What can we learn from the *Botrytis cinerea* genome sequence?

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Botrytis cinerea (also known as grey mould) is a serious pre- and post-harvest pathogen in a wide range of fruit, vegetable and ornamental crops. The application of molecular genetic tools in the past two decades has provided an increased insight into the mechanisms by which *B. cinerea* infects plants. This insight may be useful for developing novel, rational control strategies to reduce pathogen damage, either by using novel chemicals or by enhancing plant resistance.

The previous molecular-genetic studies on *B. cinerea* have resulted in the cloning and functional analysis of many dozens of genes, but cloning of individual genes can be time-consuming when the sequences are unknown. In the 1990's the genome of one *B. cinerea* strain has been determined by Syngenta. More recently, a different strain has been sequenced by an international consortium, coordinated by French partners. The genome sequences of both *B. cinerea* strains, as well as of the closely related pathogen *Sclerotinia sclerotiorum*, are in the process of annotation. An important part of the analysis is dedicated to the comparison between the two fungal species and the two *B. cinerea* isolates.

I will present an overview of the current status of the *B. cinerea* genome analysis and highlight what we have learned thus far from the sequence with respect to evolution, (sexual and asexual) reproduction and the infection strategies of *B. cinerea*.