I. THESIS ABSTRACT

Arbuscular mycorrhizal fungi (AMF) are important symbiotic partners to the majority of land plants. AMF depend on the plant community for photosynthate-derived energy. In return, AMF provide the plant with a range of nutritional benefits, increased protection against plant pathogen and environmental stresses. In natural ecosystems, AMF can significantly influence plant community structure and plant community stability. In cropping systems, AMF are important contributors to sustainable, low-input plant production. Excessive reduction in the diversity of AMF has occurred in some intensively managed soils as the result of intensive farming practices. Low taxonomic diversity in AMF communities may have important implications for ecosystem function. This thesis examined some of the whether AMF taxonomic diversity is reduced a cotton cropping system.

AMF were identified in the roots of mycorrhizal host plants and directly in field soil using PCR-based techniques. An AMF-targeted PCR primer was designed that enabled the specific amplification of AMF DNA in the presence of plant DNA and other non-target organism templates (Chapter 2). The primer was used to amplify AMF rDNA living in the roots of trap plants baited with field soil. The trap plants were grown in soil from long-term fallow, monoculture and rotation crops to examine whether rotation crops can influence the taxonomic diversity of AMF in cropped soils (Chapter 3). Trap plants harboured the same overall diversity of AMF in monoculture and rotation cropped field soils. The same taxa occurred in each of the fields. AMF in the cotton cropping vertisols appear to be robust. Spore dormancy may be common in many AMF (Chapter 5), and may account for the survival of the majority of AMF taxa in the long-term fallow soil.

TRFLP profiles were used to compare AMF communities in soil under different land management practices. DNA was extracted directly from soil to obtain community profiles. TRFLP analysis revealed that AMF are distributed more evenly in

cultivated than uncultivated soils. This finding has important implications for the design of sampling strategies for AMF community diversity studies.