

# Contents

<b>List of Figures</b>	<b>III</b>
<b>List of Tables</b>	<b>IV</b>
<b>Abbreviations</b>	<b>V</b>
<b>1. Methods</b>	<b>1</b>
1.1. Chemicals & Instruments . . . . .	1
1.2. Strain Cultivation . . . . .	3
1.2.1. Media . . . . .	3
1.2.2. <i>Escherichia coli</i> K12 and <i>Bacillus subtilis</i> 168 . . . . .	3
1.2.3. General cultivation of <i>Streptomyces</i> sp. Tü2401 . . . . .	3
1.2.4. Batch Fermentation of <i>Streptomyces</i> sp. Tü2401 . . . . .	3
1.3. Bioassays . . . . .	5
1.3.1. Agar Diffusion Bioactivity Assays . . . . .	5
1.3.2. <i>yorB</i> Reporter Gene Assay . . . . .	5
1.4. Sample Preparation and Extraction . . . . .	6
1.4.1. Preparation of medium extracts . . . . .	6
1.4.2. Determination of Extraction Conditions . . . . .	6
1.4.3. Processing of Fermentation Broth . . . . .	6
1.4.4. Agar Plate Extraction . . . . .	7
1.5. Bioactivity-guided Isolation . . . . .	8
1.5.1. Thin Layer Chromatography . . . . .	8
1.5.2. Ion Exchange Chromatography . . . . .	8
1.5.3. Trimethylsilyl Derivatization and Gas Chromatography . . . . .	9
1.5.4. Preparative HPLC . . . . .	9
1.5.5. Analytical HPLC and Mass Spectrometry . . . . .	10
1.6. Genome Analysis . . . . .	10

<b>2. Results &amp; Discussion</b>	<b>11</b>
2.1. Determination of Extraction Conditions . . . . .	11
2.2. Chromatographic Separation . . . . .	13
2.2.1. Reverse-Phase HPLC . . . . .	13
2.2.2. HPLC with Amino Column . . . . .	13
2.2.3. Hydrophilic Interaction Chromatography . . . . .	13
2.2.4. Ion exchange Chromatography . . . . .	13
2.2.5. Thin-Layer Chromatography . . . . .	13
2.3. Dereplication . . . . .	13
2.3.1. HPLC Mass Spectrometry . . . . .	13
2.3.2. Trimethylsilane Derivatization and Gas Chromatography . . . . .	13
2.4. Antibacterial Activity Spectrum . . . . .	13
2.4.1. Activity against E. coli . . . . .	13
2.4.2. Activity against B. subtilis . . . . .	13
2.4.3. Extraction of yorB-inducing Compound . . . . .	13
2.5. Species Determination and AntiSMASH Cluster Analysis . . . . .	13
2.5.1. Phylogeny of Strain Tü2401 . . . . .	13
2.5.2. AntiSMASH Cluster Identification . . . . .	13
<b>Bibliography</b>	<b>18</b>
<b>A. Appendix</b>	<b>20</b>
A.1. HPLC Methods . . . . .	20
A.2. Genomic analysis . . . . .	23
A.2.1. Phylogenetic Data . . . . .	23

# List of Figures

2.1.	K12 Bioassay results with media supernatants . . . . .	12
2.2.	Maximum likelihood tree of <i>Streptomyces</i> sp. Tü2401. . . . .	14
2.3.	Structures of known enediyne natural products . . . . .	16
A.1.	Cluster and subcluster search results for the cluster located on contig four. .	23

# List of Tables

1.1. Used chemicals and solvents . . . . .	1
1.2. Components of HPLC systems . . . . .	2
1.3. Column Specifications . . . . .	2
1.4. Media components for the cultivation of strain Tü2401 . . . . .	4
1.5. Mobile phase compositions used for Thin-Layer Chromatography . . . . .	8
1.6. Method for ion exchange chromatography . . . . .	9
A.1. Standard C18 screening method . . . . .	20
A.2. Standard aminocolumn method . . . . .	20
A.3. Aminocolumn method adapted for MS coupling . . . . .	21
A.4. The standard ZIC-HILIC method . . . . .	21
A.5. ZIC-HILIC method adapted for MS coupling . . . . .	21
A.6. Screening method for HPLC-MS . . . . .	22
A.7. Screening Method Polar-C18 . . . . .	22
A.8. Reverse Screening Method Polar-C18 . . . . .	22
A.9. Reference genomes for the construction of the phylogenetic tree . . . . .	23
A.10. Single copy genomes for tree construction . . . . .	24

# Abbreviations

Abbreviation	Description
AntiSMASH	Antibiotics & Secondary Metabolites Analysis Shell
EtAc	Ethyl acetate
GC	Gas Chromatography
MeAc	Methyl acetate
MS	Mass Spectrometry
HPLC	High Performance Liquid Chromatography
TLC	Thin Layer Chromatography
TMS	Trimethylsilane

# 1. Methods

## 1.1. Chemicals & Instruments

All chemicals and solvents were supplied by Merck, if not specified otherwise. Vendors for specific solvents are listed in Table 1.1. Water was purified prior to use by a MilliQ filtration system.

Table 1.1.: Used chemicals and solvents

Chemical	Supplier
J. T. Baker	Acetonitrile Chloroform
Alfa Aesar	Methyl acetate
Fisher Chemicals	Ethyl acetate

High performance liquid chromatography (HPLC) systems were manufactured by Agilent. The components of the HPLC systems are listed in Table 1.2. Detailed specifications of used HPLC-columns are listed in Table 1.3.

Table 1.2.: Components of HPLC systems

	<b>Component</b>	<b>Description</b>
Agilent 1100 Series	G1322A	Degasser
	G1311A	Quaternary Pump
	G1313A	Autosampler
	G1316A	Column Compartment
	G1315B	Diode Array Detector
Agilent 1200 Series	G1379B	Degasser
	G1312A	Binary Pump
	G1367B	Autosampler
	G1330B	Thermostat
	G1316A	Column Compartment
	G1315B	Diode Array Detector
Agilent 1260 Infinity	G4225A	Degasser
	G1312C	Binary Pump
	G1329B	Autosampler
	G1330B	Thermostat
	G1316A	Column Compartment
	G1315D	Diode Array Detector

Table 1.3.: Column Specifications

<b>Manufacturer</b>	<b>Line</b>	<b>Type</b>	<b>Size</b>
Merck	SeQuant®	ZIC®-HILIC 3.5 µm	150 × 4.6 mm
	Luna®	NH2 5 µm	250 × 4.6 mm
	Kinetex®	Polar-C18 2.6 µm	150 × 4.6 mm
Dr. Maisch	Nucleosil-100	C18 5 µm	100 × 2.5 mm

## 1.2. Strain Cultivation

### 1.2.1. Media

All media were prepared by solving the components listed in Table 1.4 in MilliQ-H<sub>2</sub>O and adjusting the pH with NaOH and HCl. For solid media, 2 % (w/v) agar was added. Media were sterilized by autoclaving at 121 °C and 230 kPa for 15 min. Fluid media were stored at ambient temperature, solid media at 8 °C.

### 1.2.2. *Escherichia coli* K12 and *Bacillus subtilis* 168

*Escherichia coli* K12 and *Bacillus subtilis* 168 were cultivated in LB medium (10 g peptone, 5 g yeast extract, 10 g NaCl per liter; pre-mixed by Roth) at either 37 °C (K12) or 30 °C (168). Liquid cultures were shaken at 200 rpm in flasks with baffles and spirals. Plate cultures were grown in an incubator.

### 1.2.3. General cultivation of *Streptomyces* sp. Tü2401

Agar-plate cultures of *Streptomyces* sp. Tü2401 were grown on ISP2 medium at 29 °C. 100 µL of spore solution or liquid culture were used for inoculation. Liquid cultures were incubated at 27 °C in shake flasks with aluminium caps. Pre-cultures were grown in 20 mL of NL 410 in 100 mL flasks and inoculated with plate-grown mycelium. Main cultures were grown in 100 mL medium in 500 mL flasks.

### 1.2.4. Batch Fermentation of *Streptomyces* sp. Tü2401

*Streptomyces* sp. Tü2401 was cultivated at a ten-liter scale in a continuous stirred tank bioreactor. 500 mL of pre-culture were grown in five 500 mL shake flasks containing 100 mL of NL 410 medium without CaCO<sub>3</sub>. The pre-cultures were inoculated from stored ISP-agar plates and grown for 72 h at 27 °C. The pre-cultures were pooled and used to inoculate 9.5 L of OM medium for fermentation. The temperature was kept at 27 °C with an airflow of 5 L min<sup>-1</sup> and a rotor speed of 200 rpm. Control samples of 15 mL were taken throughout the process at regular intervals. Fermentation was stopped after 125 h and the culture broth was harvested. Further processing is described in section 1.4.3.

**Table 1.4.: Media components for the cultivation of strain Tü2401.** All amounts are calculated for one liter of MilliQ-H<sub>2</sub>O. The pH was adjusted with NaOH and HCl.

Name	pH	Component	Amount	Vendor
LB		Yeast extract	5 g	Roth
		Tryptone	10 g	Roth
		NaCl	10 g	Roth
ISP2	7.3	Yeast extract	4 g	Oxoid
		Malt extract	10 g	Thermo Fisher
NL 200	7.5	D(-)Mannitol	20 g	Merck
		Cornsteep Powder	20 g	Sigma-Aldrich
NL 300	7.5	D(-)Mannitol	20 g	Merck
		Cotton Seed	20 g	Pharmamedia
NL 410	7.0	Glucose	10 g	Roth
		Glycerol	10 g	Acros Organics
		Oatmeal	5 g	Holo Bio Hafergold
		Soymeal	10 g	Hensel
		Yeast extract	5 g	Oxoid
		Bacto Casaminoacids	5 g	Difco
		CaCO <sub>3</sub>	1 g	
NL 500	8.0	Starch	10 g	Roth
		Glucose	10 g	Roth
		Glycerol	10 g	Acros Organics
		Fish Meal	15 g	Sigma-Aldrich
		Sea Salts	10 g	Sigma-Aldrich
OM	7.3	Oatmeal	20 g	Holo Bio Hafergold
		Trace metal mix	5 mL	
Trace metal mix		CaCl <sub>2</sub> · 2 H <sub>2</sub> O	3 g	
		Fe <sup>3+</sup> citrate	1 g	
		MnSO <sub>4</sub> · H <sub>2</sub> O	200 mg	
		ZnCl <sub>2</sub>	100 mg	
		CuSO <sub>4</sub> · 5 H <sub>2</sub> O	25 mg	
		Na <sub>2</sub> B <sub>4</sub> O <sub>7</sub> · 10 H <sub>2</sub> O	20 mg	
		CoCl <sub>2</sub> · 6 H <sub>2</sub> O	4 mg	
		Na <sub>2</sub> MoO <sub>4</sub> · 2 H <sub>2</sub> O	10 mg	

## 1.3. Bioassays

### 1.3.1. Agar Diffusion Bioactivity Assays

Agar diffusion bioactivity assays against *E. coli* K12 and *B. subtilis* 168 were conducted on LB-agar in petri dishes. Round petri dishes ( $\varnothing = 92$  mm) were filled with 20 mL of liquid agar, square dishes (120 × 120 mm) were filled with 40 mL. Solidified agar plates were stored at 8 °C.

400  $\mu$ L (200  $\mu$ L for round plates) of liquid culture at an optical density of 0.3 to 0.6 at 600 nm were spread on the solid agar plate with a drigalski spatula until dry. Round wells ( $\varnothing = 7$  mm) were punched out of the agar and filled with 50  $\mu$ L of sample. Finished plates were stored for 1 h at ambient temperature, before incubating them at either 30 °C or 37 °C over night.

### 1.3.2. *yorB* Reporter Gene Assay

Agar-based *yorB*-reporter gene assays were performed with *Bacillus subtilis* 1S34 pHJS105-*yorB-lacZ2*.<sup>1</sup> 20 mL of LB-agar with added 50  $\mu$ g mL<sup>-1</sup> Spectinomycin were inoculated with 500  $\mu$ L of overnight culture and grown until the stationary phase. 50 mL LB-softagar (0.7 % agarose) with 150  $\mu$ g mL<sup>-1</sup> 5-bromo-4-chloro-3-indolyl- $\beta$ -D-galactopyranoside (X-Gal) were prepared. The strain was added to a concentration of  $3 \times 10^7$  colony-forming units per milliliter and poured into a square petri-dish. After solidification, 50  $\mu$ L of test samples were filled in wells. The plates were incubated at 30 °C for 14 to 18 h and analyzed for induction.

## 1.4. Sample Preparation and Extraction

Extracts and reverse extracts of *Streptomyces* sp. Tü2401 were generally obtained through filtrated medium supernatants. After cultivating the strain for 4 to 7 days, the harvested biomass was centrifuged at 9000 rpm for 20 min. The supernatant was collected and filtered through a 0.2 µm sterile filter. The filtrate was stored at 4 °C.

### 1.4.1. Preparation of medium extracts

Medium filtrate extracts were prepared by adding an equal amount of solvent to the filtrate and shaking the mixture for 30 min. The phases were separated by centrifugation at 4000 rpm for 10 min. Both phases were collected separately and stored at 4 °C. Samples were concentrated by drying them under vacuum at either 40 °C (ethyl acetate, methyl acetate) or 60 °C (butanol, water) and resuspending them in a fifth of the initial volume. Organic phases were resuspended in methanol, aqueous phases in water.

### 1.4.2. Determination of Extraction Conditions

5 mL filtered medium aliquots of Tü2401 were transferred to three sets of five 15 mL falcon tubes. The pH of the tubes in each set was adjusted to 2, 5, 7, 9 or 11 with NaOH and HCl. Each set was extracted with either ethyl acetate, methyl acetate or ethyl formate and both phases were collected. Each phase was tested for bioactivity against *E. coli* K12.

### 1.4.3. Processing of Fermentation Broth

The harvested fermentation broth was supplemented with diatomaceous earth and filtered through Pall T 1500 filter plates (relative retention range 10 - 30 µm). The remaining filter cake was discarded and the filtrate transferred to a stirring bucket. Two liters of ethyl acetate were added to the filtrate and stirred for 30 min. After completed phase-separation, the organic phase was collected and the aqueous phase reused for further extraction. The process was repeated, until 10 L of extract had been generated. Both phases were collected seperately and concentrated in a rotary evaporator at 40 °C. The concentrated aquous phase was frozen at –20 °C and lyophilized. The organic concentrate was stored at 8 °C.

#### **1.4.4. Agar Plate Extraction**

Standard ISP2 agar plates were ground with a blender and extracted with an equal volume of butanol or ethyl acetate for 1 h. The mixture was centrifuged at 4000 rpm for 1 h and the supernatant collected. The remaining slurry was resuspended in the same amount of water, centrifuged at 4000 rpm for 1 h and the supernatant collected.

Special ISP2 agar plates with low-melting-point agarose (LMPA) were prepared by substituting the 2 % (w/v) agar of regular plates with 4 % (w/v) LMPA. 75 mL of LMPA agar plates were melted in Schott-flasks at 70 °C and extracted with either butanol or ethyl acetate for 30 min. The organic phase was collected and the remaining agar extracted again with 50 mL of water.

All collected organic extracts were dried at 40 °C (ethyl acetate) or 60 °C (butanol) and resuspended in 1 mL methanol.

## 1.5. Bioactivity-guided Isolation

### 1.5.1. Thin Layer Chromatography

Thin layer Chromatography was performed with reverse extracts of Tü2401 on TLC Silica Gel 60 F<sub>254</sub> plates by Merck. Aqueous samples were applied by pipetting 1 µL at a time and letting the plate dry until the next application. The TLC chambers were filled up to 1 cm with solvent and incubated for 12 h. The plates were run until either 75 % of the plate had been soaked or 2 h had passed. The solvents used as mobile phases are listed in Table 1.5.

Table 1.5.: Mobile phase compositions used for Thin-Layer Chromatography

Solvent	Ratio (v/v)
Acetonitrile / Water	85:15
Butanol / Acetic acid / Water	14:3:2 and 42:10:7
Butanol / Ethanol / Water	3:2:1
Ethyl acetate / 2-Propanol / Water	6:3:1
Chloroform / Methanol	8:3

The working orcin staining solution was prepared by mixing two storage solutions, solution A and B, at a ratio of 10:1 (v/v). Solution A contained 1 % (w/v) Fe<sup>III</sup>Cl in 10 % sulfuric acid, solution B contained 6 % (w/v) Orcin in ethanol. The plates were sprayed with the working solution and treated with a heat gun for a few seconds.

Preparative samples were obtained by scraping the silica off the unstained plate and collecting it in reaction tubes. The samples were then extracted with 1 mL methanol, vortexed and sonicated for 30 min. After centrifugation at 14,000 rpm for 5 min, the supernatant was transferred to a new tube and the extraction process repeated. The methanolic samples were dried at 30 °C and resuspended in an amount of water equal to the sample initially applied on the TLC plate.

### 1.5.2. Ion Exchange Chromatography

Ion exchange chromatography was performed with both a strong anion (Diaion SA11A, 20-50 mesh, Cl<sup>-</sup> form) and a strong cation exchange resin (Dowex 50WX4, 100-200 mesh, Na<sup>+</sup> form). Three solutions were used for all operations: An acidic solution (1 % (v/v) formic acid, pH 2), a neutral solution (MilliQ-H<sub>2</sub>O, pH 7) and a basic solution (2 % (v/v)

ammonium hydroxide, pH 11). Prior to column preparation, both resins were swollen for 24 h. The anion exchange resin (AnX) was swollen in the basic solution and the cation exchange resin (CatX) was swollen in the acidic solution. 12.5 mm diameter glass columns were filled with resin up to a bed height of 10 cm (AnX) or 9.5 cm (CatX). Both columns were operated at a constant flow of  $2.5 \text{ mL min}^{-1}$ . All method steps are listed in Table 1.6. The pH of the applied sample was adjusted to pH 2 (CatX) or pH 11 (AnX) with NaOH and HCl. The flow-through of each step was collected and stored at  $4^\circ\text{C}$ .

Table 1.6.: **Method for ion exchange chromatography.** pH values and relative volume of the solutions used for ion exchange chromatography with both strong anion exchange (AnX) and cation exchange (CatX) resins. Both resins were loaded with 1 mL of sample

Step	AnX pH	CatX pH	Column Volumes
Equilibration	11	2	2
Wash 1	7	7	1
Sample application	11	2	*
Wash 2	11	2	1
Wash 3	7	7	1
Elution	2	11	5

### 1.5.3. Trimethylsilane Derivatization and Gas Chromatography

The derivatization and gas chromatography (GC) measurements were performed by Dr. Dorothee Wistuba of the mass spectrometry department at the institute of organic chemistry in Tübingen. Dried HPLC fractions were suspended in  $500 \mu\text{L}$  *N,O*-Bis(trimethylsilyl)-trifluoroacetamide with added  $40 \mu\text{L}$  pyridine and heated to  $110^\circ\text{C}$ . Afterwards, the samples were dried with nitrogen gas and redissolved in dichloromethane. The derivatized samples were analyzed with a Hewlett Packard (HP) 6890 GC-system coupled to a HP 5973 mass selective detector. The Agilent DB5 column measured  $13 \text{ m} \times 0.25 \text{ mm}$  with a film thickness of  $0.1 \mu\text{m}$ . Helium was used as the carrier gas.

### 1.5.4. Preparative HPLC

Preparative HPLC was performed on either the Agilent 1100 Series or Agilent 1260 Infinity instrument coupled to an Agilent G1346C fraction collector. Occasional coupling of an

electric light scattering detector (ELSD) was achieved by mounting a 1:5-splitter after the UV-Detector. 4/5 of the flow was directed to the fraction collector, the remaining 1/5 was directed to the ELSD. The ELSD was operated at a temperature of 40 °C and with nitrogen gas at a pressure of 3.2 bar. Detailed information about the used columns and methods can be found in Table 1.3 and the appendix. The obtained data was analyzed with the Agilent Chemstation (Version B.04.03). All samples were centrifuged at 14,000 rpm, before transferring the supernatant to HPLC-vials. All fractions were collected by timeslices of 1 min and stored at 4 °C to 8 °C, before drying them at 40 °C. Dried fractions were resuspended in an amount of water equal to the amount of injected sample and stored at 4 °C to 8 °C. Detailed method descriptions are found in the appendix at section A.1.

### 1.5.5. Analytical HPLC and Mass Spectrometry

For mass spectrometry, an Agilent 1200 series HPLC system was coupled to an Agilent 6330 IonTrap LC-MS mass spectrometer. It features electrospray ionization with alternating positive and negative modes. The instrument was controlled with 6300 Series Trap Control (Version 6.1) and data was analyzed using DataAnalysis for 6300 Series Ion Trap LC-MS (Version 3.4).

## 1.6. Genome Analysis

The phylogenetic tree was constructed by using 50 sequenced *Streptomyces* genomes (Table A.9) as reference. From these genomes and the concatenated contigs of *Streptomyces* sp. Tü2401, 50 single copy genes were identified by The gene sequences were aligned using the MAFFT tool (version 7) and refined using trimAl (version 1.2).<sup>2-4</sup> The maximum-likelihood tree was constructed with RAxML (version 8).<sup>5</sup> The average nucleotide identity was calculated with the JSpeciesWS web tool.<sup>6</sup> The final tree was visualized using Interactive tree of life (iTOL) v3.<sup>7</sup>

All five contigs were uploaded individually to the Antibiotics & Secondary Metabolite Analysis Shell (AntiSMASH) webserver.<sup>8-10</sup> Clusters were identified with standard settings and ClusterFinder enabled.

## 2. Results & Discussion

### 2.1. Determination of Extraction Conditions

Preliminary experiments demonstrated, that the antibiotic compound could not be extracted with ethyl acetate. Only the medium supernatant of the complex media NL 200, NL 300, NL 500 and OM produced notable inhibition zones on plate bioactivity assays. Moreover, the compound was not retained in any matter, when the supernatant was separated by HPLC with a common C18 column. The compound is likely very hydrophilic, so that usual extraction and reverse-phase chromatography protocols are not applicable. Because of the difficulties involved in working with aqueous solvents, an extraction procedure involving organic solvents would be beneficial. Additionally, out of the four complex media, in which Tü2401 is able to produce the antibiotic, one with optimal properties has to be determined.

For determination of the optimal medium, Tü2401 was grown in each of the NL and OM media for either four or seven days. The obtained medium supernatants were filtrated by using  $0.45\text{ }\mu\text{m}$  and  $0.2\text{ }\mu\text{m}$  consecutively. OM supernatant proved to be the easiest to filtrate, while the NL media clogged the filters after few milliliters had passed through. Each filtrate was subjected to the standard bioassay against *Escherichia coli* K12 to determine the antibiotic activity. Pictures of the assay results are displayed in Figure 2.1.

Most samples cause notable ( $\varnothing > 1\text{ cm}$ ) zones of inhibition in the agar diffusion assay. NL 500 after seven days and OM in both cases possess the greatest activity with inhibition zones greater than 1.5 cm. When cultivated in NL 300, Tü2401 seems to take longer than four days to synthesize the compound.



(a) Four day growth period



(b) Seven days growth period

**Figure 2.1.: K12 Bioassay results with media supernatants**

*Streptomyces* sp. Tü2401 was grown for either four (a) or seven days (b) in four different complex media. The filtrated medium supernatant was tested against *Escherichia coli* K12. Media: (Top) NL 200 (Left) NL 300 (Right) NL 500 (Bottom) OM.

## 2.2. Chromatographic Separation

### 2.2.1. Reverse-Phase HPLC

### 2.2.2. HPLC with Amino Column

### 2.2.3. Hydrophilic Interaction Chromatography

### 2.2.4. Ion exchange Chromatography

### 2.2.5. Thin-Layer Chromatography

## 2.3. Dereplication

### 2.3.1. HPLC Mass Spectrometry

### 2.3.2. Trimethylsilane Derivatization and Gas Chromatography

## 2.4. Antibacterial Activity Spectrum

### 2.4.1. Activity against E. coli

### 2.4.2. Activity against B. subtilis

### 2.4.3. Extraction of yorB-inducing Compound

## 2.5. Species Determination and AntiSMASH Cluster Analysis

### 2.5.1. Phylogeny of Strain Tü2401

### 2.5.2. AntiSMASH Cluster Identification

One cluster was detected on contig four and identified as a Type1-PKS-NRPS hybrid. It shows a 95 % cluster identity to the C-1027 biosynthetic gene cluster from *Streptomyces globisporus* C-1027 (MiBiG accession no. BGC0000965). Additionally, three homologous

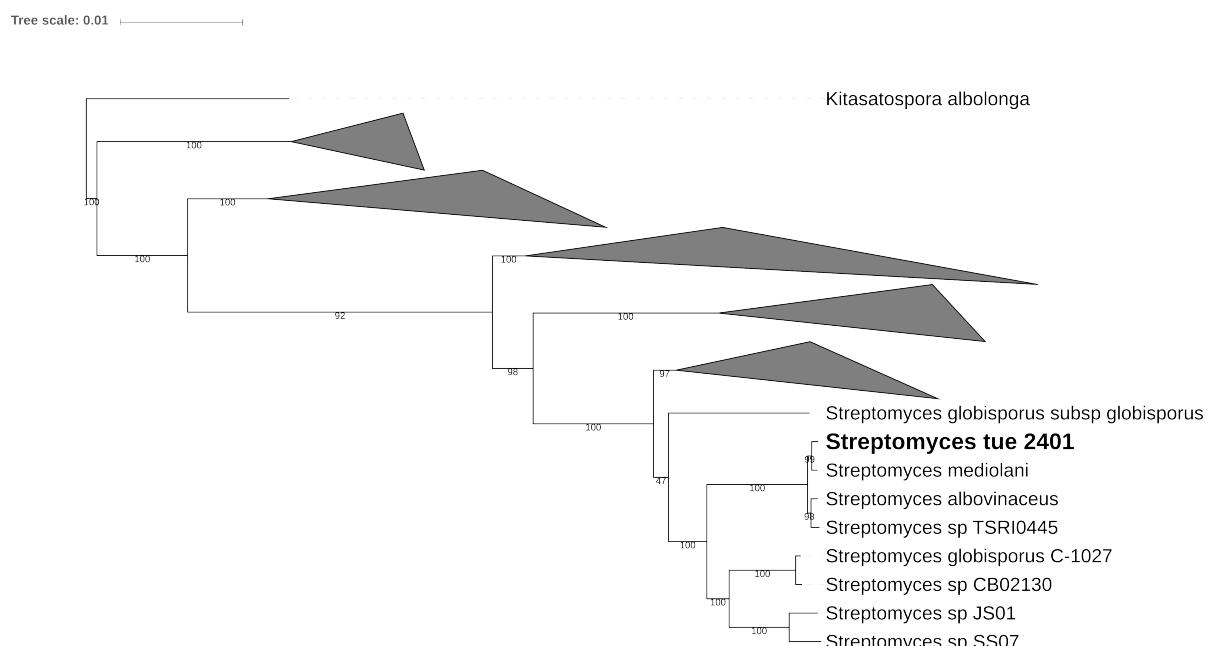


Figure 2.2.: Maximum likelihood tree of *Streptomyces* sp. Tü2401.

The tree was constructed using a multiple-sequence alignment of 50 single-copy genes across 50 *Streptomyces* reference genomes. The node belonging to *Streptomyces* sp. Tü2401 is highlighted with bold text. Only the nine most closely related nodes and the outgroup are shown. Dark triangles represent hidden, collapsed nodes.

subclusters with 100 % identity were identified, which are associated with the synthesis of C-1027, Neocarzinostatin and Maduropeptin enediynes (see Figure A.1). The presence of this cluster could indicate, that the strain Tü2401 is capable of producing a compound similar to enediyne antibiotics.

Enediyne natural products are a class of cytotoxic bacterial compounds, which cause extensive DNA-damage.<sup>11–14</sup> 11 different enediyne natural products are known, all of which feature either a bicyclo[7.3.0]dodecadienediyne core inside a nine-membered ring or a bicyclo[7.3.1]tridecadiyne core inside a ten-membered ring (Figure 2.3). The 9-membered family includes neocarzinostatin, C-1027 and maduropeptin. The 10-membered family includes calicheamicin  $\gamma_1^I$ , esperamicin A<sub>1</sub> and dynemicin A.<sup>11</sup> Enediynes are potent cytotoxic agents because of their ability to induce DNA double-strand breaks.<sup>15</sup> Electronic rearrangement of the carbocycle produces a benzenoid diradical, which abstracts hydrogen atoms from the DNA-backbone. The resulting radicals cause interstrand crosslinks or react with molecular oxygen. While the ten-membered enediyne compounds were isolated as free-standing chromophores, most of the compounds in the nine-membered family were isolated in conjunction with a protective apoprotein.<sup>11</sup> The nine-membered chromophore of C-1027, which was isolated from *Streptomyces globisporus* C-1027, is bound noncovalently to an 110 amino acid apoprotein.<sup>13,16–23</sup> The isolated chromophore has been shown to be very unstable, whereas the holo C-1027 did not lose activity under the same conditions.<sup>19–21</sup> The apoprotein binds specifically to the C-1027 chromophore, supposedly by hydrophobic pocket, which binds the benzoxazine side chain.<sup>20,24</sup> The enediyne antibiotics neocarzinostatin and maduropeptin, which were also isolated from actinomycetes, feature highly specific and protective apoproteins as well..<sup>13</sup>

The homologies of the identified cluster could be an indicator, that the strain Tü2401 is capable of synthesizing an enediyne antibiotic with a nine-membered core and a corresponding apoprotein. The potent DNA-strand-breaking capabilities of this compound-class could induce the *yorB* reporter system of *Bacillus subtilis* 1S34 pHJS105-*yorB-lacZ2* in the *yorB*-induction assay. A number of compounds, which cause DNA double strand breaks and crosslinks are reported to induce the system, though none of them belong to the family of endiyne antibiotics.<sup>1</sup> Whether this is due to inactivity or to this family not having been tested in the assay is unclear, since the compound library is not publicly accessible. Nevertheless, an endiyne compound could be responsible for the induction.

The assay in Section 2.4.3 showed, that the *yorB* inducing compound is produced when the strain is grown on an ISP2 agar plate, but it could not be extracted via ethyl acetate or

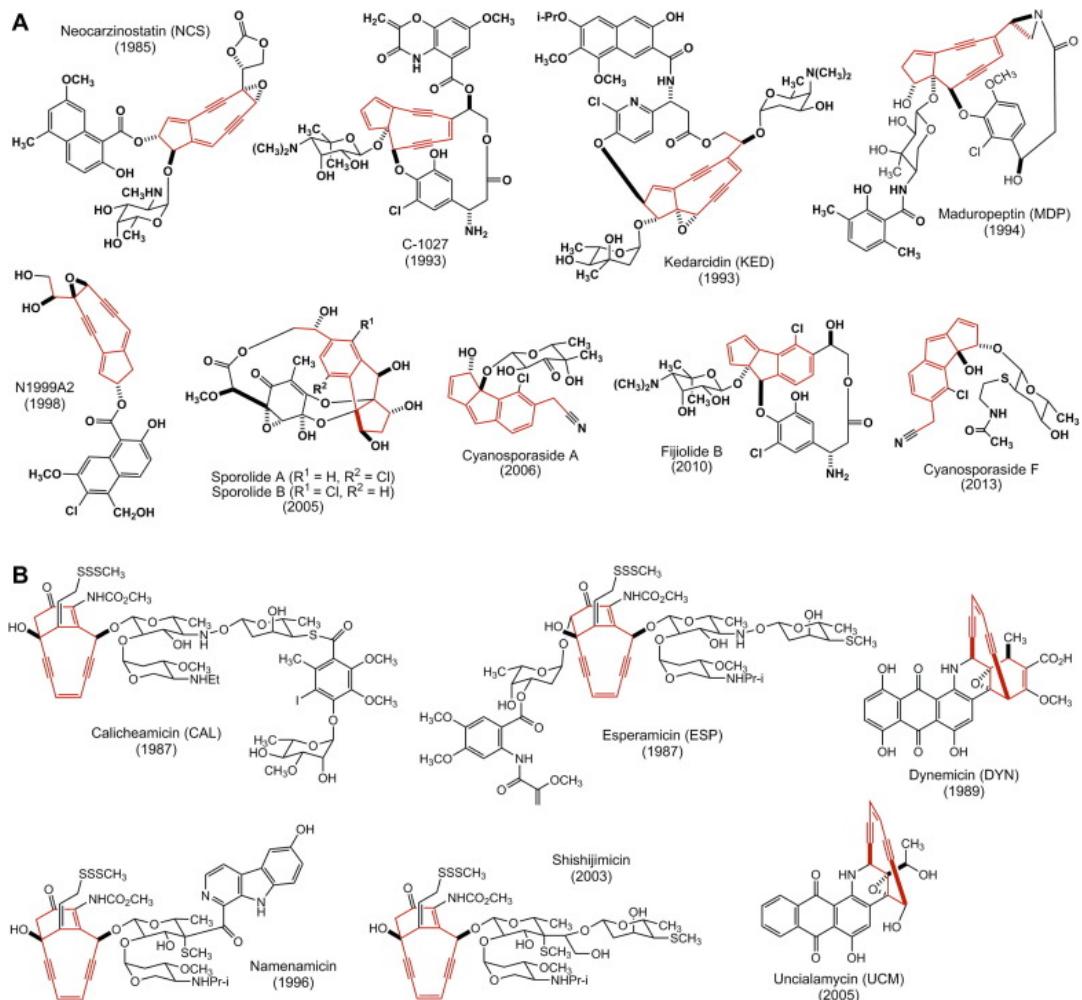


Figure 2.3.: **Structures of known enediyne natural products.** Enediyne cores are highlighted in red. (A) Compounds with nine-membered rings. (B) Compounds with ten-membered rings. The year of structure confirmation is displayed in parentheses. The sporolides, cyanosporolids and fijiolides do not contain an endiyene core, but are proposed to be derived from enediyne precursors. Reprinted from Shen *et al.* (2015) Copyright 2014 Elsevier Ltd.

butanol. Only very low activity was retained in the aqueous phase. If the compound is indeed an endiyne, this loss of activity could be due to the high instability of the chromophore. The apoprotein could have been detached during the extraction and concentration process, which also included high temperatures of 40 to 60 °C. Combined with an incubation time of several days between extraction and assay, this could have led to the degradation of the chromophore below the sensitivity threshold. The high temperatures and long storage times also apply to the numerous HPLC-fractioning samples subjected to the *yorB*-induction assay.

To verify this assumption, the putative endiyne compound has to be extracted by an adapted protocol, dereplicated and subjected to the assay in pure form. The C-1027 antibiotic protein from *S. globisporus* was precipitated from the medium supernatant by the addition of ammonium sulfate and purified by dialysis and column chromatography.<sup>22</sup> The active chromophore could be extracted from the apoprotein with methanol at 0 °C.<sup>20</sup> However, as of now, untreated medium supernatant samples of the strain Tü2401 did not induce the *yorB*-reporter system. The cultivation in liquid OM medium is probably not sufficient for production of the putative endiyene compound and the protocol would have to be adapted for the extraction from ISP2 agar plates. To circumvent this, other cultivation media could be employed and tested for *yorB*-induction. The holo endiyne-apoprotein complex should be stable enough for routine testing of media and media supernatants. The only alternative to optimizing production conditions would be heterologous expression of the biosynthetic cluster. For the endiyne compound family though, this has, as of now, only been partly achieved for the nine-membered endiyne neocarzinostatin.<sup>25</sup>

The isolation of the putative endiyne antibiotic would be a very promising target. Only eleven compounds of this class are known to this date, yet several members are in use or development as anticancer drugs with promising results.<sup>11,26</sup> Isolation of a new endiyne compound could hold a strong promise for the discovery of a new anticancer drug lead structure.

# Bibliography

- (1) Urban, A.; Eckermann, S.; Fast, B.; Metzger, S.; Gehling, M.; Ziegelbauer, K.; Rübsamen-Waigmann, H.; Freiberg, C. *Applied and environmental microbiology* **2007**, *73*, 6436–43.
- (2) Katoh, K.; Rozewicki, J.; Yamada, K. D. *Briefings in Bioinformatics* **2017**, *30*, 1072–80.
- (3) Kuraku, S.; Zmasek, C. M.; Nishimura, O.; Katoh, K. *Nucleic acids research* **2013**, *41*, W22–W28.
- (4) Capella-Gutiérrez, S.; Silla-Martínez, J. M.; Gabaldón, T. *Bioinformatics* **2009**, *25*, 1972–1973.
- (5) Stamatakis, A. *Bioinformatics* **2014**, *30*, 1312–1313.
- (6) Richter, M. F.; Drown, B. S.; Riley, A. P.; Garcia, A.; Shirai, T.; Svec, R. L.; Hergenrother, P. J. *Nature* **2017**, *545*, 299–304.
- (7) Letunic, I.; Bork, P. *Nucleic acids research* **2016**, *44*, W242–W245.
- (8) Weber, T.; Blin, K.; Duddela, S.; Krug, D.; Kim, H. U.; Brucolieri, R.; Lee, S. Y.; Fischbach, M. A.; Müller, R.; Wohlleben, W.; Breitling, R.; Takano, E.; Medema, M. H. *Nucleic Acids Research* **2015**, *43*, W237–W243.
- (9) Blin, K.; Medema, M. H.; Kazempour, D.; Fischbach, M. A.; Breitling, R.; Takano, E.; Weber, T. *Nucleic Acids Research* **2013**, *41*, W204–W212.
- (10) Medema, M. H.; Blin, K.; Cimermancic, P.; de Jager, V.; Zakrzewski, P.; Fischbach, M. A.; Weber, T.; Takano, E.; Breitling, R. *Nucleic Acids Research* **2011**, *39*, W339–W346.
- (11) Liang, Z. X. *Natural Product Reports* **2010**, *27*, 499–528.
- (12) Gredicak, M.; Jerić, I. *Acta pharmaceutica (Zagreb, Croatia)* **2007**, *57*, 133–50.
- (13) Smith, A. L.; Nicolaou, K. C. *Journal of Medicinal Chemistry* **1996**, *39*, 2103–2117.

- (14) Nicolaou, K. C.; Smith, a. L.; Yue, E. W. *Proceedings of the National Academy of Sciences* **1993**, *90*, 5881–5888.
- (15) Shen, B.; Hindra; Yan, X.; Huang, T.; Ge, H.; Yang, D.; Teng, Q.; Rudolf, J. D.; Lohman, J. R. *Bioorganic and Medicinal Chemistry Letters* **2015**, *25*, 9–15.
- (16) Minami, Y.; ichiro Yoshida, K.; Azuma, R.; Saeki, M.; Otani, T. *Tetrahedron Letters* **1993**, *34*, 2633–2636.
- (17) Yoshida, K.-I.; Minami, Y.; Azuma, R.; Saeki, M.; Otani, T. *Tetrahedron Letters* **1993**, *34*, 2637–2640.
- (18) Otani, T. *The Journal of antibiotics* **1993**, *46*, 791–802.
- (19) Sugiura, Y.; Matsumoto, T. *Biochemistry* **1993**, *32*, 5548–5553.
- (20) Matsumoto, T.; Okuno, Y.; Sugiura, Y. *Biochemical and biophysical research communications* **1993**, *195*, 659–666.
- (21) Otani, T.; Minami, Y.; Sakawa, K.; Yoshida, K.-I. *Journal of Antibiotics* **1991**, *44*, 564–568.
- (22) Otani, T.; Minami, Y.; Marunaka, T.; Zhang, R.; Xie, M. Y. *The Journal of antibiotics* **1988**, *41*, 1580–1585.
- (23) Hu, J.; Xue, Y.-C.; Xie, M.-Y.; Zhang, R.; Otani, T.; Minami, Y.; Yamada, Y.; Marunaka, T. *Journal of Antibiotics* **1988**, *41*, 1575–1579.
- (24) Okuno, Y.; Otsuka, M.; Sugiura, Y. *Journal of Medicinal Chemistry* **1994**, *37*, 2266–2273.
- (25) Zhang, J.; Van Lanen, S. G.; Ju, J.; Liu, W.; Dorrestein, P. C.; Li, W.; Kelleher, N. L.; Shen, B. *Proc Natl Acad Sci U S A* **2008**, *105*, 1460–1465.
- (26) Galm, U.; Hager, M. H.; Van Lanen, S. G.; Ju, J.; Thorson, J. S.; Shen, B. *Chemical Reviews* **2005**, *105*, 739–758.

# A. Appendix

## A.1. HPLC Methods

Vielleicht wenn hier text steht

Table A.1.: Standard C18 screening method

Parameter	Value
Column	Nucleosil-100 C18 5 µm 150×3 mm
Solvents	A: Water + 0.1 % Formic acid B: Acetonitrile + 0.1 % Formic acid
Method	Gradient 5 - 100 % B for 15 min Plateau 100 % B for 3 min
Flow	1.25 mL min <sup>-1</sup>
Temperature	25 °C
Injection Volume	50 µL

Table A.2.: Standard aminocolumn method

Parameter	Value
Column	Luna NH <sub>2</sub> 5 µm 250×4.6 mm
Solvents	A: Water + 0.1 % Formic acid B: Acetonitrile + 0.1 % Formic acid
Method	Isocratic 80 % B for 20 min + 100 % A for 10 min
Flow	2 mL min <sup>-1</sup>
Temperature	25 °C
Injection Volume	50 µL

Table A.3.: Aminocolumn method adapted for MS coupling

Component	Parameter
Column	Luna NH <sub>2</sub> 5 µm 250×4.6 mm
Solvents	A: Water + 0.1 % Formic acid B: Acetonitrile + 0.1 % Formic acid
Method	Isocratic 80 % B for 60 min.
Flow	0.5 mL min <sup>-1</sup>
Temperature	40 °C
Injection Volume	50 µL
Capillary Voltage	3500 V
Injector Temperature	350 °C
Target mass	400 m/z

Table A.4.: The standard ZIC-HILIC method

Component	Parameter
Column	ZIC-HILIC 3.5 µm 150×4.6 mm
Solvents	A: 10 mM Ammonium acetate B: Acetonitrile
Method	Isocratic 80 % B for 45 min.
Flow	0.8 mL min <sup>-1</sup>
Temperature	25 °C
Injection Volume	50 µL

Table A.5.: ZIC-HILIC method adapted for MS coupling

Component	Parameter
Column	ZIC-HILIC 3.5 µm 150×4.6 mm
Solvents	A: 10 mM Ammonium acetate B: Acetonitrile
Method	Isocratic 80 % B for 60 min.
Flow	0.5 mL min <sup>-1</sup>
Temperature	40 °C
Injection Volume	50 µL
Capillary Voltage	3500 V
Injector Temperature	350 °C
Target mass	400 m/z

Table A.6.: Screening method for HPLC-MS

Parameter	Value
Column	Nucleosil-100 5 $\mu\text{m}$ 150×3 mm
Solvents	A: Water + 0.1 % Formic acid B: Acetonitrile + 0.06 % Formic acid
Method	Gradient 0 - 100 % B for 15 min Plateau 100 % B for 2 min
Flow	0.4 mL min <sup>-1</sup>
Temperature	40 °C
Injection Volume	2.5 $\mu\text{L}$
Capillary Voltage	3500 V
Injector Temperature	350 °C
Target mass	400 m/z

Table A.7.: Screening Method Polar-C18

Parameter	Value
Column	Kinetex Polar-C18 2.6 $\mu\text{m}$ 150×4.6 mm
Solvents	A: Water + 0.1 % Formic acid B: Acetonitrile + 0.1 % Formic acid
Method	Gradient 5 - 100 % B for 20 min Plateau 100 % B for 6 min
Flow	1.2 mL min <sup>-1</sup>
Temperature	50 °C
Injection Volume	50 $\mu\text{L}$

Table A.8.: Reverse Screening Method Polar-C18

Parameter	Value
Column	Kinetex Polar-C18 2.6 $\mu\text{m}$ 150×4.6 mm
Solvents	A: Water + 0.1 % Formic acid B: Acetonitrile + 0.1 % Formic acid
Method	Gradient 100 - 5 % B for 20 min Plateau 100 % B for 6 min
Flow	1.2 mL min <sup>-1</sup>
Temperature	50 °C
Injection Volume	50 $\mu\text{L}$

## A.2. Genomic analysis

### A.2.1. Phylogenetic Data

Table including the reference genomes

Table A.9.: Reference genomes for the construction of the phylogenetic tree

1	2	3
1	2	3

Table including the identified single-copy genes

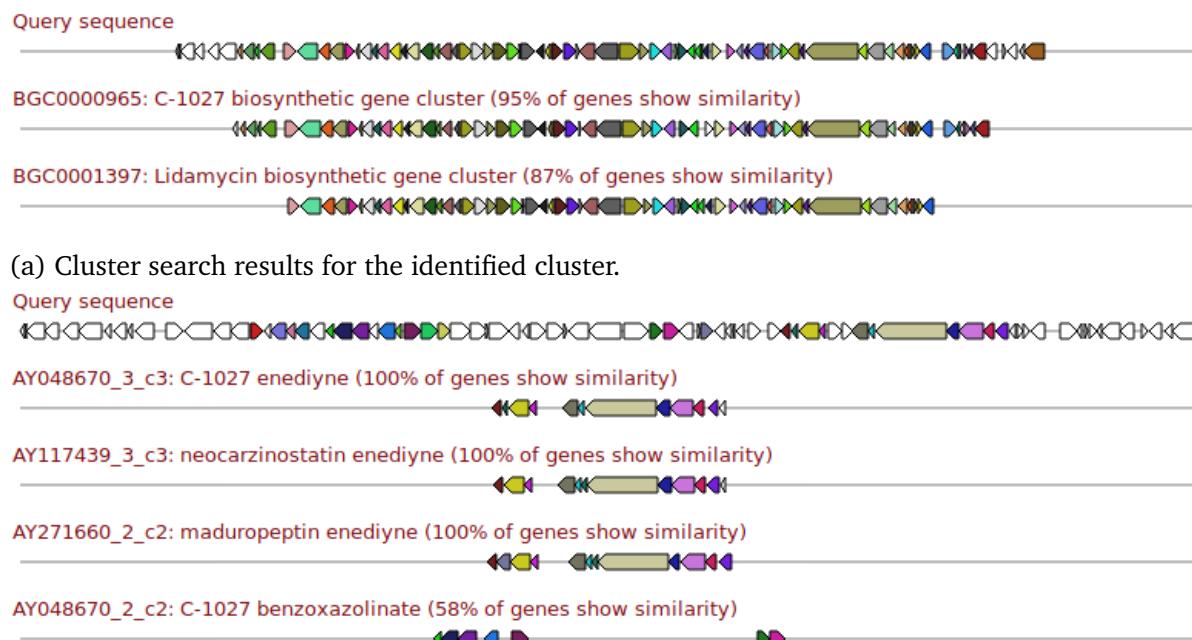


Figure A.1.: Cluster and subcluster search results for the cluster located on contig four. The 160 kb contig was submitted to AntiSMASH with the ClusterFinder option. Only the search results with the highest similarities are shown.

Table A.10.: Single copy genomes for tree construction

TIGR ID	Description
00008	translation initiation factor IF-1
00033	chorismate synthase
00060	ribosomal protein uL18
00062	ribosomal protein bL27
00118	acetolactate synthase, large subunit, biosynthetic type
00151	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
00171	3-isopropylmalate dehydratase, small subunit
00302	phosphoribosylformylglycinamide synthase, purS protein
00355	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase
00382	ATP-dependent Clp protease, ATP-binding subunit ClpX
00431	tRNA pseudouridine(55) synthetase
00484	translation elongation factor G
00615	recombination protein RecR
00631	exinuclease ABC subunit B
00708	cob(I)yrinic acid a,c-diamide adenosyltransferase
00962	ATP synthase F1, alpha subunit
00981	ribosomal protein uS12
01009	ribosomal protein uS3
01021	ribosomal protein uS5
01022	ribosomal protein bL36
01024	ribosomal protein bL19
01029	ribosomal protein uS7
01030	ribosomal protein bL34
01032	ribosomal protein bL20
01039	ATP synthase F1, beta subunit
01044	ribosomal protein uL22
01049	ribosomal protein uS10
01050	ribosomal protein uS19
01067	ribosomal protein uL14
01083	endonuclease III
01134	amidophorphoribosyltransferase
01162	phosphoribosylaminoimidazole carboxylase, catalytic subunit
01164	ribosomal protein uL16
01169	ribosomal protein uL1
01171	ribosomal protein uL2
01393	elongation factor 4
01980	FeS assembly protein SufB
02013	DNA-directed RNA polymerase, beta subunit
02027	DNA-directed RNA polymerase, alpha subunit
02156	phenylacetate-CoA oxygenase, PaaG subunit
02157	phenylacetate-CoA oxygenase, PaaH subunit
02952	RNA polymerase sigma-70 factor
03188	phosphoribosyl-ATP diphosphatase
03450	inositol 1-phosphate synthase
03631	ribosomal protein uS13
03632	ribosomal protein uS11