

Papaya Dieback in Malaysia: A Step Towards A New Insight of Disease Resistance

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A draft genome of *Erwinia mallotivora* BT-Mardi (1), the causal pathogen of papaya dieback infection in Peninsular Malaysia, has significant potential to overcome and reduce the effect of this vulnerable crop (2). The authors found that the draft genome sequence is approximately 4824 Kbp and the G+C content of the genome was 52-54%, which is very similar to the reference genomes of other *Erwinia* species. They concluded that the draft genome would be useful for understanding host-pathogen interaction and determining the mechanism of infection of the disease. In addition to this, we believe that there are some further directions that should be considered in the future.

Firstly, the comprehensive analysis of pathogenicity genes in *E. mallotivora*, which would enable the comparison of genes important in pathogenicity between species in the genus *Erwinia*, and highlight any differences. These include the most important and well-studied pathogenicity system in gram negative bacteria: the Type III Secretion (TTSS). Investigation of genes important in the pathogenesis of *E. mallotivora* will decipher the function of these genes and unravel the complex interaction of the bacteria and host, and this will enable the understanding of their capabilities to enter plant cells, overcome host resistance and induce disease. This in-depth understanding will potentially allow the identification and application of new sources of biocontrol for this disease.

Secondly, the elucidation and identification of the potential pathogen-inducible and defence-related genes in papaya. The papaya genome is available online to enable the identification of the putative immunity related genes (IRG) and it will be greatly useful for revealing the blueprint of host genes under

pathogen stress. Wee *et al.* (3) reported the expression analysis for four possible defence related genes in the *E. mallotivora* host (zinc finger protein, leucine rich protein, aquaporin and peroxidase), in order to understand the defence mechanisms in papaya. This information will be valuable for strategies in generating host resistance and understanding host-pathogen interaction.

Thirdly, the discovery of papaya microRNAs (miRNAs) is also important. Previous studies have shown that miRNAs could act in wide range of biological processes as well as in the plant's defence system towards biotic and abiotic stresses. Therefore, profiling and functional analysis of miRNAs would be important to generate novel possibilities in improving resistance to dieback. The high potential application of miRNAs in the host defence mechanism indicates that they should be used or manipulated to confer pathogen resistance in papaya.

Finally, the development of resistant plants using a genetic engineering approach is also an important tool in the control of papaya dieback disease. Currently, there is no chemical control treatment available and no resistant papaya varieties offered in order to overcome this severe disease, and generating resistant plants using a biotechnology approach could be the solution. The strategy of disruption of bacterial virulence factors, improvement of plant defence responses and the expression of antimicrobial proteins of non-plant origin could be applied in papaya to confer resistance.

The draft genome of *E. mallotivora* BT Mardi is the first step and the initial key to the understanding of the host-microbe interaction and mechanism of infection of this severe disease. This could be fundamental for

plant pathologists, molecular biologists and botanists in Malaysia - it could help them to focus on the ultimate goal of control of papaya dieback disease.

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Conflict of interest

The author declares there is no conflict of interest regarding the publication of this paper.

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