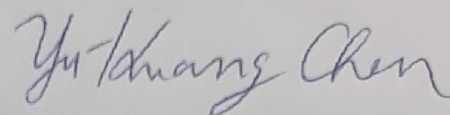


**Evaluation of guava wilt disease resistance among genotypes and
identification of molecular markers linked to guava wilt disease resistance
in guava**

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ABSTRACT

Guava wilt disease (GWD) caused by soil-borne fungus *Nalanthamala psidii* has resulted in significant losses to global guava production. Several methods have been employed to control the pathogen including the use of biological agents, chemicals, and phytosanitary measures. However, their effect on this disease has been limited. In general, the improvement of host resistance offers the most economic, sustainable, and efficient means for combating the pathogen. In addition, biotechnological advances through the use of marker-assisted selection (MAS) provide an effective strategy for the introgression of resistant genes. The aim of my study is to evaluate the response of different guava genotypes including related species to *Nalanthamala psidii* inoculation under greenhouse conditions. Furthermore, simple sequence repeat (SSR) markers associated with *Nalanthamala psidii* resistance will be identified in an F₂ population segregating for GWD resistance. Bulk segregant analysis will be conducted to identify markers tightly linked to the trait of interest. The study expects to identify markers linked with GWD resistance which could provide a platform for the development of resistant cultivars through marker-assisted selection.

Keywords: Guava wilt disease, *Nalanthamala psidii*, linkage analysis, microsatellite markers

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