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Francisco A. Macias, Department of Organic Chemistry, Faculty of Sciences, University of Cádiz, Spain
Phone: 34-956012770 Puerto real (Cadiz)
E-mail: famacias@uca.es

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

Javier Moraga (javier.moraga@uca.es)⁽¹⁾, B. Dalmais⁽²⁾, J. Aleu⁽¹⁾, M. Viaud⁽²⁾, I. G. Collado⁽¹⁾

1 University of Cadiz | Organic Chemistry Department, Campus Ciencia y Tecnología, 11510, Puerto Real, SPAIN

2 INRA, BIOGER | , 78850, Thiverval-Grignon, FRANCE

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 and a family of polyketides.

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 sesquiterpene cyclase, 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 derivati.

