

Seedling Disease – getting to the root of the problem

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Increasing our knowledge of seedling disease

Annual cotton disease surveys continue to indicate the threat posed to sustainable cotton production by seedling disease. The cost of seedling disease can be measured directly as the cost of fungicide seed dressings and indirectly as the various costs (eg. fuel and labour) associated with replants. The last comprehensive survey of cotton seedling pathogens occurred over 15 years ago, before the onset of the *Fusarium* wilt and black root rot epidemics (Ogle *et al.*, 1993). Potential pathogens were collected from Narrabri and sites in QLD, and assayed for their ability to cause disease. The fungi *Rhizoctonia solani* and *Pythium ultimum* were the most common pathogens. *Fusarium spp.* were also isolated but were not aggressive. Seedling disease and stand loss is historically higher in the southern valleys (i.e. Macquarie, Lachlan and Murrumbidgee). This is probably due to cool climatic conditions and may indicate variation in the species, aggressiveness, and tolerance to fungicide of pathogens attacking cotton seedlings. Given the potential for expansion of the cotton industry into southern NSW, a comprehensive study of seedling pathogens and their ecology is well overdue.

A substantial study is now underway to 1) isolate and identify potential pathogens and 2) investigate the ecology of *Rhizoctonia solani* associated with cotton in NSW. During the 2007/8 disease surveys, diseased seedlings and soil were collected from the Macintyre, Gwydir, Namoi, Macquarie, Lachlan and Murrumbidgee Valleys. In June 2008, a further 85 soil samples were collected from Bourke and Lake Tandou on the Darling, and from the Murrumbidgee Valley. Further sampling is anticipated in the Macquarie and Lachlan Valleys during the 2008/9 cotton season. Fungi have been isolated from diseased seedlings in the lab, and baited from soil samples in the glasshouse. 106 fungi have been isolated so far (Table 1). Isolations are ongoing and fungi are currently being tested for the ability to prevent the establishment of cotton seedlings in pots. *Fusarium oxysporum* was frequently isolated from diseased seedlings in fields with a history of *Fusarium* wilt, suggesting that the *Fusarium* wilt fungus is also a major seedling pathogen. *Rhizoctonia solani* and *Pythium sp.* have also been widely isolated. One of the most aggressive pathogens was a *Pythium* species isolated from the Lachlan valley in a field with a history of severe stand loss. At the completion of this study, we will have compiled an exhaustive list

of seedling pathogens from all valleys in NSW which will assist the future development of IDM strategies for seedling disease.

While it is important to know what is out there, it is also important to understand the level of variation within and between populations of the major pathogens. As part of a PhD though the University of Sydney, Chris Anderson is looking in more detail at populations of the seedling pathogen

Table 1: Fungi associated with seedling disease in 2008

Fungus	Valley	Pathogen of
<i>Fusarium oxysporum</i>	Macintyre	Cotton, and many other hosts.
	Gwydir	
<i>Fusarium sp.</i>	Macquarie	Cotton, and many other hosts.
	Murrumbidgee	
	Macintyre	
	Gwydir	
<i>Fusarium equiseti</i>	Namoi	Mildly pathogenic on a range of hosts
	Murrumbidgee	
<i>Pythium ultimum</i> and <i>Pythium sp.</i>	Macintyre	Cotton, and many other hosts.
	Namoi	
<i>Rhizoctonia solani</i>	Lachlan	Cotton, corn, rice, soybean, peanuts, etc
	Murrumbidgee	
	Macintyre	
<i>Macrophomina phaseolina</i>	Gwydir	Cotton, Faba Bean, Soy Bean, etc.
	Macintyre	
<i>Sclerotium rolfsii</i>	Namoi	Cotton, peanuts, cucurbits, tomato, soybean, etc
<i>Thielavia sp.</i>	Gwydir	Sesame, Cluster Beans (Guar)
<i>Chaetomium sp.</i>	Namoi	Non-pathogenic
<i>Mortierella hyalina</i>	Lachlan	Non-pathogenic
<i>Paecilomyces lilacinus</i>	Gwydir	Non-pathogenic
<i>Phialophora sp.</i>	Lachlan	Non-pathogenic

Rhizoctonia solani from soils across NSW. Chris is comparing *Rhizoctonia* from the southern valleys of NSW with *Rhizoctonia* from other areas to identify differences in aggressiveness and sensitivity to commonly used fungicides. DNA from each individual *Rhizoctonia* is extracted and compared using a process called RFLP analysis, which determines how closely individuals are related to each other. This enables the individual *Rhizoctonia* isolates to be grouped into families. It is expected that each family will reflect a geographic location (eg. individuals from Bourke will be more closely related to each other than to individuals from Warren). This technique can also help us determine whether *Rhizoctonia* in Australian cotton fields has one or many origins. We expect to find that isolates from different geographical regions will vary in aggressiveness towards cotton and sensitivity to fungicides. It is also possible that large variations will occur even within closely related populations.

While the southern valleys of NSW present a great opportunity for expansion of the cotton industry, they also present unique challenges from a plant disease perspective. This study will fill in the blanks in our knowledge of seedling pathogens from these regions and assist with the development of IDM strategies for seedling disease in the south.



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