

Supporting Information for

Elucidation of shanorellin biosynthetic pathway and functional analysis of associated enzymes

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Figure S1. SDS-PAGE analysis of the *Escherichia coli*-produced CgsF enriched by metal-affinity chromatography using Ni-NTA Sepharose resin. Lane M: molecular weight marker; lane 1: CgsF (48 kDa).

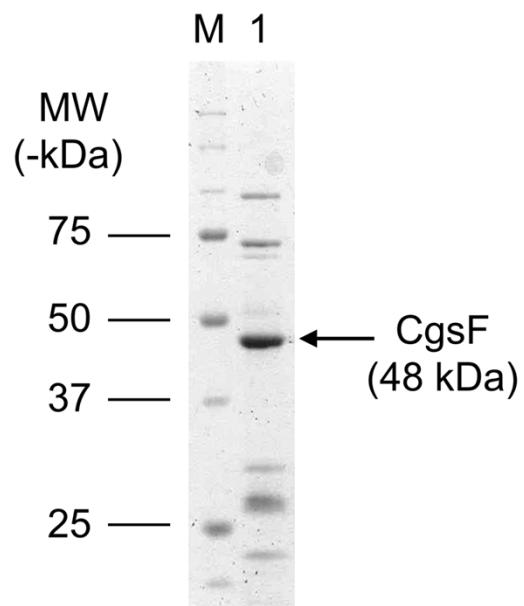
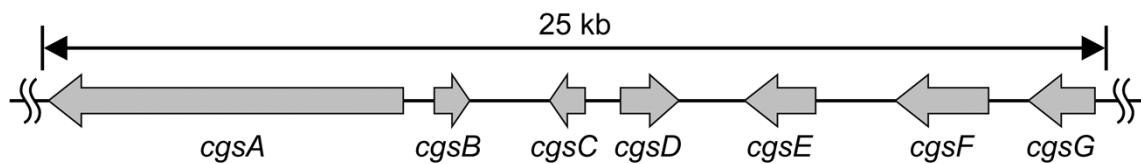


Table S1. Organization of the *cgs* gene cluster responsible for the biosynthesis of shanorellin **4**, and predicted functions of corresponding translation products.



Gene	Amino acids (no)	Proposed protein function (most homologous protein ^[a] , NCBI accession number, species)	Identity / Similarity (%)
<i>cgsA</i> (CHGG_08793)	2379	Polyketide synthase (Polyketide synthase putative, XP_002339967, <i>Talaromyces stipitatus</i>)	39/56
<i>cgsB</i> (CHGG_08794)	238	Cytochrome P450 (Unnamed protein product, BAE65443, <i>Aspergillus oryzae</i>)	68/85
<i>cgsC</i> (CHGG_08795)	262	SGNH_hydrolase (Carbohydrate esterase family 3 protein, CCD55162, <i>Botryotinia fuckeliana</i>)	40/60
<i>cgsD</i> (CHGG_08796)	378	Reverse transcriptase (Hypothetical protein, XP_001226257, <i>Chaetomium globosum</i>)	76/79
<i>cgsE</i> (CHGG_08797)	405	Hypothetical protein CHGG_08797 (Conserved hypothetical protein, XP_002483593, <i>Talaromyces stipitatus</i>)	67/79
<i>cgsF</i> (CHGG_08798)	371	Salicylate hydroxylase (Salicylate hydroxylase putative, XP_002483592, <i>Talaromyces stipitatus</i>)	43/57
<i>cgsG</i> (CHGG_08799)	472	GAL4 (C6 finger domain protein GliZ, XP_002151409, <i>Penicillium marneffei</i>)	29/44

[a] Deduced functions of the ORFs identified within the *cgs* biosynthetic gene cluster were based on the percentage sequence similarity/identity to known proteins as determined by Protein BLAST search against the NCBI non-redundant database.

Table S2. Oligonucleotide primer sequences. DNA primers were designed on the basis of sequence data obtained from the *Chaetomium globosum* and *Streptomyces hygroscopicus* (for *hph*) genome sequence database.

Primer name	Sequence (5' to 3')
19140-Fw1	GAAATTGCACCAAGATGAGCCACAACATCGCGG
19133-Rv4	CAAAGGGCGTTCCGTTGCCCG
19133-Rv3	CTAAAGGGAACAAAAGCTGGTCAAAGGGCGTTCCGTTGCCCG
19133-Fw4	GATTTCGTAGCCGACCTCGATTATGCC
19151-Fw2	CAGAAAGGCCACCAAGATGAGCCACAACATCGCGG
19151-Fw1	GATCGCAGGTCAAGGACTTCAGGCTGGTATAAGATCCAAGGC
19151-Rv1	CATCTGGTGGGCCTTCTGTAATCCTCAAAGGAGCCG
19114-Rv3	CTCCTGACCTGCGATCTCCCT
19133-Fw1	CTATAGGGCGAATTGGGTACATGATTCCGTAGCCGACCTCGATTATG
19121-Fw2	GAAGATCGCAGGTCAAGGACTTCAGGCTGGTATAAGATCCAAGGCTATCG
19121-Rv2	CACGGGTGGTGCCATTGACGGCTGGAAAGGTGC
19121-Fw3	CAAATGGCACCAACCGTGAAACTTCCGACCCGCAAGC
10121-Rv3	CAAGAGAGTAGGCGCCAATTTCATAGCCACTCAGTCTGCACTG
19121-Fw4	GAAATTGGCGCCTACTCTTGTAAAGCTGAAGATCTCTGC
19121-Rv4	CTAAAGGGAACAAAAGCTGGGAAATACAGGCCGACTACAGTTGATATAC
19153-Fw1	GGGCGAATTGGGTACGTTCAAGGGTTCTGCATTGGTTTC
19153-Rv1	CAACAGGACTGTAGCGAGACCTGGAAGAAGCGGTGGTCG
19153-Fw2	CTCCACC GTTCCATTGAGAGGGAGTTTGTGTTGC GGGGG
19153-Rv2	GAACAAAAGCTGGAGCTGGTGGAGTCTGCCCTCGATGAAAGCCG
19153-Fw3	CGAACCGCCAACACGTAGTCCTC
19153-Rv3	CTCGTATCTGGA ACTGCCCCATGAGC
19154-Fw4	GGGCGAATTGGGTACCGTGAGGTGAGATCCAGTAAGGCG
19154-Rv4	CAACAGGACTGTAGCGGGAAAGTGGCGGAGACGGTAGTATAC
19154-Fw5	CTCCACC GTTCCATTGGTCCCTCGTGC CCGTTTCAC
19154-Rv5	GAACAAAAGCTGGAGCTGGAGAAATCGCGAAAGGAAGTCGCCTC
19154-Fw3	CCAGAGCTCGGTGAGGCTGCTTAG
19154-Rv3	CAAACACGCTTAGCACGGCACTTGTC
19155-Fw1	GGGCGAATTGGGTACGAACGGGGAAAGGGGTGAGCCTTG
19155-Rv1	CAACAGGACTGTAGCGGGTTGCCGTGGTGGAGAGCAGAC
19155-Fw2	CTCCACC GTTCCATTGGTCAACGCCCTCATCGAGGAATAC
19155-Rv2	GAACAAAAGCTGGAGCTAGTGGCGTCTGGAGGGAACGAC
19155-Fw3	GTTATATCCAAGTGAGGGTGCTCGTC
19155-Rv3	CTATCAAGAGACGATCTGAGCGG
19156-Fw1	GGGCGAATTGGGTACCGCCCCAAGTCCAACGCAAAC
19156-Rv1	CAACAGGACTGTAGCTATGGATCAGCCCATGCACATAGC
19156-Fw2	CTCCACC GTTCCATTATGTTAAGAACCTCCTGC GGGGAG
19156-Rv2	GAACAAAAGCTGGAGCTCGAACCTTCAAGCGTTATTGGAGC

19156-Fw3	GCTACAGTTCAAGGAGGGAGAACTC
19156-Rv3	CAAGCCAGCCGAGTAGAGTTACATG
19157-Fw1	GGGCGAATTGGGTACGCCATTATGCCCGGTTAACATAATG
19157-Rv1	CAACAGGACTGTAGCTCCACCCCCCTCCCCCGTCCGAG
19157-Fw2	CTCCACCCTTCATTATTAGTGAGTATTAAAGCAAGGCTGAC
19157-Rv2	GAACAAAAGCTGGAGCTGTTGTCATTCCCCCAGCGACC
19157-Fw3	GTGGTCCGAGTCACTAAAGGTAG
19157-Rv3	CCCAACTCTCTTGCTCCGAGAAC
19140-Rv1	CAAGTCAGCAGCGGCAAGGATTCGGCGGGTTGTATCTTGC
pyrG Fw	TGCCGCTGCTGACTTGAGGTG
pyrG Rv	CTCCTGACCTGCGATCTCCCT
19121-Fw1	CTATAGGGCGAATTGGGTACGCTGGTTGTCAGTCTAGATCCGGCTTTG
19121-Rv1	CCTCAAGTCAGCAGCGGCAATCGAACGCGTATATAGACCGTCTTGC
hph_Fw	GCTACAGTCCTGTTGCGCCTCCGG
hph_Rv	AATGGAACGGTGGAGAAGTTCCCTGGC
Cg-KO-hph-Rv	GCACTCGTCCGAGGGCAAAGGAATAG
Cg-KO-hph-Fw	CGACAGACGTCGCGGTGAGTTCAAG
19140-Fw1	GAAATTGCAACCAAGATGAGCCACAACATCGCGG