

Journal of The Chemical Society, Chemical Communications

NUMBER 8/1980

Biosynthetic Intermediates *en route* to Mycophenolic Acid in *Penicillium brevicompactum*

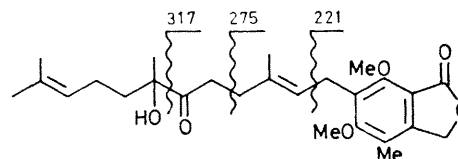
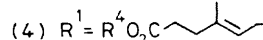
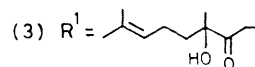
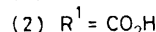
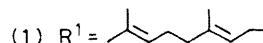
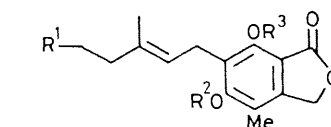
By DENNIS L. DOERFLER, LAUREN A. ERNST, and IAIN M. CAMPBELL*

(Department of Biological Sciences, University of Pittsburgh, 130 DeSoto Street, Pittsburgh, PA 15261)

Summary The farnesyl phthalide (**1**; R² = Me, R³ = H) and the mycophenolic acid prenylogue (**4**; R² = Me, R³ = R⁴ = H), but not the acyloin (**3**; R² = H or Me, R³ = H), have been found by radiogas chromatography-mass spectrometric analysis of *P. brevicompactum* cultures that were active in mycophenolic acid biosynthesis.

It appears that at least two pathways lead from the farnesyl phthalide (**1**; R² = R³ = H) to mycophenolic acid (MA, **2**, R² = Me, R³ = H). Cell-free extracts of *Penicillium brevicompactum* convert the phthalide (**1**; R² = R³ = H) into the acyloin (**3**; R² = R³ = H);¹ whole cells of the fungus convert this acyloin effectively into MA.¹ The prenylogue of MA, compound (**4**; R² = R³ = R⁴ = H),² is also converted into MA by the fungus.³ As would be required by a role for this compound, acetone and levulinic acid are produced in parallel with MA as the fermentation develops.^{4,5}

The existence of two pathways to MA raises the question of the relative importance of each. The basic metabolic opportunism^{6,7} of fungal cells coupled with uncertainties regarding relative rates of transport into cells make it doubtful that this question can be answered unambiguously by feeding isotopically labelled (**3**) and (**4**) (in both, R² = R³ = H) to *P. brevicompactum*. This communication reports preliminary results with an alternative method, based on radiogas chromatography-mass spectrometry (r.g.c.-m.s.),⁸ in which cells are exposed to primary precursors such as ¹⁴C-acetate and total cell extracts are then scanned to determine (a) if the biosynthetic pathway is



(5)

active and (b) what pathway-related compounds are present in the tissue.

P. brevicompactum was grown from spores in medium B of reference 9. At the 60th hour the culture was exposed to [¹⁴C]acetate for 3 h. Medium and biomass were separately extracted with ethyl acetate. A portion of the extracts was treated with diazoethane; the bulk was treated with diazomethane. The two alkylation procedures should allow us to determine if R² was H or Me, in compounds (**1**), (**3**), and (**4**), *in vivo*.

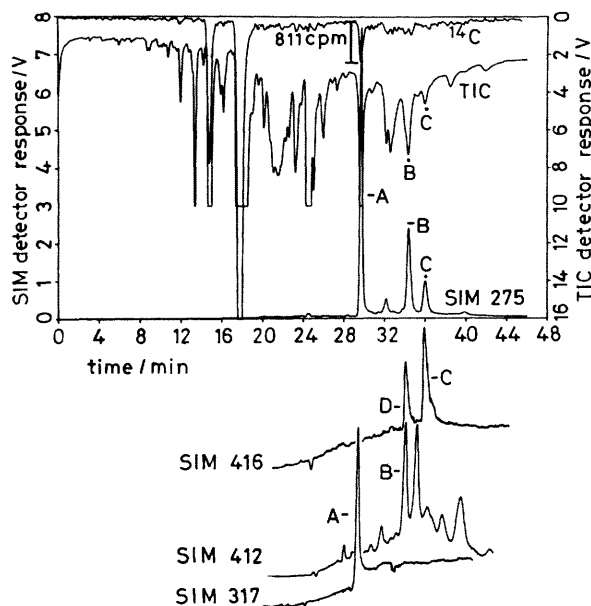


FIGURE. Radioactivity (^{14}C), total ion current (TIC), and selected ion monitoring (m/z 275, 416, 412, and 317) outputs from an r.g.c.-m.s. analysis of a total tissue extract of *P. brevicompactum*. The maximum disintegration rate in the mycophenolic acid peak (peak A) was 811 counts per minute. (Peak D in the m/z 416 profile is produced by a steroid.)

The Figure gives results obtained from the methylated tissue extract and shows the radioactivity, total ion current, and m/z 275, 317, 412, and 416 selected ion monitor (SIM)

profiles. The m/z 412 and 416 ions are the parent molecular ions of (**1**; $\text{R}^2 = \text{R}^3 = \text{Me}$) and (**4**; $\text{R}^2 = \text{R}^3 = \text{R}^4 = \text{Me}$) respectively. We expect the ion m/z 317 to be formed from the methylated acyloin as shown in (**5**). The origin of the m/z 275 ion is also shown in structure (**5**); it, together with an m/z 221 ion, is highly characteristic of the methylated MA nuclear skeleton.

In the Figure, peak A is due to MA. It is radiolabelled indicating that MA biosynthesis is active. The m/z 221 (not shown), 275, 412, and 416 SIM profiles establish that peaks B and C are due to (**1**) ($\text{R}^2 = \text{R}^3 = \text{Me}$) and (**4**) ($\text{R}^2 = \text{R}^3 = \text{R}^4 = \text{Me}$) respectively. No trace of the acyloin (**3**; $\text{R}^2 = \text{R}^3 = \text{Me}$) could be found in this or other experiments of a similar type.

Failure to find the acyloin does not preclude its involvement. However, since compound (**4**), together with acetone and levulinate are found routinely while the acyloin and 2-oxo-6-methylhept-5-ene⁵ (the presumed residue from cleaving the MA skeleton out of the acyloin in a single step) are not, it is unlikely that the biosynthetic route through the acyloin is a major one.

R.g.c./m.s. analysis of the ethylated tissue extracts reveals that the parent molecular ions associated with former peaks B and C move to m/z 426 and 444 respectively. This establishes that in the cells only the methylated forms (**1**; $\text{R}^2 = \text{Me}$, $\text{R}^3 = \text{H}$) and (**4**; $\text{R}^2 = \text{Me}$, $\text{R}^3 = \text{R}^4 = \text{H}$) exist. It confirms the fears of Muth and Nash¹⁰ that their methyltransferase is not specific for demethylmycophenolic acid.

This work was supported by the National Sciences Foundation.

(Received, 2nd November 1979; Com. 1165.)

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