Loop- mediated Isothermal Amplification (LAMP) - A new diagnostic tool for Pseudomonas syringae pathovars syringae and pisi that causes bacterial blight in field pea

Pragya Kant[1]
Mario Fruzangohar[2], Rachel Mann[1], Brendan Rodoni[1], Grant Hollaway[1] and Garry Rosewarne[1]

[1] Agriculture Victoria
[2] Biometry Hub, University of Adelaide, waite campus, Urrbrae, SA 5064

Bacterial blight (BB) is a major disease of field pea caused by the pathogen, *Pseudomonas syringae* pathovars *syringae* and *pisi*. Both pathovars cause similar symptoms and can be isolated from a single plant. Several races have been identified in the *pisi* pathovar, however there is no race specificity in the *syringae* pathovar. Due to frequent frost events, BB epidemics occurred in two consecutive years, 2017 and 2018. To understand the pathovar populations, survey samples were collected from Victoria and other states. The isolates were characterised using traditional polymerase chain reaction (PCR) to identify the pathovar specificity which was time consuming and laborious. Here we demonstrated the development of sequence based diagnostic markers for pathovar identification by utilizing whole genome sequencing of 16 *Pseudomonas syringae* pathovars including *syringae, pisi* and two outgroups. Through comparative analysis, a unique genomic region specific for the *pisi* pathovar was identified and used to develop a loop-mediated isothermal amplification (LAMP) assay. Our collaborators previously have developed a LAMP assay for pathovar *syringae* diagnostics. The LAMP assay has been validated on several *Pseudomonas* species and unrelated outgroup bacteria obtained from VPRI (Victorian herbarium). The results showed high accuracy towards *pisi* pathovars. Both LAMP assays were successfully utilised on the survey work in 2018 and historical isolates from the Horsham collection for high throughput diagnostics.