Title	Detection and classification of soft rot Erwinia of vegetables in Thailand by DNA polymerase chain
	reaction
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## Abstract

Detection and classification of soft rot Erwinia of vegetables in Thailand were conducted from ten varieties of vegetables; cauliflower, cabbage, chinese cabbage, pak-choi, spinach, carrot, chinese radish, cucumber, tomato and asparagus. To determine soft rot Erwinia, soft rot bacteria were isolated from rot symptom of these vegetables on pectate assay medium and identified by technique of DNA polymerase chain reaction. Using Y1 and Y2 primers are specific to amplify 434 bp open reading frames of pectate lyase (*pel*) genes of *E. carotovora* while ADE1 and ADE2 primers are specific to amplify 420 bp open reading frames of pectate lyase genes of *E. chrysanthemi*. The result showed that only Y1 and Y2 primers were able to amplify genomic DNA of all isolates. Amplified DNA band of each isolate was sequenced and searched similarity with DNA Data Bank of Japan (DDBJ). The results presented that a DNA band of all isolates had 90-96% similarity with *pel153* gene of *E. carotovora* and DNA band of isolates from spinach and cauliflower had 90 and 94% similarity with *pelB* gene of *E. carotovora*, respectively. Analysis of phylogenic tree indicated that all bacterial soft rot isolates were *E. carotovora* group. Disease severity of those *Erwinia* species was considered by determining the activity of tissue macerating enzymes; pectate lyase, polygalacturonase, cellulase, and protease with spectrophotometer and measuring the area of soft rot symptom on chinese cabbage after artificial inoculation. The results revealed that *Erwinia* isolated from carrot was the severest because it produced the highest tissue macerating enzymes and macerated plant tissue with largest soft rot area in compare to among of all isolates.