

RNAi as a tool to investigate *Verticillium* wilt diseases

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Verticillium albo-atrum and *V. dahliae*. are soil-borne plant pathogens that are responsible for *Verticillium* wilt diseases that worldwide occur on many, mainly dicotyledonous, plant species including many economically important crops. The fungus enters the roots of the host plant, grows into the vascular tissue (xylem) and spreads to distal parts of the plant. Infection generally leads to obstruction of xylem vessels, thus hampering water transport and causing wilting. There are currently no fungicides available to cure plants once they are infected and, besides the use of resistant cultivars if available, removal of plants diagnosed with *Verticillium* wilt disease is the most effective means of disease control.

We are studying the interaction of *Verticillium* spp. with two different host plants, tomato and Arabidopsis. Tomato is a natural host of *Verticillium* spp., while Arabidopsis is used as a model plant. *Verticillium* strains have been selected that are pathogenic on both plant species and, with the use of GFP transformants, the infection is characterized on both hosts.

Because ultimately we are interested in genes that play a determinant role in *Verticillium*-host interactions, we have investigated whether we can employ RNA interference (RNAi) as a tool for functional analysis in *Verticillium*. We have designed an inverted repeat construct to knock down GFP expression that, upon introduction into *Verticillium* strains transgenic for *GFP*, indeed resulted in reduced GFP fluorescence. Subsequently, we have designed an inverted repeat construct to target the expression of an endogenous toxin biosynthesis gene in *Verticillium*. Our preliminary data show that introduction of this construct into *Verticillium* results in reduced pathogenicity of the fungus, demonstrating that RNAi can be used in *Verticillium* to investigate putative virulence genes.