NEW ZEALAND PLANT PROTECTION SOCIETY
RESEARCH SCHOLARSHIP

Matthew Denton-Giles, recipient of the 2011/12 New Zealand Plant Protection Society Research Scholarship, is a 2nd year PhD student in the Institute of Molecular Biosciences (IMBS), Massey University. In 2006, Matthew completed his Master of Science (Plant Biology) at Massey University and has worked as an environmental chemist, gardener and teaching/research technician. In 2011, he started his PhD study in plant pathology under the supervision of Drs Paul Dijkwel, Rosie Bradshaw and Murray Cox, with funding supplied by the New Zealand Camellia Society and the Leslie and Gladys Riggall Scholarship.

Matthew’s research aims to characterise natural resistance within the Camellia genus to the host-specific fungal pathogen Ciborinia camelliae. Ciborinia camelliae is the causal agent of “Camellia flower blight” and has become rampant throughout New Zealand since its accidental introduction in the early 1990s. It specifically infects the blooms of many ornamental Camellia species causing them to turn brown and fall early. Economically, this disease has impacted heavily on the New Zealand Camellia industry leading to declining sales, export losses and an overall social disheartening. Matthew’s research uses microscopy and molecular techniques to identify and quantify physiological and genetic hallmarks of plant resistance together with pathogen virulence.

Bioassays were performed on petals of potentially resistant and susceptible Camellia species/interspecific hybrids by measuring the area of C. camelliae-associated lesion development over time. Susceptible petals of Camellia saluenensis × Camellia japonica “Donation” and Camellia japonica × Camellia pitardii var pitardii “Nicky Crisp” produced macroscopic lesions within 30 hours of inoculation and became fully enveloped by 72 hours. In comparison, resistant petals of Camellia lutchuensis produced small necrotic spots that did not develop further. These results were consistently reproduced, suggesting that a bioassay of this type could be used to determine levels of resistance to C. camelliae across the Camellia genus. Microscopic analysis of the Camellia lutchuensis/C. camelliae interaction revealed hallmarks of non-host resistance together with localised cell death. Petal epidermal cells in direct contact with fungal ascospores exhibited papilla formation, cell wall thickening and localised H2O2 accumulation. Furthermore, localised cell death was observed, which suggests Camellia lutchuensis has a complex and robust form of resistance to C. camelliae.

To identify genes involved in resistance as well as pathogen virulence, the transcriptomes of both compatible and incompatible interactions were sequenced using Illumina™ next generation sequencing technology. Samples of mRNA from compatible/infected, compatible/mock, incompatible/infected and incompatible/mock were extracted and sequenced, producing a total of 400 million 100 bp paired-end sequences. Preliminary analysis of the data confirmed a combination of C. camelliae and Camellia sequences in the compatible/infected dataset. Furthermore, fungal sequences aligned with 23 previously characterised virulence factors from Botrytis cinerea and Sclerotinia sclerotiorum. Matthew is currently assembling the transcriptomes of these interactions using the de novo assembly software Trinity. Future bioinformatics analysis will aim to identify fungal and plant genes that are differentially expressed during infection.

In summary, Matthew’s research will provide useful information regarding incompatible and compatible interactions between Ciborinia camelliae and members of the Camellia genus, which could be utilised to breed resistance into ornamental Camellia cultivars.