

MOLECULAR DISSECTION OF VIRUS RESISTANCE USING MEDICAGO TRUNCATULA

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Crop and pasture legumes play an important role in the Australian cropping system. *Medicago truncatula* has now emerged as the major model species for legumes, because it has a small diploid genome, is self-fertile, and it is amenable to efficient molecular genetics, reverse genetic studies and contains little repetitive non-coding DNA. It is related to varying degrees to other legume crops such as alfalfa, soybean, pea, fababean, lentils, lupins and clover. These species have related genome structures and organization, and so the genetics and genomics resources generated by study of *Medicago truncatula* can be applied to these related crops species to achieve desired results more rapidly. Viral disease can cause significant economic losses to legume crops where virus infection results in losses in grain production for human consumption, stock feed, pasture feed for dairy, meat and wool industries. In this project *Medicago truncatula* is being used as a model to study viruses of legume crops, and to identify new sources of natural resistance genes to these viruses. This involves screening and detailed analysis of responses of the *Medicago* core collection from SARDI to infection with alfalfa mosaic virus, cucumber mosaic virus, bean yellow mosaic virus, and subterranean clover stunt virus. So far more than 120 *Medicago truncatula* lines have been analysed for susceptibility, resistance, symptoms, and systemic and localised responses. The aim of this work is to identify new genes for virus resistance in *Medicago*, and to apply this knowledge to develop new forms of virus resistance in crops such as lupins, chickpeas and lentils.