IFB-Lactam-1, a natural compound with anti-Gloeosporium kaki Hori activity

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The title compound, IFB-Lactam-1 (systematic name: 2,15-dihydroxy-7-methyl-6-azabicyclo[11.3.0]hexadec-3-en-5-one), $C_{16}H_{27}NO_3$, is a newly characterized natural anti-Gloeosporium kaki Hori compound. It was isolated from the EtOAc extract of the fermentation broth of an endophytic fungus *Trichoderma sp.* from cabbage. It is a 13-membered macrocyclic lactam which shares a two-atom edge with a cyclopentanol ring.

Comment

In our investigations on secondary metabolites antagonistic against vegetable pathogens from endophytic fungi which live in the healthy tissues of host plants (Monnanda *et al.*, 2005) and are commonly recognized as a rich source of secondary metabolites (Evelyn *et al.*, 2004), the title compound IFB-Lactam-1, (I), was isolated from the EtOAc extract of the fermentation broth of an endophytic fungus *Trichoderma sp.* from cabbage.

(I)
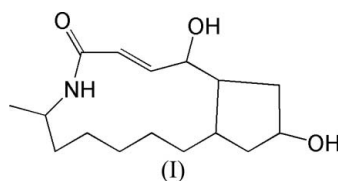
IFB-Lactam-1 is a 13-membered macrocyclic lactam, which shares one bond with a cyclopentanol ring. The molecular structure of (I) is shown in Fig. 1. In the lactam skeleton, the C=C double bond is conjugated with the carbonyl bond. There is a hydroxyl group in the α-position of the conjugated system. The cyclopentanol ring is in an envelope conformation. Atoms C5, C6, C8, and C9 constitute one distorted plane of the envelope, with a deviation of 0.082 (9) Å. Atom C7 is the cover of the envelope, and it is 0.554 (7) Å above the envelope plane.

The hydroxyl groups in (I) participate in the formation of intermolecular hydrogen bonds, which link the molecules to form a one-dimensional chain along the *a* axis (see Fig. 2).

Experimental

The endophytic fungus *Trichoderma sp.*, was cultured in Czapedox media at 298 K for 10 d. The fermentation broth (100 l) was extracted three times with ethyl acetate. The EtOAc was evaporated *in vacuo* to give a brown residue (18 g). The extract was divided into eight fractions by column chromatography on silica gel (gradient from pure chloroform to pure methanol). Fraction 3 (4.3 g) was rechromatographed on silica gel CC with the same range of solvent mixtures, to

give six fractions. Fraction 3–2 (1.0 g) was then subjected to gel filtration on Sephadex LH-20 with chloroform–methanol (1:1), followed by recrystallization from methanol to give compound (I) (5 mg).

Crystal data

$C_{16}H_{27}NO_3$
$M_r = 281.39$
Orthorhombic, $P2_12_12_1$
$a = 7.4001 (9)$ Å
$b = 12.9986 (13)$ Å
$c = 18.860 (2)$ Å
$V = 1814.1 (4)$ Å^3

$Z = 4$
$D_x = 1.034$ Mg m^{-3}
Mo $K\alpha$ radiation
$\mu = 0.07$ mm^{-1}
$T = 298 (2)$ K
Prism, colourless
$0.27 \times 0.23 \times 0.20$ mm

Data collection

Bruker SMART CCD area-detector diffractometer
φ and ω scans
Absorption correction: multi-scan (*SADABS*; Sheldrick, 1996)
$T_{min} = 0.961$, $T_{max} = 0.988$

9063 measured reflections
1859 independent reflections
1583 reflections with $I > 2\sigma(I)$
$R_{int} = 0.038$
$\theta_{max} = 25.5°$

Refinement

Refinement on F^2
$R[F^2 > 2\sigma(F^2)] = 0.074$
$wR(F^2) = 0.239$
$S = 1.04$
1859 reflections
185 parameters
H-atom parameters constrained

$w = 1/[\sigma^2(F_o^2) + (0.1522P)^2 + 1.1271P]$
where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max} < 0.001$
$\Delta\rho_{max} = 0.38$ e Å^{-3}
$\Delta\rho_{min} = -0.37$ e Å^{-3}

Table 1
Hydrogen-bond geometry (Å, °).

D—H$\cdots A$	D—H	H$\cdots A$	$D\cdots A$	D—H$\cdots A$
O3—H3$A\cdots$O4^i	0.82	1.98	2.785 (6)	167
O4—H4$A\cdots$O3^{ii}	0.82	2.45	3.257 (7)	167

Symmetry codes: (i) $x - 1, y, z$; (ii) $x + \frac{1}{2}, -y + \frac{1}{2}, -z$.

All the H atoms were positioned geometrically and constrained to ride on their parent atoms, with O—H = 0.82, N—H = 0.86 and C—H = 0.93–0.98 Å. They were treated as riding atoms, with U_{iso}(H) = $1.2U_{eq}$(C,N) or $1.5U_{eq}$(O). In the absence of significant anomalous scattering effects, Friedel pairs were merged.

Data collection: *SMART* (Siemens, 1996); cell refinement: *SAINT* (Siemens, 1996); data reduction: *SAINT*; program(s) used to solve structure: *SHELXS97* (Sheldrick, 1997); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL* (Sheldrick, 1997); software used to prepare material for publication: *SHELXTL*.

References

Evelyn, A. A., Koichi, T., Yasunori, A., Nitaro, M., Hajime, A., Motoichiro, K. & Hiroshi, O. (2004). *J. Gen. Plant Pathol.* **70**, 139–142.
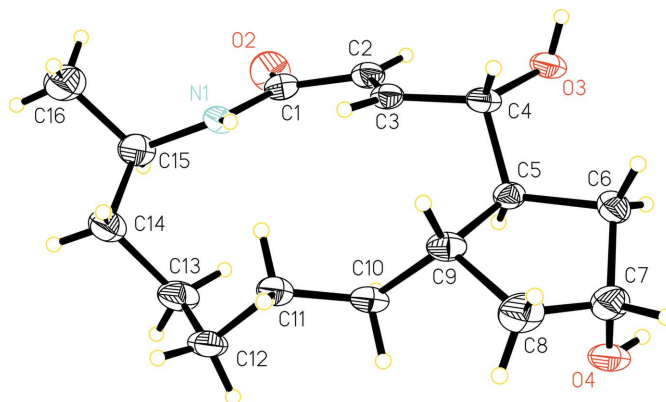
Figure 1
The molecular structure of (I), showing 30% probability displacement ellipsoids and the atom-numbering scheme.
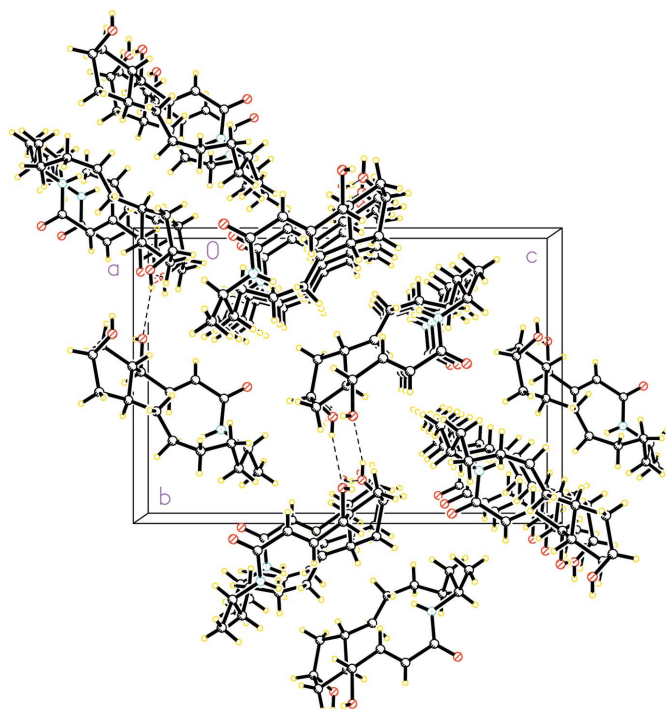

Figure 2
Packing diagram of (I), viewed along the *a* axis. Dashed lines indicate hydrogen bonds.

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