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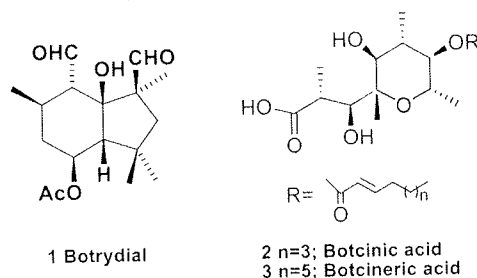
Connecting Genes to Intermediate Molecules in The Biosynthesis of Botrydial

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The growing understanding of microbial genomics has provided valuable insights into the principles of natural product biosynthesis and thus offers promising alternatives for the discovery and engineering of new chemical entities.

The fungus *Botrytis cinerea* is the causal agent of the economically important gray mould disease that affects more than 200 ornamental and agriculturally important plant species. *B. cinerea* is a necrotrophic plant pathogen that secretes nonspecific phytotoxins, including the sesquiterpene botrydial (**1**) and the polyketide botcinic acid (**2**).



We recently showed that the BcBOT1 gene, which encodes a P450 monooxygenase, is responsible for one of the final steps of botrydial biosynthesis and the region surrounding the previously characterized BcBOT1 gene was identified as the botrydial biosynthetic gene cluster.¹ So, this gene is surrounded by two other putative P450 monooxygenase-encoding genes BcBOT3 and BcBOT4, the BcBOT2 gene, encoding a sesquiterpene synthase² and a fifth expressed gene, BcBOT5, which showed high homology to known acetyl transferases.

In this communication we report the functional characterisation of the BcBOT1-5 genes and the encoded key enzymes which catalyze all steps in the biosynthesis pathway leading to botrydial and its derivatives.

- 1 V. Siewers, M. Viaud, D. Jimenez-Teja, I. G. Collado, C. S. Gronover, J. Pradier, B. Tudzynski, P. Tudzynski, *Mol Plant Microbe Interact.*, 2005, **18**, 602-612.
- 2 C. Pinedo, C. Wang, J. Pradier, B. Dalmais, M. Choquer, P. Le Pecheur, G. Morgant, I.G. Collado, D. Cane, M. Viaud, *ACS Chemical Biology*, 2008, **3**, 791-801.