

## **Multiple sequence analysis of *Erwinia papayae* isolates from six different locations of Papaya Dieback Outbreak In Malaysia**

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*Erwinia papayae* has been previously shown to be the etiological agent of the papaya dieback outbreak in Malaysia (Maktar *et al.*, 2008). Six isolates each from different locations of papaya dieback outbreak in Malaysia namely Serdang, Kuala Selinsing, Kalumpang, Semenyih, Kulim and Setiawan were subjected to 16S RNA sequencing and analysed by Multiple sequence alignment (Clustal X (1.81)) software. The Multiple sequence alignment analyses showed that all the isolates shared at least 99.4% homology suggesting that they probably originate from one source of outbreak .

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