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Cotton Research and Development Corporation Final Report

Project Grant US8C

VERTICILLIUM WILT OF COTTON: GENETIC FINGERPRINTING OF FUNGAL PATHOGENS & WILT-TOLERANT COTTON CULTIVARS

July 1992 - June 1996

1. PROJECT OVERVIEW

1.1. Introduction

Over the last five years the incidence of Verticillium wilt disease in cotton has increased and has cost the industry millions of dollars in lost yield. Information about the pathogenic races of *Verticillium dahliae* prevalent in the cotton growing areas of Australia, their mode of spread and their extent of field persistence has been lacking. Furthermore, although a few cotton cultivars developed by the CSIRO have shown some degree of tolerance to Verticillium wilt in the field, little is known about the number and kinds of defence genes that they possess.

With the advent of new molecular genetic techniques, it is now possible to identify the particular pathogen strain in an outbreak of plant disease, to characterise it, and potentially, to isolate genes associated with pathogenicity. Similarly, such techniques can also be employed to differentiate between plant cultivars and progeny in plant breeding programs and in the identification of genes implicated in improved plant resistance to diseases. In the present investigation, we have applied molecular genetic techniques to strains of *V. dahliae* isolated from cotton plants, and to cotton cultivars tolerant to Verticillium wilt, with the aim of achieving a better understanding of this pathogenic disease in cotton.