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INVESTIGATION OF PLASMODIOPHORA BRASSICAE (CLUBROOT DISEASE) IN VEGETABLE BRASSICA USING ARABIDOPSIS THALIANA AS A MODEL SYSTEM

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Clubroot, caused by *Plasmodiophora brassicae*, is the most devastating soil-borne disease of vegetable brassicas. It occurs all over the world and is responsible for crop losses of up to 10% every year. In Australia, the disease is being managed effectively with chemicals and cultural practices, but ideally control can be improved in the long term by the introduction of resistant cultivars. The life cycle of *P. brassicae* and mode of action of plant resistance has not been fully elucidated because of the technical difficulties of working with an obligate, soil-borne plant pathogen. However, *Arabidopsis thaliana*, which is a host of *P. brassicae*, has great potential as a model system for studying the life cycle, the infection process and development of resistance. We have developed a sand-liquid-culture system for growing *Arabidopsis* that allows easy observation of all life stages and, most importantly, the primary plasmodial stages within the root hair. The method was first optimised for observations of the lifecycle of the pathogen in a susceptible *Arabidopsis* ecotype (Col-3) where all stages of the lifecycle have now been observed and characterised. Further screening of *Arabidopsis* ecotypes for disease resistance has utilised one of the most virulent Australian pathotypes of brassica (ECD number 16/19/31). To date, *Arabidopsis* ecotype Ta-0 has shown a level of tolerance to the disease even though the roots get infected. It has been reported earlier that resistance to *P. brassicae* in *Arabidopsis* is due to one or a small number of genes. To examine changes in gene expression during the early, critical stages of infection, RNA was extracted from the susceptible and resistant ecotypes at two time points, 4 days and 17 days after inoculation. Microarray analysis will be used to investigate genome wide changes in gene expression during infection but also to identify candidate genes that may confer resistance to Australian isolates of the pathogen.