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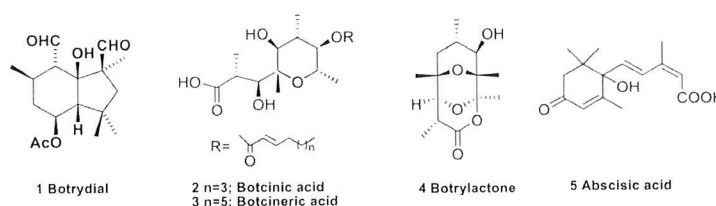
Characterization of Orphan Sesquiterpene Biosynthesis Genes in *Botrytis Cinerea*

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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.

Botrytis cinerea is a well known pathogen of a number of commercial crops and produces many structurally diverse metabolites. *Botrytis* produces two series of phytotoxic metabolites: a family of characteristic sesquiterpene metabolites which contain the basic botryane skeleton, principally botrydial (**1**) and two polyketide lactones types: botcinins (**2**, **3**) and botrylactone (**4**).¹ Additionally, abscisic acid (a phytohormone) has been isolated and reported.²



However, genomic data revealed that *B. cinerea* has 43 key enzymes involved in the biosynthesis of secondary metabolites, including many polyketides, peptides and terpenes, some of them are specific of this phytopathogen. The study displayed six genes coding for putative sesquiterpene cyclases (STC) in *B. cinerea*.³

So, we have undertaken a chemical genetic project oriented to characterization of these orphan biosynthetic genes and their corresponding cryptic metabolites from *B. cinerea*, by a molecular- and chemical-based epigenetic approach, using mutant strains which have silenced genes coding for five STCs. As a result the sesquiterpene cyclases STC1 and STC4 have been characterized and some aspect about the role played by STC1, STC2 and STC4 in the pathogenicity of *B. cinerea* determined.

- 1 J. Moraga, C. Pinedo, R. Durán-Patrón, I. G. Collado, R. Hernández-Galán, *Tetrahedron*, 2011, **67**, 8583.
- 2 V. Siewers, L. Kokkelink, J. Smedsgaard, P. Tudzynski, *Appl Environ Microbiol.*, 2006, **72**, 4619-4626.
- 3 J. Amsellem, C. Cuomo, J. van Kan, M. Viaud, et al., *PLoS Genet.*, 2011, **7**, e1002230.