Characterisation of the Fusarium wilt pathogen of cotton in Australia.

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Introduction

Fusarium wilt was first identified in cotton in the USA in 1892. It is caused by the fungus *Fusarium oxysporum* Schlecht. ex Fr. f.sp.*vasinfectum* (Atk) Snyd.& Hans (*Fov*). The disease has since been identified in all the main cotton growing areas of the world except west Africa and Turkey (Hillocks 1992). In Australia, the disease was first found in the Brookstead/Cecil Plains area in March 1993. However, in November 1994 it was found near Warra, downstream from the original area, and in December 1994 the disease was identified in wilted cotton from the Boggabilla area of NSW (Kochman 1995). In January 1995 the disease was also found on a farm between Talwood and Mungindi.

Fusarium wilt has been responsible for substantial yield losses in some developing countries (Hillocks 1984, Kelman and Cook 1977), and remains important in the USA, Egypt, Tanzania, India (Smith *et al.* 1981) and China (Chen *et al.* 1985). It caused severe losses in some cultivars grown on the Darling Downs in 1995.

Characterising *Fov* isolates

Australian isolates of *Fov* have been characterised by using: pathogenicity tests with differential and local cotton lines ; vegetative compatibility groups (VCG) analyses and DNA amplification fingerprinting (DAF) analysis. Vegetative compatibility groups and DNA fingerprints of overseas isolates of the fungus have also been compared with those of Australian isolates of *Fov.*

The Australian isolates of *Fov,* tested to date on the differential lines, were pathogenic on both *G. hirsutum* cultivars (Siokra 1-4 and Acala 44) and both *G. barbadense* cultivars (Ashmouni and Sakel). No symptoms were observed on *G. arboreum* cv Roseum. The remaining differentials (tobacco, lupin and soybean) were not apparently affected by any isolate in these tests. Hence the local isolates react like race 6 which was initially identified in Brazil (Hillocks 1992).

There is some confusion as to the number of races currently recognised. Apart from the six reported by Hillocks (1992), there appear to be an additional two races (7 and 8) in China (Chen *et al.* 1985) where a further two non-cotton hosts (alfalfa and okra) were added to the differential set. Furthermore, Assigbetse *et al.* (1994) and Fernandez *et al.* (1994) described only three races from a world-wide collection of isolates of *Fov* by using pathogenicity testing in conjunction with RAPD analysis,. They constructed a race A which includes isolates previously designated as races 1, 2 and 6. Their races 3 and 4 corresponded with those previously described

A pot test has also been developed to test the reaction of cotton cultivars to infection by *Fov*. This involves growing cotton seedlings and dipping their roots in a suspension of *Fov*. Seedlings are replanted in pots and observed for symptoms of wilt and vascular discolouration.

All cultivars tested to date are susceptible to infection, although, there is a marked range of susceptibility. Siokra L22, Sicala V-1, DP90, Exp 720 (now Deltagem) and Pima are the least susceptible. Siokra L23 and CS189+ are moderately susceptible. Siokra S324, CS50, CS7S, Sicala 34 and Siokra 1-4 are the most susceptible. Generally there appears to be a good correlation between these results and the reaction of cultivars observed in field trials conducted on the Downs. However, there were some differences in the field trial results with CS189+ being in the least susceptible group. Variations may have been due to uneven distribution of the fungus in the field soil or other factors. The pot test may also need further fine tuning to make the correlation between pot and field trials better.

There appears to be a spread of virulence or aggressiveness in the *Fov* population even though all the Downs' isolates are in the same VCG and have similar DNA banding patterns. Of seven different isolates used in the pot test, the least aggressive did not affect CS7S, Siokra L22, Siokra L23, Sicala V-1, DP90 or Pima. The most aggressive severely affected CS7S, CS50, Siokra L23, S324, Sicala 34 and DP90. This suggests that isolates used in screening trials will need to be selected carefully.

VCG analyses, both in Australia and in France, indicate that the *Fov* isolates from the Downs differs from overseas isolates. We were not able to find any compatibility between the Down's isolates and races of the fungus imported through quarantine from overseas. This was confirmed by Dr Diana Fernandez (ORSTOM, Montpellier, France) who was also unable to obtain compatibility between the Australian isolates and 52 isolates of *Fov* collected from different cotton growing areas of the world. She suggested that the Australian isolate be numbered VCG 01111. VCG analyses also indicated that the isolate from the Talwood - Mungindi area is in the same compatibility group as isolates from the Downs while the Boggabilla isolate is in a different compatibility group. Further testing is in progress.

Data from DAF analysis indicated that the banding patterns produced by the Australian isolates were significantly different to those produced by the overseas races of *Fov* tested. The Boggabilla isolate had banding patterns which differed to isolates of *Fov* from the Downs and Talwood-Mungindi areas.

Conclusions

It appears that the isolates of *Fov* from wilted cotton in Australia are similar to race 6 in their reactions on the differential lines. However, we have concerns about the use of non-cotton hosts to differentiate between races 1,2 and 6. Therefore, we prefer to use the terminology of Assigbetse *et al.* (1994) and Fernandez *et al.* (1994) to designate the Australian isolates of *Fov* as race A.

The molecular characteristics, obtained by VCG analyses and DAF analysis, of Australian isolates indicate that they differ from all isolates of *Fov* tested from overseas. Isolates from the Darling Downs and the Talwood-Mungindi area also have different molecular characteristics to those isolates from Boggabilla.

Hence we speculate that the Australian strains developed locally, both on the Darling Downs and Boggabilla, and are unique. Perhaps they developed from a minor population of *Fusarium oxysporum* in response to widescale planting of very susceptible cotton cultivars. These findings have significant implications for control of the disease and spread of the pathogen in Australia.

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