

Genetic structure of *Alternaria solani* - a new approach

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SUMMARY

The diagnostic PCR analyses of lesions with similar symptoms to early blight collected during two years (2009-2010), revealed that *Alternaria solani* probably is the major causal agent to early blight in Sweden. *Alternaria alternata* was identified in one single sample in 2009 and in the following year, 69 out of 360 samples contained *A. alternata*, of which the vast majority co-occurred with *A. solani*. In 2011 the epidemic of early blight started in the second half of July in ecologically cultivated fields and in the beginning of August in the conventional fields. The incidence of early blight was intense during September despite one or commonly two applications of fungicides based on strobilurins. In order to determine if the population had become tolerant toward strobilurins the PCR products of the samples with confirmed *A. solani* were sequenced. None of the substitutions at position 129 associated with loss of sensitivity toward strobilurins were observed.

During the collections in mid September 2011 scattered lesions with similar symptoms to early blight were found on *Solanum nigrum* in two different fields. These lesions are to be analysed together with the samples from the collections of 2011.

The genetic structure of the population *A. solani* has been primarily analysed in Germany (Leiminger *et al.*, 2010), South Africa (van der Waals *et al.*, 2004), USA (Weir *et al.*, 1998) and Brazil (Lourenzo *et al.*, 2011). The studies revealed that populations of *A. solani* had large variation both within and among fields, which is unusual for an asexually reproducing fungus. Analysis of the genetic structure may give valuable information about the range of dispersal of the conidia between areas.

The genetic structure of the Swedish and Tajikistani populations will be analysed by 8 SSRs developed for *A. alternata* (Tran-Dinh and Hocking, 2006) and *A. dauci* (Benichou *et al.*, 2009), which have shown to work on *A. solani* too. However, the method needs to be optimised for best results. Preliminary results from the Swedish population, using DNA from mycelium and lesions, show that there is some genetic diversity even within fields.

KEYWORDS

Alternaria solani, early blight, fungicide sensitivity, genetic structure, SSR

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