = 9.2, 8.4, 3.6 Hz, H-22) in emericellamide C (**2**). These results suggested that Me-31 in emericellamide A is replaced by H in emericellamide C (**2**).

Emericellamide D (**3**), a constitutional isomer of emericellamide C (**2**), also has similar  $^1H$  and  $^{13}C$  NMR spectral features with emericellamide A (**1**) (Tables S3 and S4). Emericellamide A (**1**) and D (**3**) differ only in that CH<sub>3</sub>-30 in emericellamide A (**1**) is replaced by H in emericellamide D (**3**). This generated one methylene [ $\delta_H$  2.68 (1H, dd,  $J$  = 13.6, 9.6 Hz) and 2.18 (1H, d,  $J$  = 13.6 Hz);

$\delta_C$  30.8 (t), CH<sub>2</sub>-21] in emericellamide D (**3**) instead of one methine [ $\delta_H$  2.87 (1H, dq,  $J = 9.6, 6.8$  Hz);  $\delta_C$  41.1 (d), CH-21] in emericellamide A (**1**). Emericellamides E (**4**) and F (**5**), another pair of constitutional isomers, both have the molecular formula C<sub>32</sub>H<sub>57</sub>N<sub>5</sub>O<sub>7</sub>. The <sup>1</sup>H NMR spectra of emericellamides E (**4**) and F (**5**) are superimposable with emericellamides C (**2**) and D (**3**), respectively. This result, together with the <sup>13</sup>C and DEPT spectra exhibiting two more CH<sub>2</sub> carbons, suggested that the structures of emericellamide E (**4**) and F (**5**) extended two more carbons on the aliphatic side chains of emericellamides C (**2**) and D (**3**), respectively. 2D NMR (gHMQC, gHMBC, gCOSY, and ROESY) data led to full assignments of emericellamides C – F (**2** – **5**) (Tables S3 and S4) and also confirmed the assigned structures. The absolute configurations of the amino acids in emericellamides C (**2**) and D (**3**) were determined as all L-isomers by Marfey's reagent after hydrolysis as described by Oh et al [1]. The configurations of C-21 and C-22 in emericellamides C (**2**) and E (**4**) were same as emericellamide A (**1**) because they all have large coupling constants (> 9.0 Hz) between H-21 and H-22. The configurations of C-22 and C-23 in emericellamides D (**3**) and F (**5**) were also the same as emericellamide A (**1**) because all have small coupling constants (< 4.0 Hz) between H-22 and H-23 [1]. The similar optical rotation values of these compounds also support these configurations.

## Supplemental Methods

Optical rotations were measured on a JASCO P-1010 digital polarimeter, whereas IR spectra were recorded on a Perkin–Elmer Spectrum BX. <sup>1</sup>H and <sup>13</sup>C NMR spectra were run on a Varian Unity Plus 400 spectrometer, whereas HRFABMS spectra were obtained on a JEOL MSRoute mass spectrometer. LC/MS was carried out using a ThermoFinnigan LCQ Advantage ion trap mass spectrometer with a RP C<sub>18</sub> column (Alltech Prevail C18 3  $\mu$ m 2.1 X 100mm) at a flow rate of 125  $\mu$ L/min. The solvent gradient for HPLC was 95 % MeCN/H<sub>2</sub>O (solvent B) in 5 % MeCN/H<sub>2</sub>O (solvent A) both containing 0.05 % formic acid: 0 % B from 0 to 5 min, 0 to 100 % B from 5 to 35 min, 100 to 0 % B from 35 to 40 min, and re-equilibration with 100 % B from 40 to 45 min. Positive ion electrospray ionization (ESI) was used for the detection of the analytes. Conditions for MS included a capillary voltage 5.0 kV, a sheath gas flow rate at 60 arbitrary units, an auxiliary gas flow rate at 10 arbitrary units, and the ion transfer capillary temperature at 350 °C.

## Spectral Data of Emericellamides

Emericellamide A (**1**) characterization: white powder;  $[\alpha]_D^{24}$  -50.2 (MeOH, c 0.1); IR  $\nu_{\max}^{\text{ZnSe}}$  3306, 2930, 1743, 1652, 1549 cm<sup>-1</sup>; For <sup>1</sup>H and <sup>13</sup>C NMR data, see Table S3 and S4. HRFABMS,  $[M+H]^+$   $m/z$  found 610.4154; calc. for C<sub>31</sub>H<sub>56</sub>N<sub>5</sub>O<sub>7</sub>: 610.4180.

Emericellamide C (**2**) characterization: white powder;  $[\alpha]_D^{24}$  -37.4 (MeOH, c 0.1); IR  $\nu_{\max}^{\text{ZnSe}}$  3307, 2962, 1758, 1636, 1551 cm<sup>-1</sup>; For <sup>1</sup>H and <sup>13</sup>C NMR data, see

Table S3 and S4. HRFABMS,  $[M+H]^+$   $m/z$  found 596.4026; calc. for  $C_{30}H_{54}N_5O_7$ : 596.4023.

Emericellamide D (**3**) characterization: white powder;  $[\alpha]_D^{25}$  -65.3 (MeOH, c 0.1); IR  $\nu_{\max}^{\text{ZnSe}}$  3306, 2930, 1745, 1656, 1529  $\text{cm}^{-1}$ ; For  $^1\text{H}$  and  $^{13}\text{C}$  NMR data, see Table S3 and S4. HRFABMS,  $[M+H]^+$   $m/z$  found 596.4016; calc. for  $C_{30}H_{54}N_5O_7$ : 596.4023.

Emericellamide E (**4**) characterization: white powder;  $[\alpha]_D^{25}$  -35.2 (MeOH, c 0.1); IR  $\nu_{\max}^{\text{ZnSe}}$  3307, 2962, 1758, 1636, 1551  $\text{cm}^{-1}$ ; For  $^1\text{H}$  and  $^{13}\text{C}$  NMR data, see Table S3 and S4. HRFABMS,  $[M+H]^+$   $m/z$  found 624.4324; calc. for  $C_{32}H_{58}N_5O_7$ : 624.4336.

Emericellamide F (**5**) characterization: white powder;  $[\alpha]_D^{25}$  -46.4 (MeOH/ $\text{CHCl}_3$  1:1, c 0.05); IR  $\nu_{\max}^{\text{ZnSe}}$  3306, 2930, 1758, 1637, 1549  $\text{cm}^{-1}$ ; For  $^1\text{H}$  and  $^{13}\text{C}$  NMR data, see Table S3 and S4. HRFABMS,  $[M+H]^+$   $m/z$  found 624.4312; calc. for  $C_{32}H_{58}N_5O_7$ : 624.4336.

**Table S1. *A. nidulans* Strains Used in This Study**

| strain      | genotype  | reference  |
|-------------|---|------------|
| WT (TN02A3) | <i>pyrG89; pyroA4, nkuA::argB</i>                             | [2]        |
| ΔAN0607     | <i>pyrG89; pyroA4, nkuA::argB; AN0607::pyrG A. fumigatus</i>  | this study |
| ΔAN1242     | <i>pyrG89; pyroA4, nkuA::argB; AN1242::pyrG A. fumigatus</i>  | this study |
| ΔAN2545     | <i>pyrG89; pyroA4, nkuA::argB; AN2545::pyrG A. fumigatus</i>  | this study |
| ΔAN2621     | <i>pyrG89; pyroA4, nkuA::argB; AN2621::pyrG A. fumigatus</i>  | this study |
| ΔAN8412     | <i>pyrG89; pyroA4, nkuA::argB; AN8412::pyrG A. fumigatus</i>  | this study |
| ΔAN9244     | <i>pyrG89; pyroA4, nkuA::argB; AN9244::pyrG A. fumigatus</i>  | this study |
| ΔAN2542     | <i>pyrG89; pyroA4, nkuA::argB; AN2542::pyrG A. fumigatus</i>  | this study |
| ΔAN2543     | <i>pyrG89; pyroA4, nkuA::argB; AN2543::pyrG A. fumigatus</i>  | this study |
| ΔAN2544     | <i>pyrG89; pyroA4, nkuA::argB; AN2544::pyrG A. fumigatus</i>  | this study |
| ΔAN2546     | <i>pyrG89; pyroA4, nkuA::argB; AN2546::pyrG A. fumigatus</i>  | this study |
| ΔAN2547     | <i>pyrG89; pyroA4, nkuA::argB; AN2547::pyrG A. fumigatus</i>  | this study |
| ΔAN2548     | <i>pyrG89; pyroA4, nkuA::argB; AN2548::pyrG A. fumigatus</i>  | this study |
| ΔAN2549     | <i>pyrG89; pyroA4, nkuA::argB; AN2549::pyrG A. fumigatus</i>  | this study |
| ΔAN2550     | <i>pyrG89; pyroA4, nkuA::argB; AN2550::pyrG A. fumigatus</i>  | this study |
| ΔAN10325    | <i>pyrG89; pyroA4, nkuA::argB; AN10325::pyrG A. fumigatus</i> | this study |

**Table S2. Primers Used in This Study**

| primer     | Sequence (5'→3')  |
|------------|---|
| AN0607.3P1 | GGT GTC GTA TAG GGA TCG G                                   |
| AN0607.3P2 | CAG TGA AGT GGA ACG AGT CG                                  |
| AN0607.3P3 | CGA AGA GGG TGA AGA GCA TTG CGA TGC CAA ACA CAA GGC C       |
| AN0607.3P4 | GCA TCA GTG CCT CCT CTC AGA CAG TGC ATA CAT CGC ATT GAA TGG |
| AN0607.3P5 | GCA GTC ACC CAG CAT GGG                                     |
| AN0607.3P6 | CGC ATG CGA GAG ATA AGA CC                                  |
| AN1242.3P1 | CCT TGC GTT GGC GAC TGG                                     |
| AN1242.3P2 | GCG ACT GGC CTA TCC TGG                                     |
| AN1242.3P3 | CGA AGA GGG TGA AGA GCA TTG CGT CAA TTA GGT ATT AGT AAC C   |
| AN1242.3P4 | GCA TCA GTG CCT CCT CTC AGA CAG TCG TTG TTC CAT TTG TTT GGC |
| AN1242.3P5 | CCT AGT CTA TAA AGC TCG CC                                  |
| AN1242.3P6 | CGA CGA GTC TTA TCC AAA CAC                                 |
| AN2545.3P1 | GTC ATT ATT GCA TCA GGG G                                   |
| AN2545.3P2 | GAT CGG TTT CCA TCA GTC C                                   |
| AN2545.3P3 | CGA AGA GGG TGA AGA GCA TTG GAG GCC GCT ATC AAA GGC G       |
| AN2545.3P4 | GCA TCA GTG CCT CCT CTC AGA CAG CAA ACC CCT GTA GAA GCA GG  |
| AN2545.3P5 | GCT GTT GGC AAA AGG TAA AGG                                 |
| AN2545.3P6 | CCG TTT ATT CCA GAG TCA CC                                  |
| AN2621.3P1 | GCG GCG TCG ATT TGC TGG                                     |
| AN2621.3P2 | GCT ACT CTC ATT TTG GCT GC                                  |
| AN2621.3P3 | CGA AGA GGG TGA AGA GCA TTG GGA GGG CAA AAG CCT GAG G       |
| AN2621.3P4 | GCA TCA GTG CCT CCT CTC AGA CAG AAC GTA TGC ATA ATG AGG     |
| AN2621.3P5 | CAG CTT GAC ACC ACT ATA TGC                                 |
| AN2621.3P6 | GTG ACC AAA ACG GTT ATT TGC                                 |
| AN8412.3P1 | GAC ACG GTC AAC ATG CAG G                                   |
| AN8412.3P2 | GGT ATC TGT GAA TGT CTC CC                                  |
| AN8412.3P3 | CGA AGA GGG TGA AGA GCA TTG GCA AGT ATC AAG TAA AAC TGG     |
| AN8412.3P4 | GCA TCA GTG CCT CCT CTC AGA CAG GTA TGT CTA ACT CAG CAT CCC |
| AN8412.3P5 | GGA TAT ATA CGA CGT TCC ATC                                 |
| AN8412.3P6 | GGG AGT AGC TTT GTT TGA GC                                  |
| AN9244.3P1 | GTT GCG GAT GAA GGA AAC C                                   |
| AN9244.3P2 | GCT CCA CCA GCT TTA GCC G                                   |
| AN9244.3P3 | CGA AGA GGG TGA AGA GCA TTG CGA TGC TAA CGT ACG GAC C       |
| AN9244.3P4 | GCA TCA GTG CCT CCT CTC AGA CAG GCT TGA TAG AGA TCA TTG     |
| AN9244.3P5 | CCT GCA TTC CCC AGA ATG C                                   |
| AN9244.3P6 | CCT GGT AGT TTG GCA CGC                                     |
| AN2542.3P1 | TGG ACC GGA TCT GTA CTA TGG                                 |
| AN2542.3P2 | CGG AGT TTT ACA GAG GAC AAG C                               |
| AN2542.3P3 | CGA AGA GGG TGA AGA GCA TTG AAG AGT GTG TGT GCG AAA GG      |
| AN2542.3P4 | GCA TCA GTG CCT CCT CTC AGA CAG ACA GCT GCA GCC AAT AAA CC  |
| AN2542.3P5 | CTT TCT CCC GAT TCA GTT GG                                  |
| AN2542.3P6 | GAA GCC GTG GAA CTT CTA ACC                                 |
| AN2543.3P1 | GCG CAA TGA GAC AAC AAA GG                                  |
| AN2543.3P2 | GTA AAC CCG CTG GTA CAT GG                                  |
| AN2543.3P3 | CGA AGA GGG TGA AGA GCA TTG TGA AGA CGG GAT GTT CTT GG      |
| AN2543.3P4 | GCA TCA GTG CCT CCT CTC AGA CAG AAC ATG CTA GCC CTG ACA CC  |
| AN2543.3P5 | GGC ATC AGA CGA TCA GAA GG                                  |
| AN2543.3P6 | GGA GGA GTA ATG GGA TGA AGG                                 |
| AN2544.3P1 | CGC ACC GTG TTT ACT TGT CC                                  |
| AN2544.3P2 | TCT GTG GCT GAA TTG ACA GG                                  |
| AN2544.3P3 | CGA AGA GGG TGA AGA GCA TTG TGA GGG CTC TGA AGA CAT GG      |
| AN2544.3P4 | GCA TCA GTG CCT CCT CTC AGA CAG CTG CTT CTA CAG GGG TTT GG  |

AN2544.3P5 GGC TTC CCC CAG TAT ATT TCC  
 AN2544.3P6 AGA TCT ACC AGC GCC AGT CC  
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 AN2546.3P1 ACG GCA GTA AGC AGA AGA GC  
 AN2546.3P2 ACA ACT CGA CGA AGC TGT CC  
 AN2546.3P3 CGA AGA GGG TGA AGA GCA TTG GGA TAG CCG ATG CTA GTT CC  
 AN2546.3P4 GCA TCA GTG CCT CCT CTC AGA CAG CGT CAT TCT GGG GTA AAA CG  
 AN2546.3P5 CGA CGA GTC CAA TAT TGT CG  
 AN2546.3P6 GGG ACG CCT AGA TCA TTT GG  
 -----  
 AN2547.3P1 ATC ACG TCC TCG CTT AGA GG  
 AN2547.3P2 GAG GTA CGC TGA GCT TGA CG  
 AN2547.3P3 CGA AGA GGG TGA AGA GCA TTG TGA CCG TCT GAA TAG CAT GG  
 AN2547.3P4 GCA TCA GTG CCT CCT CTC AGA CAG GTG CTA CCT CTA ATG TGT CTA  
 CGC  
 AN2547.3P5 CAC CTA CGC GAG AAA AGT GG  
 AN2547.3P6 TGG AAA CTA TGA GCG ACA CC  
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 AN2548.3P1 GTT GCG CTT CCT GAT AGT CG  
 AN2548.3P2 AGC CTC TCA CTG TCT GAC TCG  
 AN2548.3P3 CGA AGA GGG TGA AGA GCA TTG CCT GAG ATT TGG TCA CAG TCC  
 AN2548.3P4 GCA TCA GTG CCT CCT CTC AGA CAG GGA AAT GGA CCT GTA TGT GC  
 AN2548.3P5 CCT TCC AAG TTT CGA GAT CC  
 AN2548.3P6 AAC TCT CAC AAG CCC ACA CG  
 -----  
 AN2549.3P1 CTC AGC AGT GTG GTC TCA GC  
 AN2549.3P2 AGC AGT CGG TCT CCA CGT CG  
 AN2549.3P3 CGA AGA GGG TGA AGA GCA TTG GCA AGG CGA GTT GTA GAA GG  
 AN2549.3P4 GCA TCA GTG CCT CCT CTC AGA CAG TTT TAT GGA GCC AGC GTA GC  
 AN2549.3P5 CCA ACT GGA CAG ATC CAA CC  
 AN2549.3P6 CCA CCC AGT TCA CTA AAG TCG  
 -----  
 AN2550.3P1 CAG AAT GAC TGA GGG TCA TGG  
 AN2550.3P2 TTC TGG TAG AGG TCT GCT TCG  
 AN2550.3P3 CGA AGA GGG TGA AGA GCA TTG CCT AAG CTG CAC AGT GAG AGG  
 AN2550.3P4 GCA TCA GTG CCT CCT CTC AGA CAG TCG TGG TCT GCT AGT TCT TGG  
 AN2550.3P5 TTC ACA GCA CAG CGT AAA GC  
 AN2550.3P6 CTA GGC CGC TAT TTC TCA GG  
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 AN10325.3P1 CGC ATG TCT TTA TGC AGA GC  
 AN10325.3P2 GGT GGA AGA CGG TTT GAA GA  
 AN10325.3P3 CGA AGA GGG TGA AGA GCA TTG GGG TTG TGA AGA AGG TTT GC  
 AN10325.3P4 GCA TCA GTG CCT CCT CTC AGA CAG TCA TGA CGT GAC CAC TCA CC  
 AN10325.3P5 TCG CCA ATC CTC TCT TTA CC  
 AN10325.3P6 ATG ATC TTC ACC CCC AGT GC  
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Blue and red sequences are tails that anneal to the *A. fumigatus* pyrG fragment (Afp<sub>pyrG</sub>) during fusion PCR

**Table S3. <sup>1</sup>H-NMR Data for Emericellamides A and C – F (400 MHz in DMSO-*d*<sub>6</sub>)<sup>a</sup>**

|               | position | A   | C   | D   | E   | F   |
|---------------|----------|---|---|---|---|---|
| NRP (L-Ala-1) | 2        | 4.00–4.14 <sup>b</sup>                        | 4.03–4.09 <sup>b</sup>                        | 4.04–4.11 <sup>b</sup>                          | 4.01–4.09 <sup>b</sup>                        | 4.04–4.11 <sup>b</sup>                          |
|               | 3        | 1.24 (d, 6.8)                                 | 1.22 (d, 6.8)                                 | 1.24 (d, 6.8)                                   | 1.22 (d, 6.8)                                 | 1.24 (d, 6.8)                                   |
| NRP (L-Ala-2) | 2-NH     | 8.04 (br s)                                   | 7.82 (d, 4.4)                                 | 8.15 (d, 4.4)                                   | 7.85 (br s)                                   | 8.16 (d, 4.0)                                   |
|               | 5        | 4.00–4.14 <sup>b</sup>                        | 4.03–4.09 <sup>b</sup>                        | 4.09–4.17 <sup>b</sup>                          | 4.01–4.09 <sup>b</sup>                        | 4.09–4.17 <sup>b</sup>                          |
| NRP (L-Leu)   | 6        | 1.21 (d, 6.8)                                 | 1.23 (d, 6.8)                                 | 1.22 (d, 6.8)                                   | 1.23 (d, 6.8)                                 | 1.22 (d, 6.8)                                   |
|               | 5-NH     | 7.44 (d, 7.2)                                 | 7.53 (d, 7.2)                                 | 7.42 (d, 7.6)                                   | 7.55 (d, 7.2)                                 | 7.45 (d, 7.2)                                   |
| NRP (L-Val)   | 8        | 4.00–4.14 <sup>b</sup>                        | 4.01–4.04 <sup>b</sup>                        | 4.04–4.11 <sup>b</sup>                          | 4.01–4.09 <sup>b</sup>                        | 4.04–4.11 <sup>b</sup>                          |
|               | 9        | 1.54–1.62 <sup>b</sup>                        | 1.50–1.62 <sup>b</sup>                        | 1.51–1.61 <sup>b</sup>                          | 1.50–1.62 <sup>b</sup>                        | 1.51–1.61 <sup>b</sup>                          |
|               | 10       | 1.54–1.62 <sup>b</sup>                        | 1.50–1.62 <sup>b</sup>                        | 1.51–1.61 <sup>b</sup>                          | 1.50–1.62 <sup>b</sup>                        | 1.51–1.61 <sup>b</sup>                          |
|               | 11       | 0.80 (d, 6.8)                                 | 0.82 (d, 6.8)                                 | 0.82 (d, 6.8)                                   | 0.82 (d, 6.8)                                 | 0.82 (d, 6.8)                                   |
|               | 12       | 0.89 (d, 6.8)                                 | 0.89 (d, 6.8)                                 | 0.90 (d, 6.8)                                   | 0.89 (d, 6.8)                                 | 0.90 (d, 6.8)                                   |
| NRP (L-Gly)   | 8-NH     | 8.29 (d, 8.4)                                 | 8.20 (d, 7.2)                                 | 8.19 (d, 8.4)                                   | 8.32 (d, 7.2)                                 | 8.31 (d, 7.6)                                   |
|               | 14       | 3.98 (t, 7.6)                                 | 3.91 (t, 7.2)                                 | 3.93 (t, 7.6)                                   | 3.91 (t, 7.2)                                 | 3.93 (t, 7.6)                                   |
|               | 15       | 1.90 (m)                                      | 1.91 (m)                                      | 1.93 (m)  | 1.93 (m)                                      | 1.94 (m)  |
|               | 16       | 0.87 (d, 6.8)                                 | 0.89 (d, 6.8)                                 | 0.90 (d, 6.8)                                   | 0.89 (d, 6.8)                                 | 0.90 (d, 6.8)                                   |
| NRP (Gly)     | 17       | 0.88 (d, 6.8)                                 | 0.91 (d, 6.8)                                 | 0.88 (d, 6.8)                                   | 0.90 (d, 6.8)                                 | 0.88 (d, 6.8)                                   |
|               | 14-NH    | 8.22 (d, 8.4)                                 | 8.11 (d, 7.2)                                 | 8.10 (d, 7.6)                                   | 8.26 (d, 7.6)                                 | 8.25 (d, 7.6)                                   |
|               | 19       | 3.62 (dd, 17.6, 2.4);<br>4.31 (dd, 17.6, 5.2) | 3.58 (dd, 17.6, 2.0);<br>4.38 (dd, 17.6, 6.0) | 3.75 (dd, 17.2, 4.0);<br>4.09–4.17 <sup>b</sup> | 3.59 (dd, 17.6, 2.4);<br>4.35 (dd, 17.6, 6.0) | 3.76 (dd, 17.2, 4.0);<br>4.09–4.17 <sup>b</sup> |
| PK            | 19-NH    | 7.45 (br s)                                   | 7.61 (dd, 6.0, 2.0)                           | 7.54 (t, 4.0)                                   | 7.56 (br, s)                                  | 7.51 (br s)                                     |
|               | 21       | 2.87 (dq, 9.6, 6.8)                           | 2.73 (dq, 9.2, 6.8)                           | 2.18 (d, 13.6); 2.68<br>(dd, 13.6, 9.6)         | 2.72 (dq, 9.2, 6.8)                           | 2.18 (d, 13.6); 2.68<br>(dd, 13.6, 9.6)         |
|               | 22       | 4.93 (br d, 9.6)                              | 4.81 (ddd, 9.2, 8.4,<br>3.6)                  | 5.04 (dd, 9.6, 3.6)                             | 4.82 (ddd, 9.2, 8.4,<br>3.6)                  | 5.05 (dd, 9.6, 2.4)                             |
|               | 23       | 1.67 (m)                                      | 1.42 (m); 1.50–1.62 <sup>b</sup>              | 1.54–1.68 <sup>b</sup>                          | 1.42 (m); 1.50–1.62 <sup>b</sup>              | 1.54–1.68 <sup>b</sup>                          |
|               | 24       | 1.05–1.16 <sup>b</sup>                        | 1.14–1.30 <sup>b</sup>                        | 1.02 (m); 1.18–1.34 <sup>b</sup>                | 1.14–1.30 <sup>b</sup>                        | 1.02 (m); 1.18–1.34 <sup>b</sup>                |
|               | 25       | 0.98–1.06 <sup>b</sup>                        | 1.14–1.30 <sup>b</sup>                        | 1.18–1.34 <sup>b</sup>                          | 1.14–1.30 <sup>b</sup>                        | 1.18–1.34 <sup>b</sup>                          |
|               | 26~28    | 1.18–1.34 <sup>b</sup>                        | 1.14–1.30 <sup>b</sup>                        | 1.18–1.34 <sup>b</sup>                          | 1.14–1.30 <sup>b</sup>                        | 1.18–1.34 <sup>b</sup>                          |
|               | 29       | 0.84 (t, 6.8)                                 | 0.85 (t, 6.8)                                 | 0.86 (t, 7.6)                                   | 1.14–1.30 <sup>b</sup>                        | 1.18–1.34 <sup>b</sup>                          |
|               | 30       | 0.90 (d, 6.8)                                 | 0.93 (d, 6.8)                                 | 0.83 (d, 7.6)                                   | 1.14–1.30 <sup>b</sup>                        | 1.18–1.34 <sup>b</sup>                          |
|               | 31       | 0.82 (d, 6.8)                                 |   |   | 0.85 (t, 6.8)                                 | 0.86 (t, 7.6)                                   |
|               | 32       |   |   |   | 0.93 (d, 6.8)                                 | 0.83 (d, 7.6)                                   |

<sup>a</sup> Figures in parentheses are multiplicities and coupling constants (*J*) in Hz.<sup>b</sup> Data obtained from gHMQC spectrum and/or compared with the spectral data of emericellamide A (1) from literature [1].

**Table S4. <sup>13</sup>C-NMR Data for Emericellamides A and C – F (100 MHz in DMSO-*d*<sub>6</sub>)<sup>a</sup>**

|               | position | A         | C         | D         | E                     | F                     |
|---------------|----------|-----------|-----------|-----------|-----------------------|-----------------------|
| NRP (L-Ala-1) | 1        | 171.4 (s) | 171.6 (s) | 171.8 (s) | 171.4 (s)             | 171.9 (s)             |
|               | 2        | 48.2 (d)  | 48.2 (d)  | 48.4 (d)  | 48.3 (d)              | 48.4 (d)              |
|               | 3        | 16.3 (q)  | 16.2 (q)  | 16.1 (q)  | 16.2 (q)              | 16.1 (q)              |
| NRP (L-Ala-2) | 4        | 171.5 (s) | 171.4 (s) | 171.4 (s) | 171.6 (s)             | 171.4 (s)             |
|               | 5        | 47.2 (d)  | 47.8 (d)  | 47.4 (d)  | 47.7 (d)              | 47.3 (d)              |
| NRP (L-Leu)   | 6        | 18.3 (q)  | 17.4 (q)  | 18.1 (q)  | 17.5 (q)              | 18.2 (q)              |
|               | 7        | 170.9 (s) | 170.9 (s) | 170.8 (s) | 171.0 (s)             | 170.9 (s)             |
|               | 8        | 51.7 (d)  | 51.8 (d)  | 51.6 (d)  | 51.8 (d)              | 51.6 (d)              |
|               | 9        | 39.4 (t)  | 38.9 (t)  | 39.4 (t)  | 39.0 (t)              | 39.5 (t)              |
|               | 10       | 24.5 (d)  | 24.5 (d)  | 24.4 (d)  | 24.5 (d)              | 24.4 (d)              |
| NRP (L-Val)   | 11       | 20.7 (q)  | 20.7 (q)  | 20.7 (q)  | 20.7 (q)              | 20.7 (q)              |
|               | 12       | 23.2 (q)  | 23.3 (q)  | 23.2 (q)  | 23.2 (q)              | 23.2 (q)              |
|               | 13       | 171.2 (s) | 171.2 (s) | 171.2 (s) | 171.2 (s)             | 171.3 (s)             |
|               | 14       | 60.2 (d)  | 60.2 (d)  | 60.2 (d)  | 60.3 (d)              | 60.3 (d)              |
|               | 15       | 30.1 (d)  | 29.8 (d)  | 29.8 (d)  | 29.8 (d)              | 29.8 (d)              |
|               | 16       | 18.8 (q)  | 18.7 (q)  | 18.6 (q)  | 18.7 (q)              | 18.7 (q)              |
|               | 17       | 19.1 (q)  | 19.0 (q)  | 19.1 (q)  | 19.0 (q)              | 19.1 (q)              |
| NRP (Gly)     | 18       | 168.7 (s) | 169.4 (s) | 169.0 (s) | 169.4 (s)             | 169.0 (s)             |
|               | 19       | 42.5 (t)  | 42.2 (t)  | 42.4 (t)  | 42.2 (t)              | 42.3 (t)              |
| PK            | 20       | 172.9 (s) | 172.9 (s) | 169.3 (s) | 172.8 (s)             | 169.3 (s)             |
|               | 21       | 41.1 (d)  | 42.7 (d)  | 38.0 (t)  | 42.8 (d)              | 38.1 (t)              |
|               | 22       | 76.6 (d)  | 75.0 (d)  | 74.4 (d)  | 75.0 (d)              | 74.4 (d)              |
|               | 23       | 33.2 (d)  | 28.8 (t)  | 36.4 (d)  | 28.8 (t)              | 36.5 (d)              |
|               | 24       | 33.5 (t)  | 31.1 (t)  | 32.0 (t)  | 31.3 (t)              | 32.0 (t)              |
|               | 25       | 26.6 (t)  | 23.5 (t)  | 26.3 (t)  | 23.5 (t)              | 26.4 (t)              |
|               | 26       | 28.9 (t)  | 28.6 (t)  | 28.9 (t)  | 28.9 <sup>b</sup> (t) | 29.2 <sup>b</sup> (t) |
|               | 27       | 31.2 (t)  | 30.9 (t)  | 31.2 (t)  | 28.8 <sup>b</sup> (t) | 28.7 <sup>b</sup> (t) |
|               | 28       | 22.1 (t)  | 22.1 (t)  | 22.1 (t)  | 28.7 <sup>b</sup> (t) | 28.9 <sup>b</sup> (t) |
|               | 29       | 14.0 (q)  | 14.0 (q)  | 14.0 (q)  | 30.9 (t)              | 31.3 (t)              |
|               | 30       | 14.3 (q)  | 14.4 (q)  | 14.7 (q)  | 22.1 (t)              | 22.1 (t)              |
|               | 31       | 12.9 (q)  |           |           | 14.0 (q)              | 14.0 (q)              |
|               | 32       |           |           |           | 14.4 (q)              | 14.7 (q)              |

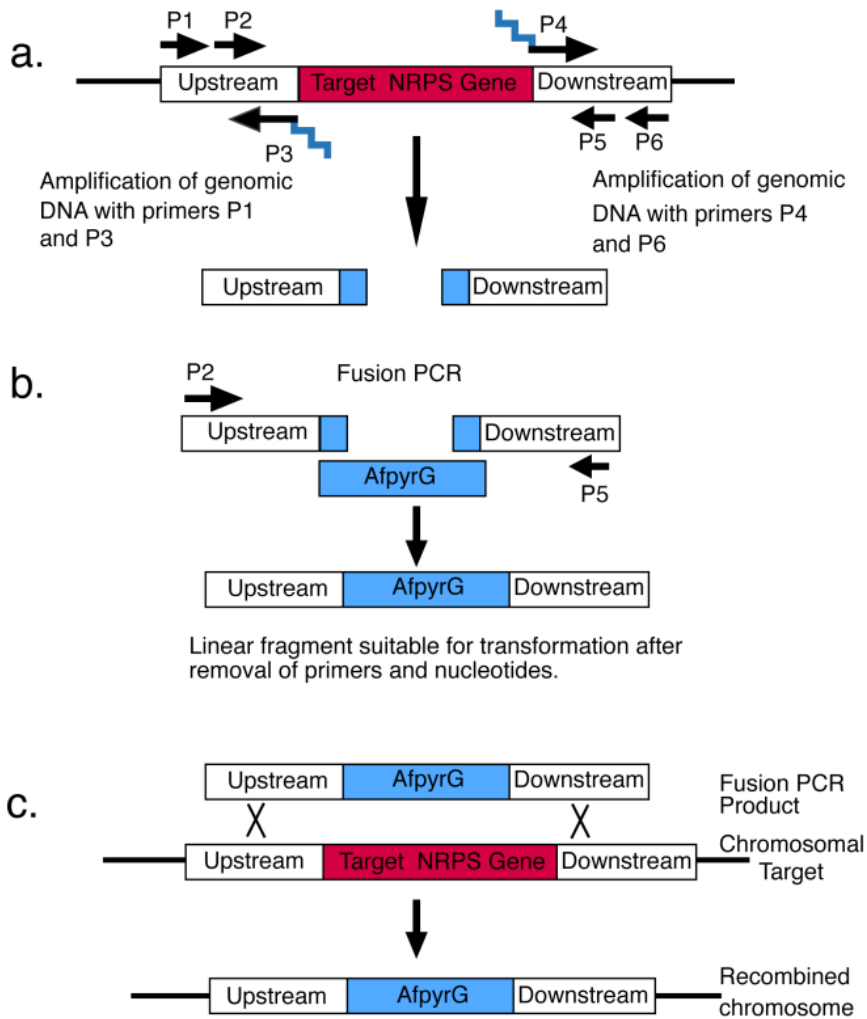
<sup>a</sup> Figures in parentheses are multiplicities assigned by DEPT NMR methods.

<sup>b</sup> Values in the same column may be interchanged.

## Supplemental References

1. Oh, D.C., Kauffman, C.A., Jensen, P.R., and Fenical, W. (2007). Induced production of emericellamides A and B from the marine-derived fungus *Emericella* sp. in competing co-culture. *J Nat Prod* *70*, 515-520.
2. Nayak, T., Szewczyk, E., Oakley, C.E., Osmani, A., Ukil, L., Murray, S.L., Hynes, M.J., Osmani, S.A., and Oakley, B.R. (2006). A versatile and efficient gene-targeting system for *Aspergillus nidulans*. *Genetics* *172*, 1557-1566.





**Figure S1. A Schematic Diagram of the Use of Fusion PCR to Target an NRPS Gene in *A. nidulans***

(a) DNA fragments flanking upstream and downstream of the target NRPS genes are amplified with primers P1 and P3 and with P4 and P6. P3 and P4 are designed to have tails that anneal to the *A. fumigatus pyrG* fragment (AfpyrG) during fusion PCR. (b) The two fragments and the AfpyrG cassette are mixed and fused together by PCR using nested primers P2 and P5 creating a linear fragment suitable for transformation. (c) Replacement of the targeted NRPS gene with the AfpyrG gene via homologous recombination.

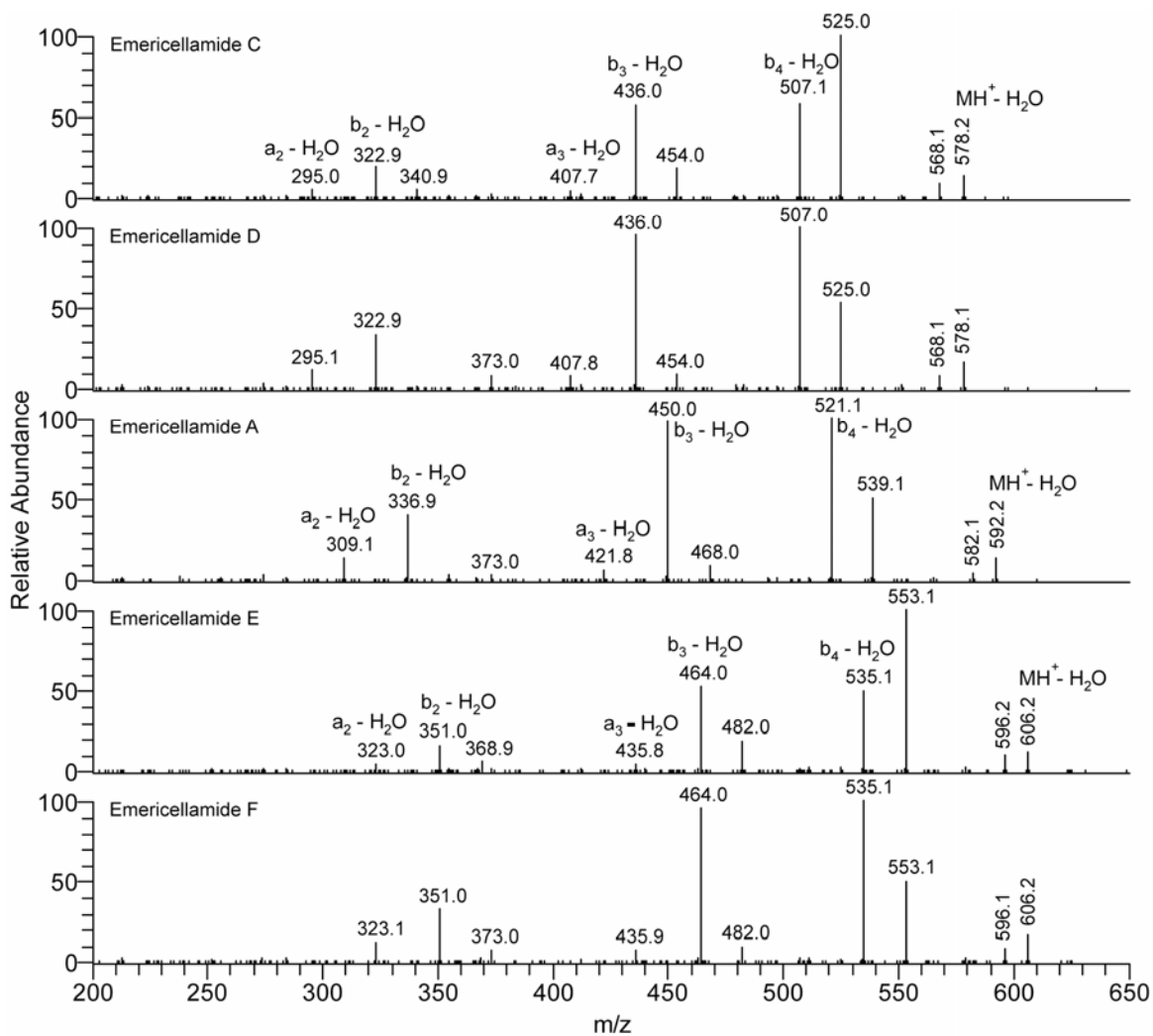
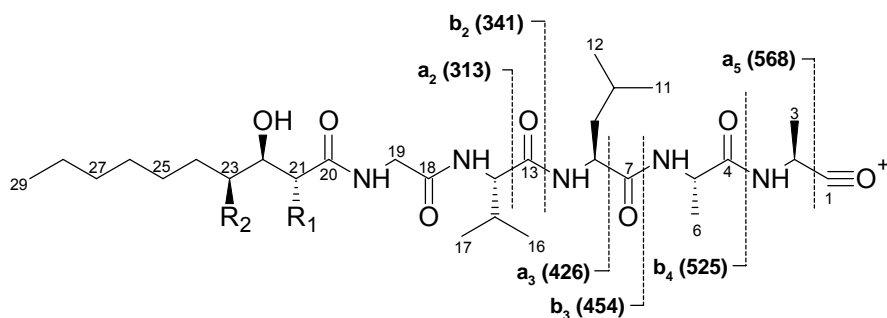


Figure S2. MS/MS Spectra of Emericellamide A (1) , C-F (2-5)

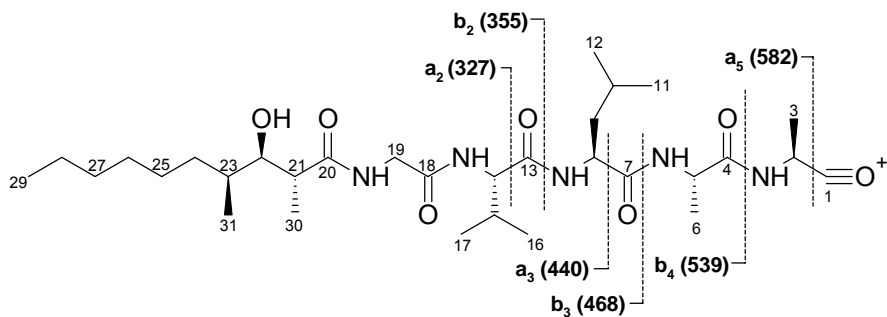
### Emericellamides

1. protonation
2. ring opening

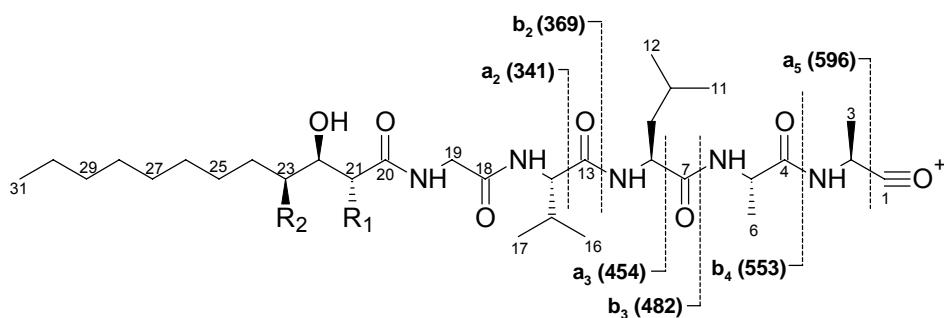


Emericellamide C (2): R<sub>1</sub> = Me, R<sub>2</sub> = H

Emericellamide D (3): R<sub>1</sub> = H, R<sub>2</sub> = Me



Emericellamide A (1)



Emericellamide E (4): R<sub>1</sub> = Me, R<sub>2</sub> = H

Emericellamide F (5): R<sub>1</sub> = H, R<sub>2</sub> = Me

**Figure S3. Assignment of Emericellamide MS/MS Fragmentation**

















