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**Supplementary Information**

# Molecular genetic analysis of the cichorine gene cluster in *A. nidulans*

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**Supplementary Table 1.Primers Used in This Study.**

| AN11921 | *cicA* |
|---|---|
| AN11921P1: GCT ACA ACC AGT ATC CGC AC | *cicA*P1: TCA ACG AGC ATA TTC CAG CC |
| AN11921P2: CTG TTC TAC CTC CAC CAT GC | *cicA*P2: ATC ACT GCG GAT CGG AAG AC |
| AN11921P3: *CTG GGG TTG TTG AAA TCG AGT | *cicA*P3: *AGT CTA GCC GAT GCT TTT GC |
| AN11921P4: **GAC GAC GTT TCT CGT TCT TTG | *cicA*P4: **ATT GGA TGG AGT GAG GTT GG |
| AN11921P5: CAT CGG AAT CGT CGG ACG AAC | *cicA*P5: TGG TGT TGA GAG CAC CAA TG |
| AN11921P6: CAT TTG ACA ACG TCG CCA TGC | *cicA*P6: CGT CTA TCA TGC TTG CCA TTG |
| | |
| *cicB* | *cicC* |
| *cicB*P1: GAT GTG ACA AAG TTC CAA TCG | *cicC*P1: CAA TGA TGG CTG CTG CAG AG |
| *cicB*P2: GTG ACA AAG TTC CAA TCG ACA AG | *cicC*P2: AGG AGA CTG TTG ATA GCA GG |
| *cicB*P3: *GTT TCG AGC CAT GGC TGA G | *cicC*P3: *CGC GTT CTT TTG TTG CGA TG |
| *cicB*P4: **TGC GGT TGC TAG ACG TTA TC | *cicC*P4: **ATC TTT CAC ATT TGT GGG CTC |
| *cicB*P5: CAG ATA TCC TGC AAT TCC AGC | *cicC*P5: TAC CAG CCG TAA TCA TGA GG |
| *cicB*P6: CTT CGT CAA AAC GTC GAC C | *cicC*P6: GCA TGG GAG ATA CCA GAC TG |
| | |
| *cicD* | *cicE* |
| *cicD*P1: CAT GAT GGT CTC ACG TGT GC | *cicE*P1: CAA CCG ACA CTG CTG TGA G |
| *cicD*P2: TGA CGA ACT GCA GGT AAG AAG | *cicE*P2: CGA ACG GCT CTG AGA ACA TC |
| *cicD*P3: *GAG GTA TTC TGG AAG G | *cicE*P3: *GAA GCG TTC CAT GAT GGT CT |
| *cicD*P4: **GAG GAA TCG GCA AGT TCT TG | *cicE*P4: **GGT GTC TGT CCA CTT GTT G |
| *cicD*P5: GAT GAG ATC GTC GAG TGG CT | *cicE*P5: GAA TTT AGC CAC GGC TTT GC |
| *cicD*P6: CGA TGG CTG GCA TTA CGC TT | *cicE*P6: GAG AAG TTC GTA CTG AAA GCC |
| | |
| *pkbA* | *cicG* |
| *pkbA*P1: GCT CAC AGT ATG ATT TGG ATC | *cicG*P1: ATC AGA AGA CGC AGC CTC G |
| *pkbA*P2: GGA AAG CAC TTG GAA GCA TAC | *cicG*P2: GAC TAG GGT CGT CCA TTT GC |
| *pkbA*P3: *CGG AGC CAT GAT GAA AGA AC | *cicG*P3: *GTT AAT CGA TGA AAT TGG CAC C |
| *pkbA*P4: **ACC TAG TCA TCT CGC TTA GAG | *cicG*P4: **AGA GAT CAA GAC ATG CGT GC |
| *pkbA*P5: GAC GAC GTG AAC AGC CTA GT | *cicG*P5: GTG CAG ACG CAG ATA CCT G |
| *pkbA*P6: CCT CTC CAT GGT AAA TGC TG | *cicG*P6: CTG TGC ATC GTG ACC GTG A |
| | |
| *cicH* | AN6450 |
| *cicH*P1: CAG ACA TTG ATC GCC TGG TG | AN6450P1: CTA TCC ATC AAG TCG AGT CAG |
| *cicH*P2: TCG GCA AGA TCG ACA TCC TC | AN6450P2: TTC TGC ATA TCA GCG CTT CC |
| *cicH*P3: *CTC GGT ACC AAT GCA ACA CA | AN6450P3: *ACT AGC TGT AGA GGG AGA TTA G |
| *cicH*P4: **AAA GGG AGG GCT GAT CTG TAG | AN6450P4: **AGA GGA CGC TGG TCT TTT GG |
| *cicH*P5: CCC CTC TTA ATT GGA CAT GTC | AN6450P5: CGA AAT TAC AGA CCT TGC CAG |
| *cicH*P6: GGT TTC TTC TCA TGG ATT CCT | AN6450P6: AGT CGT CTG GAG AAT GTG ATC |

*All P3 sequences begin with CGA AGA GGG TGA AGA GCA TTG.
**All P4 sequences begin with GCA TCA GTG CCT CCT CTC AGA CAG.
These P3/P4 beginning sequences are tails that anneal to the *A. fumigatus* pyrG fragment (AfpyrG) during fusion PCR.

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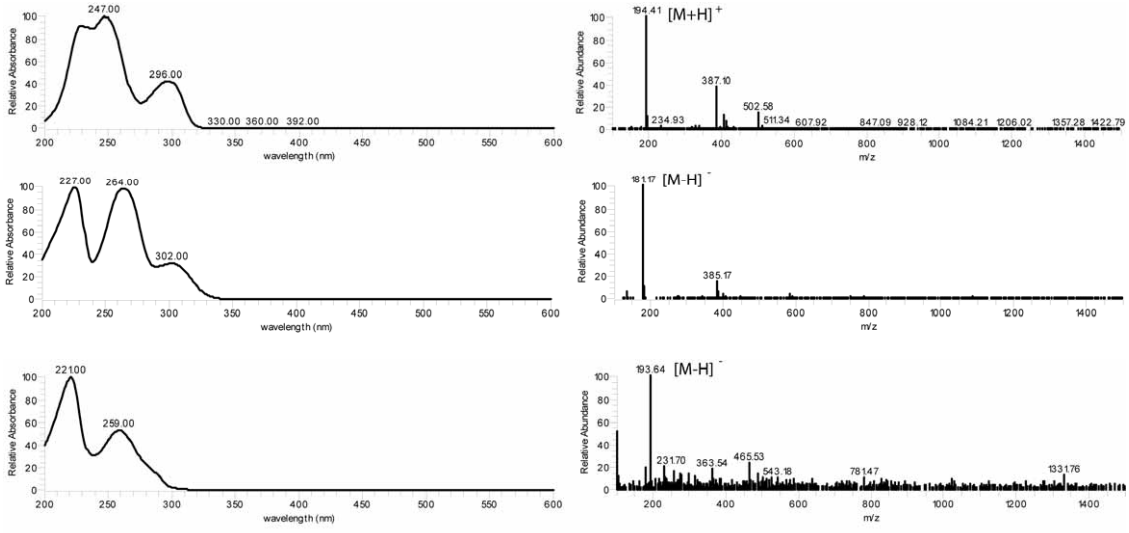
**SupplementaryMethods**

NMR spectra were run on a Varian Mercury Plus 400 spectrometer. IR spectra were obtained on a Bruker Vertex 80 FTIR spectrometer. For all structural determinations twenty-five 150x15 mm petri dishes containing solid YES media were inoculated with an *A. nidulans* strain. All compounds, from crude extract, were initially applied to a $SiO_2$ column (Merck 230-400 mesh, ASTM) and eluted with 1 L fractions. All collected fractions were further purified by reverse phase HPLC [Phenomenex Luna 5 µm C18 (2), 250 x 10 mm] with a flow rate of 10.0 mL/min and measured by a UV detector at 250 nm. Solvent A was 5% acetonitrile in water with 0.05% trifluoroacetic acid. Solvent B was 100% acetonitrile with 0.05% trifluoroacetic acid.

For the isolation of compounds **1**, **5**, and **6** LO2026, *cicB*Δ, and *cicC*Δ, respectively were cultivated. For **1** and **5** 2:98 methanol:dichloromethaned was the eluent for silica gel chromatography, and for **6** 100% dichloromethane was the eluent. The HPLC gradient system was 10 to 33% B from 0 to 23 min, 33 to 100% B from 23 to 25 min, 100% B from 25 to 28 min, 100% B to 10% B from 28 to 30 min, and re-equilibration to 10% B from 30 to 33 min.




**Supplementary Figure 1.** UV and ESIMS profiles of **1** (m/z = 193), **5** (m/z = 182), and **6** (m/z = 194).