

Project Title: DNA monitoring tools for disease suppressive microflora

S0206R Final Report

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Executive Summary

Quantitative DNA tests were successfully developed for beneficial microorganisms implicated in suppression of Rhizoctonia root rot and included the bacterial groups *Pantoea agglomerans*, *Exiguobacterium acetylicum* and *Microbacterium* spp. Assays were also developed for two sub-groups of the fungus *Trichoderma*. These tests cover the majority of known *Trichoderma* species with biological control activity. These tests were developed to monitor target populations in soil and on plant roots, and were shown to be more sensitive and efficient than existing techniques to quantify these organisms.

The assays were used to assess a number of experiments and field trials. They detected treatment differences in the Mallee Sustainable Farming Project (MSFP) core site. Of interest were higher *Exiguobacterium* and *Microbacterium* DNA levels in the canola-wheat rotation which had the least Rhizoctonia disease compared to other rotation options. Also, in several low clay-high coarse sand soils from Eyre Peninsula, increased *Microbacterium* and *Trichoderma* levels were correlated with reduced disease.

A preliminary experiment indicates that across a broad range of soil types the absolute levels of Rhizoctonia and beneficials were not correlated with either disease or suppression. It is not likely that disease suppression is associated with levels of specific organisms; however, the DNA monitoring tests developed in this project are being used to understand the role of these groups in disease suppression. Future research should examine if the ratio of specific microbes to each other, or as a proportion of total microbial population, is a better indicator.