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## The functional characterization of BcBOT3-BcBOT5 genes involved in the biosynthesis of the toxins botrydial

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**4<sup>th</sup> Spanish-Moroccan Symposium on  
Organic Chemistry  
(SMSOC-4)**

*and*

**7<sup>th</sup> Andalusian-Moroccan Meeting on  
Natural Products Chemistry  
(AMMNPC-7)**

**20-22<sup>nd</sup> September 2012  
Universidad de Almería, Almería (Spain)**

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## THE FUNCTIONAL CHARACTERIZATION OF *BcBOT3-BcBOT5* GENES INVOLVED IN THE BIOSYNTHESIS OF THE TOXINS BOTRYDIAL

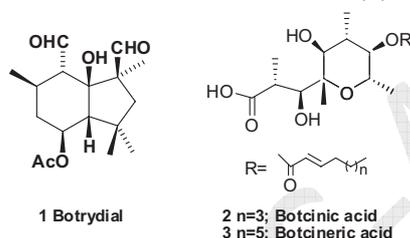
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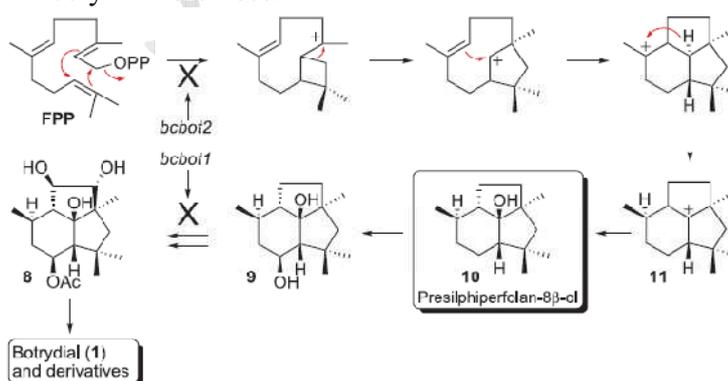
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*Botrytis cinerea* is a well-known pathogen affecting a number of commercial crops, which produces a variety of structurally diverse metabolites. There is no evidence for the production of host-specific toxins by this fungus, which is in accordance with the broad host range of this pathogen. *B. cinerea* produces two series of phytotoxic metabolites: a family of sesquiterpenes which contain the basic botriane skeleton (1) and a family of polyketides (2,3).



Advances in genomic studies, in combination with increased access to DNA sequencing, are providing a wealth of information about how natural products are assembled, mechanisms by which natural product gene clusters can be manipulated to yield new product diversity, and the genetic potential of individual organisms.

In previous works we provided the functional characterization of *BcBOT1* and *BcBOT2* genes, which encode a P450 monooxygenase and a sesquiterpenecyclase, respectively. The region surrounding the previously characterized *BcBOT1* gene was identified as the botrydial biosynthetic gene cluster: *BcBOT 2* to *BcBOT 5* genes. Wherein *BcBOT3* and *BcBOT4* genes encode two P450 monooxygenases and *BcBOT5* shows high homology to known acetyl transferases.



In this communication we report the functional characterisation of the *BcBOT3-5* genes and the encoded key enzymes which catalyze intermediate steps in the biosynthesis pathway leading to botrydial and its derivatives.

