



**THE CAMELLIA MEMORIAL TRUST  
INCORPORATED UNDER THE CHARITABLE TRUSTS ACT 1957  
(Charities Commission Registration number CC11067**

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Article for the New Zealand Camellia Society Inc. Web Site

In 2010 the Camellia Memorial Trust became aware of the possibility of support funding for research on camellias from a Trust established by the late Leslie Riggall, and his wife Gladys, who still lives in Panama. At this time the Trust had committed funding for a research project on camellia flower flight, but had insufficient funds for a scholarship to provide a stipend for a postgraduate student to research for a three-year PhD. A research proposal had been received from Dr Paul Dijkwel at the Institute of Molecular Biosciences at Massey University for a PhD project involving the use of a Solexa sequencing machine, to determine which genes control resistance to flower blight in certain *Camellia* species. This knowledge has the potential to be then used to speed the process of breeding resistant cultivars. Previous research at Massey University had identified at least 8 such species. An application to the Riggall's Trust was made, stressing that flower blight is by far the major problem faced by camellias worldwide.

The Camellia Memorial Trust's application was accepted, and Mrs Riggall and her adviser Michelle de Carles agreed to grant \$NZ 54,000 to the project, to be named the **Leslie and Gladys Riggall Scholarship**.

The costs to the Camellia Memorial Trust of the project, to be conducted at Massey University under the guidance of Professor Paul Dijkwel, are as follows

1. NZ\$48,600 towards the costs of consumables for this project.
2. NZ\$20,000 per annum for each of 3 years towards a scholarship for a PhD student. The scholarship is to be named "**The Leslie and Gladys Riggall Scholarship**".
3. In addition the trust will provide NZ\$6000 per annum for each of 3 years to cover university fees.

The Trust will thus be contributing a total of NZ\$74,600 over the full 3 year period in addition to the Grant from the Riggall Estate.

Massey University also estimates its contribution over the 3 year period as \$45,000.

In November 2010 Dr. Dijkwel, gave the Board a superb presentation on what he proposed to research with the aid of his PhD student financially supported by the Trust. He explained that

*Camellia japonica* has about 3,814,000,000 DNA bases. From this about 25 million pieces will be separated, of which 75 bases will be investigated in particular. Paul had 257 applicants for the PhD studentship, from which he had made a shortlist., Subsequently we were advised that the New Zealand applicant, Matthew Denton-Giles, had been offered and had accepted the position. Matthew starts with an advantage of previous experience with DNA sequencing

Matt Denton-Giles commenced on 1 May 2011 and he presented the Board with an outline of his project at their Board meeting later in May. Matt's presentation began with a brief introduction about himself, including his previous studies on native ferns at Massey University. A basic life-cycle of *Ciborinia camelliae* (the Camellia flower blight fungus) was described indicating the sclerotia, apothecia, ascospore and infection stages. Matt then talked about past research on Camellia flower blight and described how the new project has shifted the research focus from actively trying to kill the fungus to utilizing naturally occurring resistance. Recent Camellia flower blight research carried out by Drs Christine Taylor and Valipuram Vingnanasingam was described, including pictures of the infection in Camellia petals and possible mechanisms for resistance. Matt then went on to describe his current work status. He had purchased 36 young Camellia plants and had begun monitoring their flowering patterns in a temperature controlled glasshouse. Matt described why he had chosen the selected species and what he hoped to do with them over the 2011 blight season.

Matt is scheduled to update us again in May 2012. He hopes to have carried out the Solexa sequencing by the end of 2011 and should be well on the way to identifying candidate resistance genes.