THE STRUCTURE OF CHAETOGLOBOSIN K.

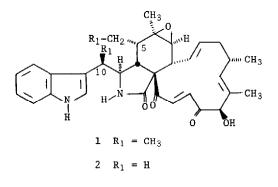
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Summary: The structure of chaetoglobosin K, a toxic metabolite from Diplodia macrospora, has been determined by single crystal X-ray analysis.

The cytochalasins are a group of cytostatically-active fungal metabolites which were first isolated in 1966, but which are generating interest both as mycotoxins and as research tools in cellular biology.^{1,2} In addition to the unique responses triggered by these compounds in animal cells, selective responses in plants have also been described.³ A new fungal metabolite, chaetoglobosin K (1), isolated from *Diplodia maerospora* (ATCC No. 36896), inhibits growth in wheat coleoptiles at 10^{-7} M and has an LD₅₀ in day-old chicks of 25-62.5 mg/kg.⁴



Previously reported mass spectral data indicated that chaetoglobosin K (1) has a formula of C₃₄H₄₀N₂O₅. Mass spectral fragmentation, U.V. and I.R. absorptions revealed the presence of a 3-substituted indole moiety. Initial analysis of both the ¹H and ¹³C NMR spectra indicated that 1 was a chaetoglobosin; however, additional resonances and shifted resonances precluded a straightforward interpretation of the data. As a consequence, single crystal X-ray diffraction experiments were undertaken to completely define the structure and stereochemistry.

Suitable crystals of 1 formed from acetone solutions as skewed parallelepipeds with symmetry P1 and $\alpha = 10.302(6)$, b = 10.569(4), c = 9.689(4)Å, $\alpha = 116.23(3)$, $\beta = 103.29(4)$ and $\gamma = 100.80(4)^{\circ}$. For Z = 1 the calculated density was 1.14 g/cc with one molecule of acetone in the unit cell (vide infra). Of the 2358 reflections measured with graphite-monochromated CuK α (λ = 1.5418Å) radiation having 20 \leq 114°, 2047 (87%) were observed (I \geq 30I). The structure was solved using a multi-solution tangent formula approach.⁵ After a number of attempts, a recognizable fragment was expanded using tangent formula refinement 6 to give coordinates for most of the atoms. Fourier difference maps using all of the data gave coordinates for the remainder of the atoms in the molecule as well as for a solvated molecule of acetone. The structure was refined using full matrix least squares techniques by minimizing Ew $(|F_0| - |F_c|)^2$ with w = $(1/\sigma F_0)^2$ and including anisotropic temperature parameters for the nonhydrogen atoms and fixed isotopic temperature parameters for the hydrogens to give a final R factor of .051.⁷ Figure 1 is a perspective drawing of the molecule generated from the final coordinates. 8 The absolute configuration of the figure is drawn to conform with the previously described cytochalasins.9,10

Tables I, II and III containing the fractional coordinates and temperature parameters, bond distances and bond angles are available.¹¹ OI' is involved in two intermolecular hydrogen bonds, one of length 2.96Å with NI' and the other of length 2.65Å with O19'. Curiously, the solvent molecule of acetone is not in a position to hydrogen bond since there are no suitable contacts less than 3.5Å.

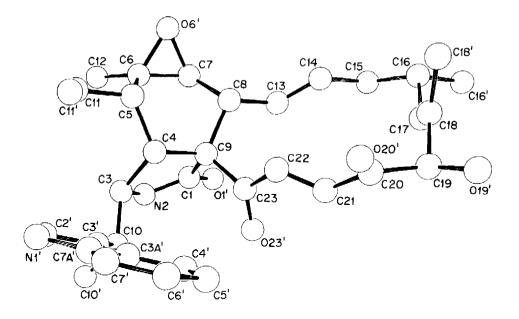


Figure 1. A computer generated perspective drawing of chaetoglobosin K (1). Hydrogens have been omitted for clarity.

Chaetoglobosin K (1) is found to be an indol-3-yl [13] cytochalasin similar to chaetoglobosin A (2)^{10,12} with additional unique features. Instead of a methyl substituent at C5, $\frac{1}{2}$ has an ethyl group; an additional methyl substituent is also found on C10. Since none of the more than 20 cytochalasins described in the literature has these additional methyl groups, an interesting biosynthetic question is raised. Biogenesis of the cytochalasins has been shown to result from the union of an aromatic amino acid, a 16- or 18-membered polyketide and several additional carbons from the C₁ pool.² The methyl group C10' undoubtedly came from the C₁ pool; however, the additional carbon C11' could have come from methionine, degradation and reduction of a 20-membered polyketide, or most likely from a propionate starting unit on the polyketide chain.

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