

Fusarium Wilt of cotton in Australia

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Introduction

Fusarium wilt of cotton (*Gossypium* L. spp.) is caused by the fungus *Fusarium oxysporum* Schletend. f.sp. *vasinfectum* (Atk.) Snyder and Hansen (*Fov*). The disease has been recorded in most of the world's major cotton growing areas and causes significant losses in the USA, Tanzania, Egypt, and India (Smith *et al.*, 1981) and China (Chen *et al.*, 1985). Australia was considered to be free from the wilt pathogen until 1993, when it was confirmed in Queensland (Kochman, 1995). *Fov* was also recently discovered in the Philippines.

Wilted cotton plants have been collected from field sites throughout the Queensland and New South Wales growing areas since 1993. Several hundred isolates of *Fov* have been recovered from such material and examined in laboratory and glasshouse studies to determine the range of genetic and pathogenic diversity in the Australian fungal population. Where possible, Australian isolates have also been compared with isolates of *Fov* imported under quarantine from other countries.

Materials and Methods

Vegetative compatibility group (VCG) analysis is used to assess isolates of *Fov* recovered from wilted cotton plants in Australia using the technique described by Correll *et al.* (1987). DNA profiles have also been generated for Australian isolates of *Fov* using the technique known as DNA Amplification Fingerprinting (DAF) (Bentley and Bassam, 1996).

Differential cotton cultivars have been used in inoculation studies to examine the extent of pathogenic diversity in Australian populations of *Fov*. In glasshouse inoculation studies and resistance evaluations, cotton-seed is germinated in moist vermiculite. Two-week old seedlings are then removed, washed and the roots dipped for 5 minutes in an inoculum containing 10^6 conidia mL⁻¹. The inoculated seedlings are then transplanted to individual pots and grown in the glasshouse for 6 weeks. The plants are then removed and assessed externally for the presence of wilt symptoms and internally for the extent of vascular discoloration using a 5-point scale.

A fusarium wilt infested field site has been established near Cecil Plains on the Darling Downs in Queensland to evaluate cotton germplasm for resistance to *Fov*.

Results and Discussion

Initially the disease was identified only on the Darling Downs. In 1995, wilted plants were observed near Goondiwindi in southern Queensland and then, in 1997, from near Moree in northern New South Wales. During subsequent seasons, the incidence of fusarium wilt became much greater and more widespread in these districts. Some cases appeared to be related to overland water flows. At the end of the 1997/98, the first case of *Fov* was confirmed at one

location near Theodore in Central Queensland, several hundred kilometres from previously affected areas. The cotton growing regions near St George and Emerald in Queensland and all regions south of Moree in New South Wales remain free from *Fov*.

VCG and DNA testing have revealed that two distinct strains of *Fov* (VCGs 01111 and 01112) are present in Australia. DNA analysis confirms that isolates within each of these VCGs are very closely related but that isolates within VCG 01111 give a significantly different DNA banding pattern to that of isolates in VCG 01112. Both groups appear to be equally pathogenic to current commercial cotton varieties. VCG 01111 occurs throughout the Darling Downs and near Theodore in Queensland and Moree in New South Wales. VCG 01112 appears to have a more limited distribution having only been recorded on a small number of properties in the Goondiwindi district in Queensland and at Moree in New South Wales.

Based on comparative analyses with a limited number of isolates of *Fov* from other countries, it appears that the Australian strains of *Fov* are distinctly different from overseas strains of the pathogen. This raises the possibility that the Australian strains of *Fov* may have evolved locally, perhaps in response to the widespread planting of susceptible varieties.

Resistance among local cotton varieties to the Australian strains of *Fov* ranges from highly susceptible to moderately resistant. Glasshouse and field evaluations of germplasm are being carried out in association with the major cotton breeding programs in Australia. Selections from F1 populations, which appear to be segregating for resistance to *Fov*, are also being evaluated.

In addition to breeding and evaluating germplasm for resistance to *Fov*, other disease management options are being adopted to contain outbreaks of the disease and prevent spread of the pathogen to disease-free farms and districts. Future research aims to identify a range of disease management strategies for industry including cultural practices such as stubble management and pathogen-limiting crop rotations.

References

- Bentley, S. and Bassam, B. J. (1996) A robust DNA fingerprinting system applied to analysis of genetic variation within *Fusarium oxysporum* f.sp. *cubense*. *Journal of Phytopathology* **144**: 207-213.
- Chen, Q., Ji, X., and Sun, W. (1985). Identification of races of cotton wilt *Fusarium* in China. *Agricultural Science China*. Number 6.
- Correll, J. C., Klittich, C. J. R., and Leslie, J. F. (1987). Nitrate non-utilising mutants of *Fusarium oxysporum* and their use in vegetative compatibility tests. *Phytopathology* **77**, 1640-6
- Kochman, J.K. (1995). *Fusarium* wilt in cotton - a new record in Australia. *Australasian Plant Pathology* **24**, p. 74.
- Smith, S. N., Ebbels, D. L., Garber, R. H., and Kappelman, A. J. (1981). *Fusarium* wilt of cotton. In 'Fusarium: diseases, biology, and taxonomy.' (Eds P. E. Nelson, T. A. Toussoun and R. J. Cook.) pp. 29-38. The Pennsylvania State University Press: University Park, PA, USA