lower valleys of the Yangtze River, with little gene flow. We observed a strong association between this genetic population subdivision and the mycotoxin produced. Our results show that the dramatic decline in trichothecene chemotypes may be explained by a recent and significant sweep of 3ADON producers in FHB pathogen composition in the middle valley. Using Bayesian statistics we found a biased gene flow from 3ADON to NIV populations.

In addition, we observed significant genetic differentiation and linkage disequilibrium between NIV and 3ADON producing isolates at the same sampling sites. We discuss the impact of this shift on the increase of FHB in Southern China.

**Session Scientific tools and pathogen detection**

**Trends in plant science: detecting air-borne chemicals sent off by plants to monitor their state of health**

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Traditional inspections of greenhouse crops are done by greenhouse personnel and rely on the presence of visual symptoms on the crop. This method has its limitations. Namely, visual symptoms are often difficult to observe, or when seen, it may be too late to remedy the problem. For example, early signs of pathogen infections and herbivore infestations often appear on the abaxial side of leaves or on stem parts that are hidden by the foliage. When these symptoms remain unnoticed, such infections or infestations may disperse rapidly and result in irrevocable crop damage. These limitations have led to the emergence of a wide range of methods to improve the inspection of greenhouse crops. Ideally, such methods would enable continuous monitoring of individual plants in order to reveal early pathogen problems at an early stage. This would enable a grower to take early action, and prevent further crop damage. One approach to monitor the health status of plants is based on the volatile organic compounds (VOCs) emitted from them. This approach was successfully tested at both laboratory-scale (Jansen et al., 2009a) as well as greenhouse-scale (Jansen et al., 2009b, Gijzen et al., 2009c).

In general, measurement of plant emission consists of three steps: (1) collection of plant-emitted VOCs, (2) separation of plant-emitted VOCs in the mixture, and (3) identification, and/or quantification of separate VOCs.

In the first step, a fraction of the compounds emitted from the plants is collected. This sampling step is usually combined with pre-concentration of the VOCs in the air to achieve the detection limits of commonly applied analytical instruments. Two methods are generally applied to pre-concentrate VOCs present in air. The first method is based on the dynamic pre-concentration of VOCs. This method is referred to as dynamic because the air is actively swept from the plants is collected. This sampling step

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**.