## Biosynthesis of the Meroterpenoid Metabolites, Austin and Terretonin: Incorporation of 3,5-Dimethylorsellinate

## C. Rupert McIntyre,<sup>a</sup> Thomas J. Simpson,<sup>\*a</sup> Desmond J. Stenzel,<sup>a</sup> Alan J. Bartlett,<sup>b</sup> Eugene O'Brien,<sup>b</sup> and John S. E. Holker<sup>b</sup>

<sup>a</sup> Department of Chemistry, University of Edinburgh, West Mains Road, Edinburgh EH9 3JJ, U.K. <sup>b</sup> Robert Robinson Laboratories, University of Liverpool, P.O. Box 147, Liverpool L69 3BX, U.K.

<sup>14</sup>C and <sup>2</sup>H Labelling experiments, together with <sup>2</sup>H n.m.r. spectroscopy show that 3,5-dimethylorsellinic acid is a specific precursor of austin and terretonin in *Aspergillus ustus* and *Aspergillus terreus*, respectively, and so substantiate the mixed polyketide–terpenoid origin proposed for these metabolites from the incorporation of <sup>13</sup>C-labelled simple precursors.

<sup>13</sup>C and <sup>2</sup>H Labelling studies<sup>1-3</sup> have shown that andibenin B (1), andilesin A (2), and anditomin (3),  $C_{25}$  metabolites of *Aspergillus variecolor* are formed by a mixed polyketide-terpenoid biosynthetic pathway in which the key step is alkylation of 3,5-dimethylorsellinic acid (4) by farnesyl pyrophosphate to give (5). We suggested that the mycotoxins austin (6) and terretonin (7), metabolites of *Aspergillus ustus* and *Aspergillus terreus*, respectively, could also be formed *via* intermediate (5), and incorporations of singly and doubly

labelled [<sup>13</sup>C]acetates and [<sup>13</sup>C]methionine into austin and terretonin result in labelling patterns consistent with these proposals.<sup>4,5</sup> However, as the suggested pathways require unprecedented degrees of modification<sup>6</sup> of the tetraketide-derived phenolic precursor, we have carried out and now report studies to show that 3,5-dimethylorsellinate is indeed a specific precursor of both austin and terretonin (Scheme 1).

Ethyl [*carboxy*,2-<sup>14</sup>C<sub>2</sub>]-3,5-dimethylorsellinate (8) (39.7  $\mu$ Ci mmol<sup>-1</sup>)<sup>2</sup> was fed to static cultures of *A. ustus* (24 mg to



## Scheme 1

0.4 l) and A. terreus (33 mg to 1 l), respectively, to give austin (36 mg, 1.60  $\mu$ Ci mmol<sup>-1</sup>) and terretonin (34 mg, 1.01  $\mu$ Ci mmol<sup>-1</sup>), specific incorporations of 4.0 and 2.5%, respectively. Interestingly, the 2-deoxyorsellinate (9) which was incorporated<sup>2</sup> into andibenin B with comparable efficiency to (8) was not incorporated into austin to any significant extent (specific incorporation, 0.06%). As with andibenin B, the complexity of the metabolites precluded the degradative studies essential to establish specificity of labelling, so the trideuteriomethyl analogue (10)<sup>2</sup> was fed, and the resultant enriched metabolites analysed by 55 MHz <sup>2</sup>H n.m.r. spectroscopy. Austin showed only one signal at  $\delta$  1.68 p.p.m.,



chemical shifts corresponding in each metabolite to the 10'methyl hydrogens,† in agreement with our proposed pathways.<sup>4,5</sup> Thus it is clear that 3,5-dimethylorsellinate is a specific precursor to both austin and terretonin and so their meroterpenoid<sup>7</sup> origins are established beyond doubt.

Further evidence for the common biogenetic origins of these metabolites comes from the isolation of austin and dehydroaustin (11), a co-metabolite of austin in *A. ustus*,<sup>8</sup> from a chance mutant of the andibenin producing culture of *A. variecolor* which no longer produced andibenin. Another observation to note is the recent isolation of the austalides [*e.g.* (12)] from a toxigenic strain of *A. ustus*.<sup>9</sup> Structural analysis suggests they are biosynthesised via alkylation of 5-methylorsellinic acid by farnesyl pyrophosphate, *cf.* mycophenolic acid,<sup>10</sup> followed by cyclisation of the farnesyl moiety and oxidative modifications analogous to those occurring in the andibenins and andilesins.

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<sup>†</sup> Control experiments show that the 10'-methyl signals in the <sup>2</sup>H n.m.r. spectra of universally deuteriated austin and terretonin are sufficiently well resolved from other signals to ensure specificity of labelling.