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摘要(中)	<p>本章的實驗目的為研發 <i>Xanthomonas</i> 屬植物病原細菌的種子檢測法。在研發此屬病原細菌的鑑別性培養基方面，首先以 mTBM 選擇性培養基做測試，並加以改良研發成 <i>Xanthomonas</i> 之鑑別性培養基，命名為 mTBM-42。以 <i>Xanthomonas</i> 屬病原細菌共 8 個種 19 個病原小種作測試，結果顯示在 28°C 培養 3-5 天，菌株均呈現淡綠色至深綠色、水亮、上突、菌株周圍有透明與白霧狀兩種暈圈。由植物葉片與種子分離出來的黃色而非 <i>Xanthomonas</i> 菌株，如 <i>Pantoea</i> sp.、<i>Pseudomonas</i> sp.、<i>Erwinia</i> sp.、<i>Arthrobacter</i> sp.，在鑑別性培養基上，菌株型態均為黃色且扁平，除屬於 <i>Arthrobacter</i> sp. 菌屬的菌株，周圍只含有透明暈圈外，其餘均無透明與白</p>

霧狀兩種型態的暈圈。將此研發出的鑑別性培養基，應用於罹病甘藍葉片病原菌的分離，在培養 3-4 天即可分離出具有明顯特徵的 *Xanthomonas* 屬病原細菌，可避免選到黃色而非 *Xanthomonas* 屬的細菌。另外，應用此鑑別性培養基在種子檢測上，以 *X. campestris* pv. *campestris* XCC1-1 菌株在此培養基與 LA 培養基上菌落數之比值，顯示不含抗生素的 mTBM-42(A)培養基與 LA 培養基上菌落數之比值為 128%，含抗生素 cephalixin (65 ppm) 與 5-fluorocil (12 ppm) 的 mTBM-42(B)與 LA 培養基上菌落數之比值之回收率為 120%，外加抗生素 cycloheximide mTBM-42(C)與 LA 培養基上菌落數之比值為 109%。以香菜葉枯細菌 *X. campestris* pv. *coriandri* NCPPB 1457 在此培養基與 LA 培養基上菌落數之比值，顯示在 mTBM-42(A)其比值為 109%，在 mTBM-42(B)之比值為 101%，在 mTBM-42(C)之比值為 95%。由此結果得知 XCC1-1 或 NCPPB1457 在此選擇性培養基上生長比 LA 培養基好，培養基所加的抗生素也對這兩個菌株只有輕微抑制作用。此實驗同時觀察到這兩個菌株在不含抗生素的培養基上，約 4 天可變綠色，在含抗生素的培養基上，約 5 天可變綠色。將 *X. campestris* pv. *campestris* XCC1-1 菌株混合青江菜 (*Brassica chinensis*) 種子，或 *X. campestris* pv. *coriandri* NCPPB 1457 混合香菜種子，再使用 mTBM-42、mTBM-42A 與 mTBM-42B 培養基分離。結果顯示，雖然此培養基不能抑制所有腐生菌生長，但在 28°C 培養 3-4 天仍可發現具有明顯特徵的 *Xanthomonas* 屬病原細菌。再利用此鑑別性培養基檢測進口香菜種子之 *Xanthomonas* 屬細菌。結果顯示只有代號為高雄-1 的種子，可發現到少數具有明顯特徵的 *Xanthomonas* 屬細菌。挑選 2 個代表性菌株 K1-A-27 與 K1-A-37 進行 16S rDNA 序列，結果顯示與 *X. campestris* 有高達 99 % 的相似性，對煙草也會產生過敏反應，證實分離菌株為 *Xanthomonas* 屬植物病原細菌。再將以上 4 個代表性菌株, K1-A-4、K1-A-9、K1-A-27 與 K1-A-37，與香菜葉片分離菌株 C2-2-1、C4-3、B3-7、B5-5 及 *X. campestris* pv. *coriandri* NCPPB 1457，以 PFGE 進行分子類型區分分析，結果顯示進口香菜種子 (高雄-1) 所分離之菌株與香菜葉片分離菌株呈現不同的 PFGE pattern。除利用鑑別性培養基檢測外，亦研發 PCR 的檢測法。使用 DNeasy? Tissue Kit 抽取種子萃取液的 total DNA，再以 hrpG-F+hrpG-R 進行 PCR 反應，結果顯示 PCR 靈敏度約為 104-105 cell/ml。本論文的實驗目的是比較使用 IS-RFLP (IS-restriction fragment length polymorphism analysis) 及 PFGE (pulsed field gel electrophoresis) 兩種方法，在台灣分離之 *Xanthomonas campestris* pv. *campestris* (XCC) 菌株的分型之結果。利用 IS1404 (IS3 family)、IS1479 (IS5 family) 以及 ISXac3 做 probe，進行 IS-RFLP 分析。結果顯示使用 IS1404-RFLP 方法，在所測試的 XCC 菌株中有 8 個分子類型。使用 IS1479-RFLP 與 ISXac3-RFLP 方法，也是分成 8 個分子類型，此結果顯示不管使用那種 IS 進行 IS-RFLP 分析，在 XCC 菌株的分型上，所得到的結果是相同的。再將這些菌株的 total DNA，以限制酵素 SpeI 處理後，再以 PFGE 進行分子類型區分分析，也可將其分成 8 個分子類型。進一步使用 PFGE 在香菜 (*Coriandrum sativum*) 葉枯病原菌株的分型上。因為推測 2000 年夏天在台灣首先發現的病原菌，可能藉由進口種子引入。所以比較在台灣香菜病葉所分離之 14 株疑似的 *X. campestris* pv. *coriandri* 菌株，以及最早在印度發現的葉枯病原菌 *X.*

	<p>campestris pv. coriandri NCPPB 1457 的 PFGE pattern。結果顯示台灣分離的菌株可分成五種 PFGE pattern，而其中一種 type 與 <i>X. campestris</i> pv. <i>coriandri</i> NCPPB 1457 有高度相似性。此結果顯示台灣分離的菌株可能來自包括印度的不同國家，而印度為台灣香菜種子最主要的進口國家。這些菌株進一步使用 <i>hrpG</i> 和 <i>virD4</i> 基因做探針，進行 Southern hybridization。結果顯示大多數的菌株都含有這兩個基因，但有一些菌株則沒有，而含有 <i>hrpG</i> 和 <i>virD4</i> 的菌株呈現多種 RFLP patterns。</p>
<p>摘要 (英)</p>	<p>The purpose of this chapter was to develop methods for detection of the plant pathogenic <i>Xanthomonas</i> spp. in plant seeds. The mTBM semi-selective media was chosen to develop a differential medium of <i>Xanthomonas</i> spp., mTBM-42. The nineteen pathovars of eight species of <i>Xanthomonas</i> were tested on mTBM-42. Colonies of <i>Xanthomonas</i> spp. were light green and deep green, glistening, convex with entire margins, and surrounded by a large clear zone and a smaller milky zone after 3-5 days of incubation at 28oC. Some yellow-pigmented non-xanthomonads isolated from plant leaves and seeds, such as the <i>Pantoea</i> sp., <i>Pseudomonas</i> sp., <i>Erwinia</i> sp., <i>Arthrobacter</i> sp., grew on the differential media as yellow, flat, and without clear and milky zones, except <i>Arthrobacter</i> sp., which was surrounded by a large clear zone only. The mTBM-42 differential medium was used to isolate plant pathogenic <i>Xanthomonas</i> spp. from infected cabbage leaves. The characteristic colonies of <i>Xanthomonas</i> sp. were observed after 3-4 days of incubation at 28oC. The medium could differentiate <i>Xanthomonas</i> spp. from yellow-pigmented non-xanthomonads and avoid isolation of non-xanthomonads. Furthermore, the differential medium was used to detect <i>Xanthomonas</i> spp. in plant seeds. The recovery of <i>X. campestris</i> pv. <i>campestris</i> XCC1-1 on mTBM-42 medium was 128%, compared with LA medium. The recovery was 120% on mTBM-42 medium supplemented with cephalexin (65 ppm) and 5-fluorocil (12 ppm) (mTBM-42A), and 109% on mTBM-42A medium with further addition of cycloheximide (75 ppm) (mTBM-42B). The recovery of <i>X. campestris</i> pv. <i>coriandri</i> NCPPB 1457 was 109% on mTBM-42, 101% on mTBM-42 A, and 95% on mTBM-42B. Thus, the addition of antibiotics had a slight inhibitive effect on the growth of <i>Xanthomonas</i> spp. The <i>Xanthomonas</i> spp. tested developed the characteristic colonies in 4 days on media without antibiotics and 5 days on media with antibiotics. The seeds of <i>Brassica chinensis</i> and coriander were artificially inoculated with <i>X. campestris</i> pv. <i>campestris</i> XCC1-1 and <i>X. campestris</i> pv. <i>coriandri</i> NCPPB 1457, respectively. The seed extracts were plated on mTBM-42, mTBM-42A, and mTBM-42B. Although the media did not eliminate growth of all saprophytes, the characteristic colonies of <i>Xanthomonas</i> spp. could still be observed after 4-5 days of incubation at 28oC. The differential media were further used for the detection of <i>Xanthomonas</i> sp. in imported coriander seeds. A few characteristic colonies of <i>Xanthomonas</i> spp. were found in the coriander seeds of Kaohsiung-1. Two isolates, which K1-A-27 and K1-A-37, were chosen for 16S rDNA sequence analysis. The sequences were highly identical (99%) to that of <i>X. campestris</i>. The hypersensitive reactions were observed in <i>Nicotiana benthamiana</i> inoculated with K1-A-27 and K1-A-37. The</p>

results indicated that the characteristic colonies isolated on the media were plant pathogenic *Xanthomonas* sp. The molecular types of K1-A-4, K1-A-9, K1-A-27, and K1-A-37 isolates, and strains C2-2-1, C4-3, B3-7, B5-5, NCPPB 1457 of *X. campestris* pv. *coriandri* which were isolated from coriander leaves were determined by using pulsed field gel electrophoresis (PFGE). There were two PFGE patterns among isolates from imported seeds of Kaohsiung-1, which were different from the patterns of strains isolated from coriander leaves. PCR assays for seed detection of *Xanthomonas* spp. was also developed. The total DNA of seed extracts was isolated by DNeasy? Tissue Kit and used in PCR amplification using primer set, *hrpG*-F/*hrpG*-R. The sensitivity of PCR assay was approximately 10<sup>4</sup>-10<sup>5</sup> cell/ml. The purpose of this study is to compare the insertion sequence-restriction fragments length polymorphism (IS-RFLP) and pulsed field gel electrophoresis (PFGE) methods in the molecular typing of *Xanthomonas campestris* pv. *campestris* (XCC) strains in Taiwan. Three insertion sequences, IS1404 (IS3 family), IS1479 (IS5 family), and ISXac3, were used as probes for IS-RFLP analyses. There were at least eight molecular types in IS1404-RFLP analysis. The number of molecular types was almost the same by using IS1479-RFLP and ISXac3-RFLP methods, indicating that the results of molecular typing would be the same regardless of what IS used in IS-RFLP analysis. PFGE analysis also obtained the same number of molecular types using *SpeI* for digestion of total DNAs. PFGE was further used to characterize the suspected strains of coriander (*Coriandrum sativum*) leaf blight pathogen. The pathogen was first found during the summer of 2000 in Taiwan and might be introduced from imported seeds. PFGE patterns of fourteen isolates of *X. campestris* pv. *coriandri* from diseased coriander leaves in Taiwan were compare with that of *X. campestris* pv. *coriandri* NCPPB 1457, which was isolated in India where coriander leaf blight first occurred. There were five PFGE pattern types in the strains isolated in Taiwan, and one type is highly similar to that of *X. campestris* pv. *coriandri* NCPPB 1457. The results indicated that the strains in Taiwan might be from different foreign countries including India, which is the major exported country of coriander seeds. The strains were further characterized by Southern hybridization using the *hrpG* and *virD4* as probes. The result showed that most strains contained both genes but some did not, and various RFLP patterns were found in strains with *hrpG* and *virD4*.

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