Fusarium Wilt of Cotton in Australia

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ABSTRACT

Fusarium wilt of cotton caused by the fungus Fusarium oxysporum Schletend. f.sp. vasinfectum (Atk.) Snyder and Hansen (Fov) was first recorded in Australia in 1993. Several hundred isolates of Fov have since been examined in laboratory and glasshouse studies to determine the range of genetic and pathogenic diversity in the Australian Fov populations. Vegetative Compatibility Group (VCG) and DNA Amplification Fingerprint analysis have confirmed that two distinct strains of Fov (VCG 01111 and 01112) occur in Australia and that these groups differ from the overseas isolates tested to date. Glasshouse and field evaluations have identified tolerant varieties for adoption by industry. The Australian cotton industry has implemented a range of measures to prevent the spread of Fov to disease-free regions and to reduce the incidence of disease on affected farms. Future research will focus on evaluation of germplasm for resistance to Fov, comparative analysis of isolates of Fov from other countries and a series of long-term field trials to assess options for stubble management and pathogen-limiting crop rotations.

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 this wilt pathogen until 1993, when it was confirmed in the state of Queensland (Kochman, 1995). The disease was also confirmed in the Philippines at around the same time.

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

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* DNA Amplification Fingerprinting (DAF) (Bentley and Bassam, 1996). A database of DNA fingerprints has been compiled allowing comparisons of the DNA from Australian isolates of *Fov* with that of other strains of *Fov* and other formae speciales of *F. oxysporum*.

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, cottonseed was germinated in moist vermiculite. Two-week-old seedlings were then removed, washed and the roots dipped for 5 minutes in an inoculum containing 10_6 conidia mL_{-1}. The inoculated seedlings were then transplanted to individual pots and grown in the glasshouse for 6 weeks. The plants were then removed and assessed externally for the presence of wilt symptoms and internally for the extent of vascular discoloration using a 5 point scale.

An eight-hectare 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

Disease distribution

Initially the disease was identified only in the Darling Downs region of southern Queensland. In 1995, wilted plants were observed near Goondiwindi, also in southern Queensland and then, in 1997, from near Moree in northern New South Wales. During subsequent seasons, the incidence of fusarium wilt became more widespread in these districts. Some cases appeared to be related to overland water flows. At the end of the 1997/98 season, 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 of St George and Emerald in Queensland and all regions south of Moree in New South Wales remain free from *Fov*.

Pathogen diversity

VCG and DNA testing have revealed that two distinct strains of *Fov* (VCGs 01111 and 01112) are present in Australia (Davis *et al.*, 1996). DNA analysis confirms that isolates within each of these VCGs are very closely related and 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 the current commercial cotton varieties used in Australia. VCG 01111 occurs throughout the Darling Downs and near Theodore in Queensland and Moree in New South Wales. VCG 01112 has 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. In comparisons with a small number of isolates from other countries, Davis *et al.* (1996) concluded that isolates in VCG 01111 most closely resembled the behaviour of isolates in Race 6 (Armstrong and Armstrong, 1978, Chen *et al.*, 1985) but questioned the rationale of using a differential set containing secondary non-*Gossypium* hosts. On the basis of DNA analysis and pathogenicity to a differential set containing only *Gossypium* species and cultivars, Assigbetse *et al.* (1994) grouped isolates in Races 1, 2 and 6 into a single group which they called Race A.

From other comparative analyses including volatile production and aesculin hydrolysis, Davis *et al.* (1996) concluded that the Australian strains of *Fov* behaved differently from races of the pathogen described elsewhere and suggested that the Australian populations may have evolved locally, possibly in response to the widespread planting of susceptible varieties. Further comparative analyses with strains of *Fov* from other countries will continue as cultures become available. Representative cultures belonging to the Australian VCGs 01111 and 01112 have been deposited in the collection held at the Fusarium Research Centre at the Pennsylvania State University in the USA. One isolate representing VCG 01111 has also been lodged with the American Type Culture Collection held in Maryland, USA (ATCC number).

Host resistance

Reaction of local cotton varieties to the Australian strains of *Fov* ranges from highly susceptible (eg. Siokra 1-4, DeltaJEWEL) to moderately resistant (e.g. Sicot 189, DeltaEMERALD). Glasshouse and field evaluations of germplasm are being carried out in association with the major cotton breeding programs in Australia (CSIRO cotton breeding team and Delta Pine Australia) to evaluate germplasm for reaction to *Fov* as well as yield. Selections from F1 populations which appear to be segregating for resistance to *Fov* are also being evaluated.

Future research

In addition to breeding and evaluating germplasm for resistance to *Fov* and the adoption of more tolerant cultivars, the Australian industry is also implementing other disease management options including on-farm hygiene measures to contain disease outbreaks and prevent the pathogen spreading to disease-free farms and districts. The location of pure seed production sites is also being closely monitored, since seed transmission of this disease has been confirmed in other countries. Further research has also commenced to identify a range of disease management strategies for industry including cultural practices such as stubble management and pathogen-limiting crop rotations, to reduce the incidence of disease on affected farms.

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