## Functional Characterization of TtnD and TtnF Unveiling New Insights into Tautomycetin Biosynthesis

Yinggang Luo,<sup>†,Ω</sup> Wenli Li,<sup>†</sup> Jianhua Ju,<sup>†</sup> Qiuping Yuan,<sup>⊥</sup> Noel R. Peters,<sup>⊥</sup> F. Michael Hoffmann,<sup>⊥</sup> Shengxiong Huang,<sup>†</sup> Tim S. Bugni,<sup>†</sup> Scott Rajski,<sup>†</sup> Hiroyuki Osada,<sup>¥</sup> and Ben Shen<sup>\*†,‡,§</sup>

<sup>†</sup>Division of Pharmaceutical Sciences, <sup>⊥</sup>University of Wisconsin Paul P. Carbone Comprehensive Cancer Center Small Molecule Screening Facility, <sup>§</sup>University of Wisconsin National Cooperative Drug Discovery Group, and <sup>‡</sup>Department of Chemistry, University of Wisconsin, Madison, Wisconsin 53705-2222, <sup>Ω</sup>Center for Natural Products Research, Chengdu Institute of Biology, Chinese Academy of Sciences, Chengdu 610041, China, and <sup>¥</sup>Antibiotics Laboratory, Chemical Biology Department, Advanced Science Institute, RIKEN, Wako-shi, Saitama 351-0198, Japan

\*To whom correspondence should be addressed: Division of Pharmaceutical Sciences, School of Pharmacy, University of Wisconsin-Madison, 777 Highland Ave., Madison, WI 53705. Tel.: (608) 263-2673; Fax: (608) 262-5345; E-mail: bshen@pharmacy.wisc.edu

## **Supporting Information**

#### **Table of Contents**

1.	Table S1.	Targeted gene inactivation by use of DIRECT technology	
		in S. griseochromogenes	<b>S</b> 2
2.	Table S2.	Southern blot analysis confirming mutant genotypes	<b>S</b> 2
3.	Table S3.	Expression constructs for complementation to the $\Delta ttnD$	
		and $\Delta ttnF$ mutants	<b>S</b> 2
4.	References		<b>S</b> 2
5.	Figure S1.	Inactivation of <i>ttnD</i> by gene replacement	<b>S</b> 3
6.	Figure S2.	Inactivation of <i>ttnF</i> by gene replacement	<b>S</b> 3
7.	Figure S3.	<sup>1</sup> H NMR spectrum for TTN F-1 ( <b>3</b> )	<b>S</b> 4
8.	Figure S4.	$^{13}$ C NMR spectrum for TTN F-1 ( <b>3</b> )	S5
9.	Figure S5.	<sup>1</sup> H NMR spectrum for TTN D-1 (4)	S6
10.	Figure S6.	<sup>13</sup> C NMR spectrum for TTN D-1 (4)	<b>S</b> 7
11.	Figure S7.	<sup>1</sup> H NMR spectrum for TTN D-2 ( <b>5</b> )	<b>S</b> 8
12.	Figure S8.	<sup>13</sup> C NMR spectrum for TTN D-2 ( <b>5</b> )	<b>S</b> 9
13.	Figure S9.	<sup>1</sup> H NMR spectrum for TTN D-3 ( <b>6</b> )	S10
14.	Figure S10.	<sup>13</sup> C NMR spectrum for TTN D-3 ( <b>6</b> )	S11
15.	Figure S11.	<sup>1</sup> H NMR spectrum for TTN D-4 (7)	S12
16.	Figure S12.	<sup>13</sup> C NMR spectrum for TTN D-4 (7)	S13

# **TABLE S1.** Targeted gene inactivation by the REDIRECT technology in S. griseochromogenes

		/	
Gene	Primers <sup>a</sup>	Cosmid <sup>b</sup>	Strain
ΔttnD	<pre>ttnDF1: 5'-AATGAAGCGACTCAAGGATCTCCGCGAGTACCTGGCGGTGATTCCGGGGGATCCGTCGACC-3' ttnDR1: 5'-TGTCAGGCAAGGAGCTCGATGACCCGCTGCCGCACCGGCTC TGTAGGCTGGAGCTGCTTC-3'</pre>	pBS13025	SB13013
$\Delta ttnF$	<pre>ttnFF1: 5'-GGTGACGAGCACACGAAGCGAGACGGATCTGACCGGCCGG</pre>	pBS13026	SB13014
9x x 1 11			

<sup>a</sup>Underlined letters represent the nucleotide homologous to the DNA regions internal to targeted genes.

<sup>b</sup>pBS13025 and pBS13026 are based on cosmid pBS13009 that carries a part of the *ttn* cluster.<sup>1</sup>

## **TABLE S2**. Southern analysis confirming the genotypes of mutant Strains<sup>a</sup>

	Cana		Fragment replaced (bp)	Restriction Site used	Signal Size (kbp)	
Strains	targeted	Probe			WT	mutant
SB13013	$\Delta ttnD$	2200-bp <i>Bam</i> HI fragment from pBS13027 <sup>b</sup>	1380	XhoI	3.63	2.29
SB13014	$\Delta ttnF$	1370-bp <i>Bam</i> HI fragment from pBS13028 <sup>b</sup>	1440	XhoI	3.06	3.53

<sup>a</sup>See Figures S1 and S2 for details.

<sup>b</sup>pBS13027 and pBS13028 were constructed by subcloning *Bam*HI fragments containing *ttnD* and *ttnF*, respectively, from cosmid pBS13012 that carries a part of the *ttn* cluster<sup>1</sup> into the same site of pUC18.<sup>2</sup>

### **TABLE S3.** Expression constructs for complementation to the $\Delta ttnD$ and $\Delta ttnF$ mutants

Mutant strain	Gene mutated	Primers used to make the expression constructs <sup>a</sup>	Construct <sup>b</sup>	Complemented strain
SB13013	ΔttnD	<i>ttnD</i> FP3: 5'-CCA <u>ATGCAT</u> GAAGCGACTCAAGGAT-3' <i>ttnD</i> P3: 5'-GC <u>TCTAGA</u> TCAGGCAAGGAGCTCGAT-3'	pBS13029	SB13015
SB13014	$\Delta ttnF$	<i>ttnF</i> FP3: 5'-GCA <u>ATGCAT</u> ATGACGAGCACACGAAGCG-3' <i>ttnF</i> RP3: 5'-GC <u>TCTAGAT</u> CAGTCGATCCACTCCGG-3'	pBS13030	SB13016

<sup>a</sup>The *ttnD* and *ttnF* genes were amplified with the primers listed (*Nsi*I and *Xba*I restriction sites are underlined), respectively, from cosmid pBS13012.<sup>1</sup>

<sup>b</sup>The PCR-amplified *ttnD* and *ttnF* genes from pBS13012 were digested with *Nsi*I and *Xba*I and cloned into the same sites of pBS6027<sup>3</sup> to afford pBS13029 and pBS13030, respectively, in which the expression of *ttnD* and *ttnF* is under the control of the *ErmE*\* promoter.

## REFERENCES

- 1. Li, W.; Luo, Y.; Ju, J.; Rajski, S. R.; Osada, H.; Shen, B. J. Nat. Prod. 2009, 72, 450-459.
- 2. Sambrook, J. E.; Fritsch, E. F.; Maniatis, T. *Molecular cloning: a Laboratory Manual*, 3rd Ed.; Cold Spring Harbor Laboratory Press: Cold Spring Harbor, NY, 2000.
- 3. Li, W.; Ju, J.; Rajski, S. R.; Osada, H.; Shen, B. J. Biol. Chem. 2008, 283, 28607-28617.

**FIGURE S1.** Inactivation of *ttnD* in *S. griseochromogenes* by gene replacement using the REDIRECT Technology. (A) Construction of the  $\Delta ttnD$  gene replacement mutant and restriction maps of *S. griseochromogenes* wild-type and SB13013 mutant strains showing the predicted fragment sizes upon *XhoI* digestion. (B) Southern analysis of the wild-type (lane 5) and SB13013 (lanes 2, 3 and 4 are three individual isolates) digested genomic DNAs and using the 2198-bp *Bam*H1 fragment as a probe. Lane 1, molecular weight standard.



**FIGURE S2.** Inactivation of *ttnF* in *S. griseochromogenes* by gene replacement using the REDIRECT Technology. (A) Construction of the  $\Delta ttnF$  gene replacement mutant and restriction maps of *S. griseochromogenes* wild-type and SB13014 mutant strains showing predicted fragment sizes upon *XhoI* digestion. (B) Southern analysis of the wild-type (lane 5) and SB13014 (lanes 2, 3 and 4 are three individual isolates) digested genomic DNAs and using the 1370-bp BamH1 fragment as a probe. Lane 1, molecular weight standard.





**Figure S3.** <sup>1</sup>H-NMR of TTN F-1 (**3**) in CDCl<sub>3</sub>.



Figure S4. <sup>13</sup>C-NMR of TTN F-1 (3) in CDCl<sub>3</sub>.



Figure S5. <sup>1</sup>H-NMR of TTN D-1 (4) in CDCl<sub>3</sub>.



**Figure S6.**  $^{13}$ C-NMR of TTN D-1 (4) in CDCl<sub>3</sub>.



**Figure S7.** <sup>1</sup>H-NMR of TTN D-2 (**5**) in CDCl<sub>3</sub>.



Figure S8. <sup>13</sup>C-NMR of TTN D-2 (5) in CDCl<sub>3</sub>.



**Figure S9.** <sup>1</sup>H-NMR of TTN D-3 (6) in CDCl<sub>3</sub>.



**Figure S10.** <sup>13</sup>C-NMR of TTN D-3 (6) in CDCl<sub>3</sub>.



**Figure S11.** <sup>1</sup>H-NMR of TTN D-4 (7) in CDCl<sub>3</sub>.



**Figure S12.** <sup>13</sup>C-NMR of TTN D-4 (7) in CDCl<sub>3</sub>.