

Comprehensive Genomic Analysis of One Marine Strain *Streptomyces* sp. 891, an Excellent Producer of Chrysomycin A with Therapeutic Potential

Xu Hu ^{1,2,†}, Yuqi Tang ^{1,†}, Yuanyuan Liu ¹, Xinwei Pei ¹, Ziwei Huang ¹, Fuxing Song ³ and Huawei Zhang ^{1,*}

¹ School of Pharmaceutical Sciences, Zhejiang University of Technology, Hangzhou 310014, China

² College of Life and Environmental Sciences, Hangzhou Normal University, Hangzhou 311121, China

³ School of Light Industry, Beijing Technology and Business University, Beijing 100048, China

* Correspondence: hwzhang@zjut.edu.cn

† These authors contributed equally to this work.

Table S1. Information associated with the different chrysomycin (A)-producing species.

Strain	Source	Yield of chrysomycin A	Ref.
<i>Streptomyces</i> sp. A-419	Soil (New York Botanical Garden, USA)	5~10 mg/L	[1]
<i>Streptomyces virens</i>	Soil (Russia)	/	[2]
<i>Streptomyces albaduncus</i> C38291 (ATCC 14698)	Soil (Colombia)	/	[3]
<i>Streptomyces albaduncus</i> AD819	Soil (New York Botanical Garden, USA)	3 mg/L	[4,5]
<i>Streptomyces sporoverrucosus</i> strain CR1	Soil (Jammu Hill, India)	5 mg/L	[6]
<i>Streptomyces</i> sp.OA161	Mixed sample (India)	/	[7]
<i>Streptomyces</i> sp. 891	Sediment (South China Sea)	3,600 mg/L	[8]

Table S2. The statistical results of sequence-length distribution of the third-generation sequencing data of strain 891.

Sample Name	Sequence
Total Number (#)	187,835
Total Length (bp)	1,461,334,907
Max Length (bp)	50,211
Min Length (bp)	200
N20 (bp)	12,425
N50 (bp)	9,471
N90 (bp)	5,502
Sequences Number (≥1kb)	180,244
GC content %	68.87

Table S3. CRISPR arrays in strain 891.

No.	Start	End	Number of Spacer	Length (bp)	Genome (%)
1	7,701,174	7,702,715	23	1,541	0.0197
2	7,712,784	7,714,256	22	1,472	0.0189

3	3,190	3,397	3	207	0.0027
4	1,539,060	1,539,188	1	128	0.0016
5	1,796,106	1,796,192	1	86	0.0011
6	2,722,200	2,722,317	1	117	0.0015
7	2,734,535	2,734,645	1	110	0.0014
8	3,081,958	3,082,182	1	224	0.0029
9	3,235,213	3,235,352	1	139	0.0018
10	4,248,405	4,248,516	1	111	0.0014
11	5,500,464	5,500,577	1	113	0.0014
12	5,508,296	5,508,404	1	108	0.0014
13	5,661,901	5,662,010	1	109	0.0014
14	6,161,260	6,161,392	1	132	0.0017
15	6,347,661	6,347,778	1	117	0.0015

Table S4. Putative biosynthetic gene clusters (BGCs) coding for secondary metabolites in strain 891.

BGC	Core potentials	From	To	Most similar known cluster (%)
Cluster 1	thiopeptide, LAP	32,672	60,344	-
Cluster 2	Terpene, RiPP	268,772	300,586	citrulassin E (66%)
Cluster 3	NRPS, NRPS-like	359,628	412,242	enduracidin (8%)
Cluster 4	Terpene	457,490	477,651	-
Cluster 5	ladderane, Other	571,337	612,704	spiroindimicin/indimicin/lynamicin (6%)
Cluster 6	lanthipeptide	853,073	875,787	SapB (75%)
Cluster 7	Terpene	1,103,217	1,126,499	hopene (61%)
Cluster 8	lanthipeptide	1,352,217	1,371,434	-
Cluster 9	RiPP-like	1,693,792	1,704,652	-
Cluster 10	siderophore	1,873,704	1,887,891	-
Cluster 11	T3PKS, NRP	2,405,467	2,446,510	echoside (35%)
Cluster 12	lassopeptide, RiPP	2,595,968	2,618,593	aborycin (50%)
Cluster 13	NRPS, Other	2,758,394	2,801,884	2'-chloropentostatin / 2'-amino-2'-deoxyadenosine (6%)
Cluster 14	Terpene	3,273,143	3,295,228	isorenieratene (85%)
Cluster 15	T1PKS, butyrolactone	5,346,521	5,395,065	reveromycin A (15%)
Cluster 16	Terpene	5,550,835	5,568,424	geosmin (100%)
Cluster 17	lanthipeptide, Polyketide	5,797,742	5,894,239	xantholipin (61%)
Cluster 18	Ectoine	6,022,782	6,031,572	ectoine (100%)
Cluster 19	siderophore, Other	6,100,486	6,110,067	desferrioxamine E (100%)
Cluster 20	lanthipeptide	6,262,668	6,285,460	-
Cluster 21	T2PKS, Polyketide	6,529,403	6,601,876	chrysomycin (74%)
Cluster 22	T1PKS, Polyketide	6,837,722	6,884,576	marineosin (100%)
Cluster 23	NRPS-like	7,073,517	7,115,564	echoside (11%)
Cluster 24	NRPS-like, Saccharide	7,235,261	7,278,035	paromomycin (5%)
Cluster 25	siderophore, Polyketide	7,302,042	7,318,494	macrotetrolide (33%)
Cluster 26	NRPS	7,519,764	7,606,851	marformycin (8%)

Table S5. Putative function of Virulence Factors in strain 891.

VFs	VF_id	VF_Funcation
<i>KatA</i>	VFG001861	1. A periplasmic catalase, expressed maximally during the post-exponential phase. 2. Important for intracellular survival and transmission.
<i>ClpC</i>	VFG000079	1. An ATPase promoting early escape from the phagosome of macrophages. 2. ClpC is also required for adhesion and invasion, possibly by modulating the expression of InlA, InlB and ActA.
<i>IdeR</i>	VFG001406	Repressor of iron acquisition genes, activator of iron storage genes and a positive regulator of oxidative stress responses.
<i>RelA</i>	VFG001826	Associated with stationary phase adaptation and long-term survival.
<i>Mycobactin</i>	VFG001818	Cell-association mycobactin participates in iron internalization and/or to serve as a temporary iron-holding molecule to prevent sudden influx of excess iron if the metal suddenly becomes available after a period of iron limitation.

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