

1 A Benzaldehyde Derivative Obtained from
2 *Hypoxylon truncatum* NBRC 32353 Treated with
3 Hygromycin B

4 Hitoshi Kamauchi^{1*}, Mitsuaki Suzuki², Koichi Takao¹, Yoshiaki Sugita¹

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6 ¹Department of Pharmaceutical Sciences, Faculty of Pharmacy and Pharmaceutical Sciences,
7 Josai University, 1-1 Keyaki-dai, Sakado, Saitama 350-0295, Japan

8 ²Department of Chemistry, Faculty of Science, Josai University, 1-1 Keyaki-dai, Sakado,
9 Saitama 350-0295, Japan

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11 * To whom correspondence should be addressed. E-mail: kamauchi@josai.ac.jp.

1 **KEYWORDS**

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3 oxidase

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ABSTRACT

The ribosome-targeted antifungal agent hygromycin B (HygB) alters the secondary metabolite profiles of fungi. *Hypoxylon truncatum* NBRC 32353 fermented in the presence of hygromycin B in barley medium activated secondary metabolite synthesis. A new benzaldehyde derivative truncaaldehyde (**1**) was obtained, along with thirteen known compounds (**2-14**). The structures of the new compounds were revealed using NMR and single-crystal X-ray crystallography. The total synthesis of (\pm)-**1** was achieved using a four-step sequence, and chiral separation was accomplished. The isolated compounds were tested for their monoamine oxidase (MAO) -A and -B inhibitory activities, with six compounds ((\pm)-**1**, **4**, **5**, **7**, **8** and **10**) showing inhibitory activity.

Introduction

Microbes were much diversity in secondary metabolisms. They were adaptable for various survival conditions and different genes for secondary metabolisms were activated in each condition (ref. 1, 2). Gaining drug resistant was one of the adaptations to survival condition. Rifampicin resistant *Streptomyces* sp. had a mutation of RNA polymerase β -subunit genes. This mutation modulate bacterial gene expression, including natural product biosynthetic pathways and yielded new alkaloids inducamide A–C (ref. 3).

Hygromycin B (HygB) is the antifungal agents targeted to ribosome and inhibiting protein producing. Mutants resistant to ribosome-targeted drugs frequently possess mutations within a ribosomal component. This mutation could also change fungal secondary metabolisms (ref. 4).

Most microbial genes involved in secondary metabolite production are not expressed under laboratory growth conditions. These silent genes can be activated by epigenetic modulating agents such as histone deacetylase inhibitors (ref. 5). HygB also could activate fungal secondary metabolites without mutating the ribosomal DNA sequence like to epigenetic modulating agents. The production of secondary metabolites of *Fusarium* sp. RK97-94 was induced by HygB. HygB could activate self-resistance gene for a toxic secondary metabolites and compounds that were not expressed under laboratory growth conditions were discovered (ref. 6). Therefore, addition of HygB in the culture medium might induce new fungal secondary metabolites.

Fungi from the family Xylariaceae produce a variety of structurally unusual secondary metabolites (ref. 7). Benzo[j]fluoranthene derivatives isolated from *Hypoxylon* and *Annulohypoxylon* spp. show anti-angiogenesis activity (ref. 8, 9 and 10). The fruiting bodies of mushrooms can be harvested only during certain seasons. In Japan, fruiting bodies of *H. truncatum*

usually grow in the autumn. Fungal-type mushrooms are easy to grow in the laboratory year-round, making fungal-type mushrooms an attractive resource for chemical investigation.

In this study, we report the examination of secondary metabolites of fungal-type *H. truncatum* NBRC 32353 treated with HygB and evaluate their monoamine oxidase inhibitory activities.

Results

Fermentation of *H. truncatum* NBRC 32353

H. truncatum was fermented under several conditions, including agar (PGY agar medium; 2% peptone, 2% glucose, 1% yeast extract and 2% agar), liquid (PGY agar medium; 2% peptone, 2% glucose and 1% yeast extract), and solid media (Barley medium; 200 g of commercially available barley immersed with distilled water in a 1000 mL Roux flask). Barley medium provided the most efficient fermentation and the largest amount of extract. The phenotype of the original *H. truncatum* was white mycelia but under HygB conditions (200 g of barley immersed with distilled water containing HygB at a concentration of 31.2 µg/mL in a 1000 mL Roux flask) the color of barley was changed to yellow under the presence of HygB. HPLC profiles for a CHCl₃ extract of *H. truncatum* showed differences in secondary metabolites. The CHCl₃ extract from the barley medium without HygB showed principal constituent peaks around retention time of 32.0, 34.5 and 52.5 min, whereas the extract from *H. truncatum* fermented in the presence of HygB exhibited several newly discovered peaks (Figure 1).

Isolation

The CHCl₃ extract of *H. truncatum* NBRC32353 fermented under 31.2 µg/mL of HygB was subjected to silica-gel column chromatography (Si C. C.), octadecylsilyl silica-gel (ODS) C. C.,

and preparative HPLC. A pair of racemic compounds (\pm)-truncaaldehyde (**1**) was obtained along with thirteen known compounds. The structures of the known compounds brasilane D (**2**) (ref. 11), brasilane A (**3**) (ref. 11), trichobrasilenol (**4**) (ref. 12), 8-methoxy-1-naphthol (**5**) (ref. 13), sphaeropsidin A (**6**) (ref. 14), 5-hydroxy-8-methoxy-1-naphthol (**7**) (ref. 15), 3-methylorcilaldehyde (**8**) (ref. 16), xylarenone (**9**) (ref. 17), diketopiperazines (**10-13**) (ref. 18, 19, 20 and 21) and phenylethane-1,2-diol (**14**) (ref. 22) were identified on the basis of their spectroscopic data, as well as by comparison with published data (Figure 2).

Structure elucidation of (\pm)-truncaaldehyde (**1**)

(\pm)-Truncaaldehyde (**1**) was obtained as colorless needles by liquid-liquid diffusion using ethyl acetate and *n*-hexane. The molecular formula $C_{14}H_{20}O_5$ was determined the basis of HRFABMS. The IR spectrum of **1** suggested the presence of hydroxy group (3419 cm^{-1}) and carbonyl group (1635 cm^{-1}). The ^1H NMR spectrum showed signals attributable to four methyl protons at δ_{H} 2.06 (s, 3-Me), δ_{H} 2.56 (s, 6-Me), δ_{H} 1.30 (s, H-4'), and δ_{H} 1.35 (s, H-5'), a pair of oxy methylene protons at δ_{H} 4.10 (dd, $J = 9.6, 7.4\text{ Hz}$, H-1') and δ_{H} 4.22 (dd, $J = 9.6, 3.2\text{ Hz}$, H-1'), an aromatic proton at δ_{H} 6.28 (s, H-5), an aldehyde derived proton at δ_{H} 10.13 (s, 1-CHO), an oxymethine proton at δ_{H} 3.85 (dd, $J = 7.4, 3.2\text{ Hz}$, H-2') and a chelated hydroxyl group at δ_{H} 12.41 (s, 2-OH). The ^{13}C -NMR spectra showed four methyl groups at δ_{C} 7.3 (3-Me), δ_{C} 18.4 (6-Me), δ_{C} 25.1 (C-4') and δ_{C} 26.6 (C-5'), three carbons bonded to oxygen at δ_{C} 69.5 (C-1'), δ_{C} 76.7 (C-2') and δ_{C} 71.6 (C-3'), six aromatic carbons at δ_{C} 113.7 (C-1), δ_{C} 162.9 (each C-2 and C-4), δ_{C} 111.4 (C-3), δ_{C} 105.9 (C-5) and δ_{C} 141.6 (C-6) and an aldehyde at δ_{C} 193.3 (1-CHO) (Table. 1).

These spectral data suggested that compound **1** comprised a five-substituted benzaldehyde (C-1 to C-6) and a hydroxylated prenyl (C-1' to C-5') group. HMBC spectra showed correlations from

H-5 to C-4, 1-CHO to C-1, 2-OH to C-1 and C-2, 3-Me to C-3 and C-4, 6-Me to C-1, C-5 and C-6, H-5' to C-2', and a weak correlation from H-1' to C-4. These data indicated a planar structure of **1** comprising a 3-methylorcilaldehyde with a 2',3'-dihydroxyprenyl moiety connected to C-4 (Figure 3). We succeeded in the single-crystal X-ray crystallography of **1**, which has a chiral center at C-2'. This result showed **1** was a racemic mixture because the crystal structure of **1** has the centric space group *C2/c* (#15). (Figure 4, Figure S9).

Synthesis and chiral separation of (±)-truncaaldehyde (**1**)

To determine its absolute configuration, the total synthesis of (±)-**1** and its separation using chiral HPLC were performed. The novel benzaldehyde (±)-**1** was synthesized from commercially available 4-methylorcinol (**15**) using a four-step sequence (Scheme 1). Formylation was conducted using POCl₃/DMF to yield aldehyde (**8**). The prenyl ether at C-4 (**16**) was obtained by reaction using prenyl bromide and K₂CO₃. Epoxidation at C-2' to C-3' using *m*CPBA provided **17**. Finally, ring opening using HCl yielded (±)-**1** as colorless needles. The NMR data for synthetic (±)-**1** matched those for the isolated natural product.

The antipodes **1a** and **1b** were separated as scalemic mixture by chiral phase HPLC (Figure S10). These scalemic mixtures were optically active and their optical rotation was $[\alpha]_D^{19} +17.2$ (MeOH *c* 0.005, **1a**) and $[\alpha]_D^{19} -38.4$ (MeOH *c* 0.0025, **1b**) respectively. The absolute configurations of **1a** and **1b** were considered by comparing their optical rotation with the calculated rotation. The calculated optical rotation for (2'*S*)-**1** and experimental **1b** showed a negative orientation ((2'*S*)-**1** -95.9, **1b** -38.4), suggesting that the absolute configuration of **1b** was 2'*S*. In contrast, the absolute configuration of **1a** was 2'*R*.

Biological activity

Monoamine oxidases A and B (MAO-B) play a critical role in neurological disease. The MAO-A inhibitor moclobemide is a moderately effective antidepressant drug (ref. 23). The MAO-B inhibitors selegiline and resagiline are approved treatments for Parkinson's disease worldwide (ref. 24).

MAO-A and -B inhibitory tests were performed using the isolated compounds, initially at concentrations of 25 and 100 μ M. The IC₅₀ values of the compounds that inhibited MAO-A or -B over 50% at 25 μ M were tested (Table 2). The MAO-A inhibitory test showed that five compounds (**1**, **4**, **5**, **7** and **8**) were active and their IC₅₀ values were 19.0, 6.1, 1.6, 3.4 and 1.1 μ M, respectively. Four compounds (**6**, **10**, **12** and **14**) showed mild inhibitory activity. The MAO-B inhibitory test showed that four compounds (**4**, **5**, **8** and **10**) were active, with IC₅₀ values of 5.4, 13.7, 25.5 and 24.8 μ M, respectively. Three compounds (**2**, **6** and **12**) showed mild inhibitory activity. Compound **4** equally inhibited both MAO-A and -B, whereas **1**, **7** and **8** showed MAO-A selectivity. In contrast, only **10** showed MAO-B selectivity.

Discussion

The isolated compounds were categorized as being newly synthesized by HygB activation or as being biosynthesized under the original condition. The HPLC data suggested that the peaks for all isolated compounds except **5** and **6** were observed or increased in intensity under HygB conditions. Based on the structures of the isolated compounds and the HPLC data, we speculated regarding the biosynthetic pathway activated. The biosynthetic pathway for **1** was similar to their total synthetic process. Starting compound **8** was biosynthesized from a malonyl CoA, three acetyl CoA and an *S*-adenosyl methionine. Prenylation at 4-OH, epoxidation at C-2' to C-3' and ring-opening

of the epoxide generated (\pm)-**1**. Based on the HPLC profiles, the production of **8** was increased, indicating that this biosynthetic pathway was newly activated by HygB.

In bioactivity for MAO-A or -B the presence of a hydroxyl group at C-5 in the naphthalene derivatives (**5** and **7**) showed different inhibitory activities: **7** showed only MAO-A inhibitory activity, but **5** inhibited both MAO-A and B activity. In the brasilane sesquiterpenoids **2-4**, only the aglycone **4** showed both MAO-A and B inhibitory activity. The benzaldehyde derivatives (**1** and **8**) showed inhibitory activity with MAO-A selectivity.

In conclusion, activation of secondary metabolism in *H. truncatum* by HygB resulted in the production of MAO-A and -B inhibitors and new compounds. The activation method involved the addition of HygB to normal fermentation medium is usually used for liquid medium. Our results discovered activation with HygB was also effective for solid medium. This method is promising for the discovery of new natural and medicinal lead compounds.

Materials and Methods

General and Experimental Procedures

All reagents and solvents were purchased from commercial suppliers and used without further purification. Melting points were determined on a MP apparatus (Yanaco Technical Science Corp., Tokyo, Japan). Optical rotation was measured with a P-2000 polarimeter (Jasco Corp., Tokyo, Japan). IR spectra were recorded with a FT/IR-4600typeA spectrophotometer (KBr, Jasco Corp.). UV spectra were recorded with a UV-1280 spectrophotometer (Shimazu Corp., Kyoto Japan). 1D and 2D NMR spectra were measured with a Varian 400-MR (400 MHz) spectrometer (Agilent Technologies Japan, Ltd., Tokyo, Japan), using tetramethylsilane as the internal standard. Low- and high-resolution EI and FABMS spectra were measured with a JMS-700 spectrometer (JEOL,

Tokyo, Japan). Column chromatography was performed using Wakogel C-200 (FUJIFILM Wako Pure Chemical Corporation, Osaka, Japan) and ODS silica gel (YMC-GEL ODS-A, YMC Co., Ltd., Kyoto, Japan). Analytical and preparative HPLC was performed on a Jasco PU-4580 equipped with a Jasco UV-4570 detector (Jasco Corp.) at 210 nm (analytical) and 254 nm (preparative). Preparative HPLC columns were a PEGASIL ODS sp100 column ($\phi 10 \times 250$ mm, 5 μ m, Senshu Scientific Co. Ltd., Tokyo, Japan) and a CHIRALCELL OD-H column ($\phi 4.6 \times 250$ mm, 5 μ m, Daicel Corp., Osaka, Japan). X-ray diffraction measurements were performed at 90 K on a Bruker D8 Venture diffractometer equipped with a PHOTON II detector with Mo K α radiation ($\lambda = 0.71073$ Å, Bruker Japan K.K., Kanagawa, Japan).

Fermentation and extraction

The fungus *H. truncatum* NBRC32353 was purchased from the Biotechnology Center of the National Institute of Technology and Evaluation (Chiba, Japan). *H. truncatum* NBRC32353 was pre-incubated on PGY agar medium (2% peptone: Kyokuto Pharmaceutical Industrial, Tokyo, Japan; 2% glucose: FUJIFILM Wako Pure Chemical Corp.; 1% yeast extract: Becton Dickinson and Company, Franklin Lakes, NJ and 2% agar: Becton Dickinson and Company) at 27°C. After pre-incubation, *H. truncatum* NBRC32353 was inoculated into 1000 mL Roux flasks (12 flasks) containing barley (200 g per flask, Hakubaku, Yamanashi, Japan) immersed in hygromycin B dissolved in water (31.2 μ g/mL). Flasks were statically incubated at 26°C for 28 days. The fermented substrate was extracted with CHCl₃.

Analytical HPLC conditions

The analytical HPLC column was a CAPCELL PAK C18 ACR column ($\phi 4.6 \times 250$ mm, 5 μ m, Osaka Soda Co., Ltd., Osaka, Japan). The solvent conditions were acetonitrile and water (0–10 min: 20:80, 10–50 min: from 20:80 to 100:0, 50–60 min: 100:0) and the flow rate was 1.0 mL/min. The CHCl_3 extracts obtained following growth with or without HygB were dissolved at a concentration of 1 mg/mL, and 50 μ L was injected onto the column. Following purification, the isolated compounds were each dissolved at a concentration of 1 mg/mL, and 20 μ L was injected for analysis.

Isolation and purification

The CHCl_3 extract (18.8 g) was fractionated by silica-gel column chromatography (Si C. C.) with $\text{CHCl}_3/\text{MeOH}$ (100:1, 50:1, 25:1 and 10:1, followed by MeOH) to yield five fractions (a-e). Fraction a (3.4 g) was further subjected to Si C. C. (*n*-Hex/EtOAc) and octadecylsilyl (ODS) C. C. (MeOH/ H_2O), yielding the six fractions aa-af. Compounds **4** (30.4 mg), **5** (279.6 mg) and **6** (10.8 mg) were isolated as fraction aa, ac and ae. Fraction b (1.8 g) was subjected to Si C. C. (*n*-Hex/EtOAc) to yield eight fractions (ba-bi). Compound **1** (40.3 mg) was obtained from fraction bd (164.0 mg) by ODS C. C. (MeOH/ H_2O). ODS C. C. (MeOH/ H_2O) and preparative HPLC of fraction bb (300.5 mg) yielded **7** (4.2 mg, t_R 15 min) and **8** (2.7 mg, t_R 18 min). ODS C. C. (MeOH/ H_2O) of fraction bf (213.1 mg) yielded six fractions, and **9** (25.4 mg) was isolated as fraction bfb. Preparative HPLC for fraction bfe (95.7 mg) yielded **10** (19.1 mg, t_R 14 min), **11** (2.0 mg, t_R 18 min) and **12** (33.4 mg, t_R 20 min). Fraction bi (374.7 mg) subjected to Si C. C. ($\text{CHCl}_3/\text{MeOH}$) to yield **13** (139.2 mg). Fraction c (1.2 g) was subjected to Si C. C. ($\text{CHCl}_3/\text{MeOH}$) and ODS C. C. (MeOH/ H_2O) to yield **14** (42.0 mg). Fraction d (477.7 mg) Si C. C. ($\text{CHCl}_3/\text{MeOH}$) and ODS C. C. (MeOH/ H_2O) yielded **2** (8.7 mg) and **3** (52.4 mg).

Compound **1** (3.0 mg) was subjected to chiral phase HPLC with *n*-Hex/isopropanol (15:1), yielding **1a** (0.6 mg, *t_R* 16 min) and **1b** (0.3 mg, *t_R* 17.5 min) as scalemic mixture.

(±)- Truncaaldehyde (**1**)

Colorless needles, m.p. 90-92°C, $[\alpha]_D^{19} +17.2$ (MeOH *c* 0.005, **1a** (2'*R*)), $[\alpha]_D^{19} -38.4$ (MeOH *c* 0.0025, **1b** (2'*S*)), UV (MeOH) λ_{\max} (log ϵ) 206 (4.01), 296 (4.05) nm, IR (KBr) ν_{\max} 3419, 2964, 1635 cm^{-1} , ^1H and ^{13}C NMR data, see Table 1. HRFABMS m/z 269.1390 $[\text{M}+\text{H}]^+$ (calculated for $\text{C}_{14}\text{H}_{21}\text{O}_5$, 269.1389).

Synthesis of (±)-**1**.

Preparation of **16**

Compound **8** was prepared using the same procedure performed by Summer *et al.* (ref. 16). To a solution of **8** (210.0 mg, 1.27 mmol) in acetone (10.0 mL) was added potassium carbonate (282.4 mg 2.05 mmol) and 3,3-dimethylallyl bromide (290.3 mg, 1.95 mmol). The reaction mixture was stirred at room temperature for 12 h. Excess water was added and the reaction mixture was extracted using EtOAc. The organic layer was dried over Na_2SO_4 , yielding **16** (164.2 mg, 0.70 mmol, 55%) after purification by Si C. C. (*n*-Hex-EtOAc 5:1).

^1H -NMR (400 MHz, CDCl_3) δ 12.41 (s, 2-OH), 10.11 (s, 1-CHO), 6.27 (s, H-5), 5.47 (m, H-2'), 4.59 (brd, $J = 6.6$ Hz, H-2'), 2.56 (s, 6-Me), 2.05 (s, 3-Me), 1.80 (s, H-5'), 1.75 (s, H-4'); ^{13}C -NMR (100 MHz, CDCl_3) δ 193.1 (1-CHO), 163.6 (C-4), 162.9 (C-2), 141.3 (C-6), 138.3 (C-3'), 119.2 (C-2'), 113.3 (C-1), 111.5 (C-3), 106.2 (C-5), 65.3 (C-1'), 25.8 (C-4'), 18.5 (C-5'), 18.3 (6-Me), 7.1 (3-Me); HRFABMS m/z 234.1255 $[\text{M}]^+$ (calculated for $\text{C}_{14}\text{H}_{18}\text{O}_3$, 234.1256).

Epoxidation of **16**

To a solution of **16** (100.0 mg, 0.43 mmol) in dichloromethane (5.0 mL) was added sodium hydrogen carbonate (15.0 mg, 0.18 mmol) and *m*-chloroperoxybenzoic acid (103.2 mg, 0.60 mmol). The reaction mixture was stirred at room temperature for 12 h and extracted with dichloromethane-water. The organic layer was dried over Na₂SO₄, yielding **17** (40.4 mg, 0.16 mmol, 38%) with slight impurities after purification by Si C. C. (*n*-Hex-EtOAc 5:1).

¹H-NMR (400 MHz, CDCl₃) δ 12.41 (s, 2-OH), 10.13 (s, 1-CHO), 6.28 (s, H-5), 4.23 (dd, *J* = 11.1, 4.4 Hz, H-1'), 4.13 (dd, *J* = 11.1, 5.8 Hz, H-1'), 3.16 (dd, *J* = 5.8, 4.4 Hz, H-2'), 2.56 (s, 6-Me), 2.08 (s, 3-Me), 1.41 (s, H-5'), 1.38 (s, H-4'); ¹³C-NMR (100 MHz, CDCl₃) δ 193.3 (1-CHO), 163.0 (C-4), 159.4 (C-2), 141.5 (C-6), 120.0 (C-3), 113.6 (C-1), 106.0 (C-5), 67.5 (C-1'), 61.1 (C-2'), 58.2 (C-3'), 24.6 (C-4'), 19.1 (C-5'), 18.5 (6-Me), 7.2 (3-Me); HRFABMS *m/z* 250.1197 [M]⁺ (calculated for C₁₄H₁₈O₄, 250.1205).

Epoxide ring-opening reaction of **17**

To a solution of **17** (14.0 mg 0.056 mmol) in methanol (0.5 mL) and water (0.5 mL) was added 10% HCl (0.5 mL). The reaction was stirred at room temperature for 15 min. The crude mixture was purified by Si C. C. (*n*-Hex-EtOAc 5:1) to yield (±)-**1** (6.1 mg 0.023 mmol, 41%)

X-ray crystallographic data for **1**.

Crystal data: C₁₄H₂₀O₅, space group C2/c (#15), *a* = 17.3939(11) Å, *b* = 17.5658(11) Å, *c* = 10.4425(7) Å, β = 122.941(2) °, *V* = 2677.6(3) Å³, *Z* = 8, crystal size 0.143 × 0.190 × 0.232 mm, *T* = 90 K, reflections collected 21249, independent reflections 3169; 2534 with *I* > 2σ(*I*); *R*₁ = 0.0556 [*I* > 2σ(*I*)], *wR*₂ = 0.1484 (all data), GOF = 1.079. Crystallographic data for **1** reported in

1 this paper have been deposited at the Cambridge Crystallographic Data Centre under reference
2 number CCDC 2093272. These data can be obtained free of charge from The Cambridge
3 Crystallographic Data Centre via <https://www.ccdc.cam.ac.uk/structures/>

4 5 Computational analyses

6 Conformational analyses of **1b** were carried out in the MMFF94S (ref. 25 and 26) molecular
7 mechanics force field using CONFLEX software (ref. 27, 28 and 29). The geometries obtained
8 within a 1.0 kcal/mol energy range were further optimized using the semi-empirical PM6 (ref. 30)
9 method available in the Gaussian 09 program (ref. 31). The geometries were further optimized by
10 the density functional theory method at the B3LYP/6-31G (d) level (ref. 32, 33, 34 and 35) using
11 the Gaussian 09 program package to give two predominant conformers. Optical rotation was
12 obtained from the most stable conformation with the B3LYP/DGDZVP basis set (ref. 36).

13 14 Bioassay

15 MAO-A and -B inhibitory assay

16 MAO-A and MAO-B inhibitory activities were assayed using the method in our previous report
17 with slight modification (ref. 37). 3 μ L of human recombinant MAO-A solution (M7316, Sigma-
18 Aldrich) or 7 μ L of MAO-B solution (M7441, Sigma-Aldrich) was diluted with 1100 μ L of
19 potassium phosphate buffer (0.1 M, pH 7.4). 140 μ L of potassium phosphate buffer, 8 μ L of
20 kynuramine (final concentration is 30 μ M, Sigma-Aldrich, St. Louis, MO) in potassium phosphate
21 buffer, and 2 μ L of a dimethyl sulfoxide (DMSO) inhibitor solution (final DMSO concentration
22 of 1% (v/v)), were mixed and pre-incubated at 37°C for 10 min. 50 μ L of diluted MAO-A or MAO-
23 B solution was then added to each well. The reaction mixture was further incubated at 37°C and

1 the reaction was stopped after 20 min by the addition of 75 μ L of 2 M NaOH. The product
2 generated by MAO-A or MAO-B, 4-quinolinol, is fluorescent and was measured at Ex 310 nm/Em
3 400 nm using a microplate reader (SPECTRA MAX M2, Molecular Devices, Tokyo, Japan).
4 DMSO without test compound was used as the negative control, and pargyline (Sigma-Aldrich)
5 was used as a positive control. The IC₅₀ values were estimated using Prism software (version 5.02;
6 GraphPad, San Diego, CA).

Supplementary information

Supplementary information (¹H NMR, ¹³C NMR, 2D NMR data, for the new compounds) is available at Journal of Antibiotics website <https://>

Compliance with ethical standards

Conflict of interest

The authors declare that they have no conflict of interest.

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10

Figure legends

Fig. 1 HPLC profiles of the CHCl₃ ext. of *H. truncatum* cultured on barley medium with and without HygB.

Fig. 2 Chemical structures of compounds **1–14**.

Fig. 3 HMBC correlations of **1**.

Fig. 4 X-ray crystal structure of **1**.

Scheme legends

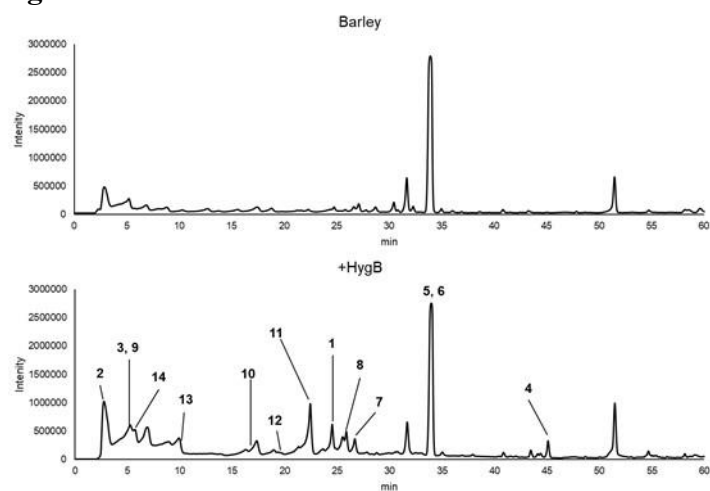
Scheme 1 Synthesis of (±)-**1**

Table legends

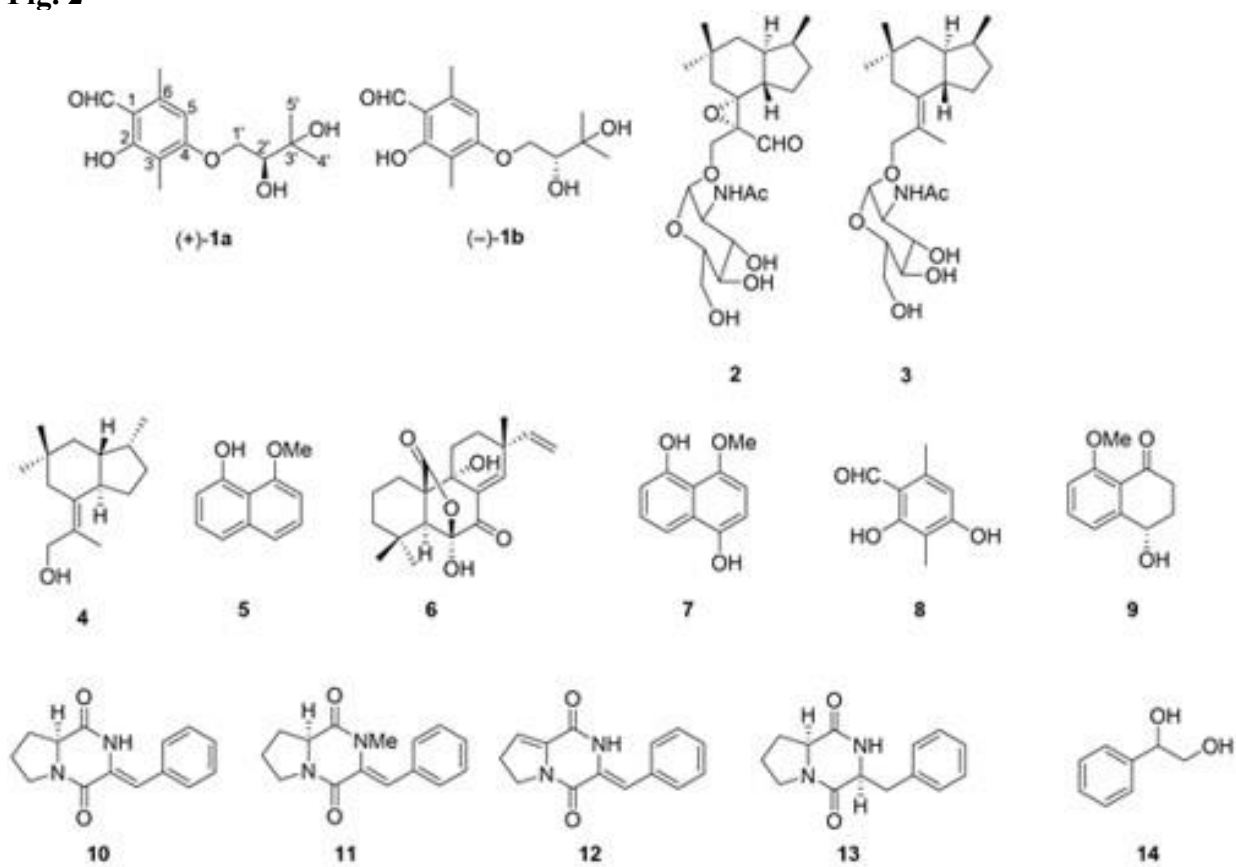
Table 1 NMR spectroscopic data of **1**.

Table 2 Inhibitory effects of compounds **1–14** on MAO-A and -B.

1 **Fig. 1**

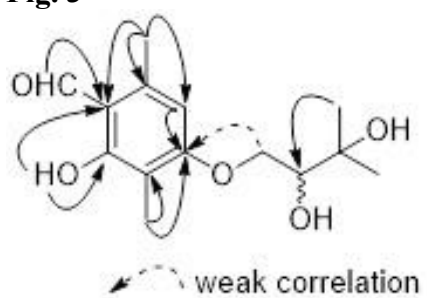


2 **Fig. 2**
3



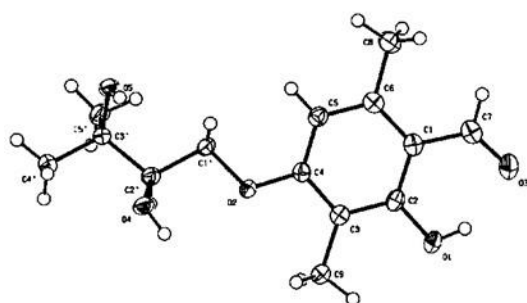
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1 **Fig. 3**

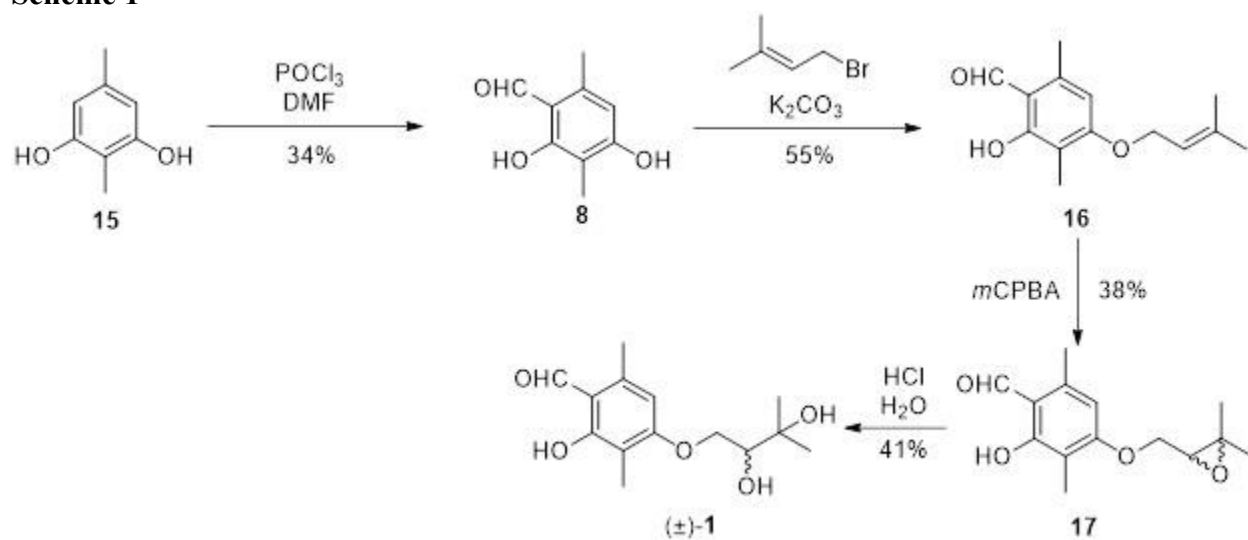


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2 **Fig. 4**



4 **Scheme 1**



6
7

Table 1

truncaaldehyde (1)		
Pos.	δ_C	δ_H (<i>J</i> in Hz)
1	113.7	
2	162.9 ^a	
3	111.4	
4	162.9 ^a	
5	105.9	6.28 (s)
6	141.6	
1-CHO	193.3	10.13 (s)
3-Me	7.3	2.06 (s)
6-Me	18.4	2.56 (s)
1'	69.5	4.10 (dd, 9.6, 7.4)
		4.22 (dd, 9.6, 3.2)
2'	76.7	3.85 (dd, 7.4, 3.2)
3'	71.6	
4'	25.1	1.30 (s)
5'	26.6	1.35 (s)
2-OH		12.41 (brs)
2'-OH		2.30 (brs) ^b
3'-OH		2.75 (brs) ^b

Measured in CDCl₃, ^{a, b} may be interchanged between two signals.

Table 2

	MAO-A			MAO-B			selectivity ^c
	Inhibition rate (%, Mean ± SE)		IC ₅₀ (μM)	Inhibition rate (%, Mean ± SE)		IC ₅₀ (μM)	
	25 μM	100 μM		25 μM	100 μM		
1	52.9±0.6	86.0±0.4	19.0	n.d.	44.7±0.7	n.d.	MAO-A
2	n.d.	28.6±2.5	n.d.	28.7±1.3	53.8±0.6	n.d.	
3	n.d.	n.d. ^b	n.d.	n.d.	20.2±1.9	n.d.	
4	79.9±0.8	96.1±0.2	6.1	84.1±0.5	94.4±0.0	5.4	
5	93.2±0.5	98.2±0.6	1.6	70.9±1.4	94.3±0.7	13.7	MAO-A
6	33.7±0.6	78.6±1.2	n.d.	30.1±3.0	69.5±0.7	n.d.	
7	87.9±1.4	97.0±0.1	3.4	n.d.	30.4±2.5	n.d.	
8	96.7±0.6	99.1±0.9	1.1	50.9±1.3	88.0±0.3	25.5	
9	n.d.	24.0±3.9	n.d.	n.d.	20.2±1.0	n.d.	MAO-B
10	14.3±3.0	58.0±0.4	n.d.	52.9±0.7	87.2±0.2	24.8	
11	n.d.	42.9±1.9	n.d.	n.d.	47.6±1.3	n.d.	
12	1.5±4.6	63.6±0.6	n.d.	9.4±4.5	88.0±0.0	n.d.	
13	n.d.	10.2±1.0	n.d.	n.d.	13.0±1.7	n.d.	
14	5.7±13.9	99.6±0.5	n.d.	n.d.	8.6±2.3	n.d.	
Pargyline ^a	62.4±1.2 (10 μM)			86.9±0.3 (1 μM)			

^a used as positive control. ^b Not determined due to the inhibition rate was under 0%. ^c IC₅₀ (MAO-A)/IC₅₀ (MAO-B) <0.1 (MAO-A selective), >10 (MAO-B selective).