記錄編號	5437
狀態	NC093FJU00105029
助教查核	
索書號	
學校名稱	輔仁大學
系所名稱	生命科學系
舊系所名稱	
學號	492546135
研究生(中)	李京倫
研究生(英)	Ching-Lun Lee
論文名稱(中)	Xanthomonas 屬植物病原細菌之兩段基因間序列之分析及應用
論文名稱(英)	Sequence analysis and application of two intergenic regions of Xanthomonas spp.
其他題名	
指導教授(中)	李永安
指導教授(英)	Yung-An Li
校內全文開放日期	
校外全文	

開放日期	
全文不開放理由	
電子全文送交國圖.	
國圖全文開放日期.	
檔案說明	
電子全文	
學位類別	博士
畢業學年度	94
出版年	
語文別	中文
關鍵字(中)	黃原桿菌屬 核酸陣列 分子分型
關鍵字(英)	Xanthomonas DNA array molecular typing
摘要(中)	本實驗室在研究十字花科黑腐病菌(Xanthomonas campestris pv. campestris 1-1；XCC 1-1)內插入序列 IS1404 座落位置時，發現其中一個 IS1404 座落於 NTPase 基因內，與已公佈的 X. campestris pv. campestris ATCC33913 (XCC ATCC33913)、X. axonopodis pv. citri 306 (XAC 306)及 X. oryzae pv. oryzae KACC10331 (XOO KACC10331)三個基因體序列分析比對，發現在 XCC ATCC33913 中，NTPase 基因內亦有一個 IS1404 插入，但 XAC306 卻無 NTPase 基因，NTPase 在 XCC ATCC33913 中兩端基因存在的情形為 mrdB-NTPase-chp-hp-peh-1，XAC 306 則為 mrdB-peh-1，缺少 NTPase-chp-hp 約 8-kb 的 DNA 片段(簡稱 NTPase 片段)，而 XOO KACC10331 則為

	mrdB-ucp1-hp-ucp2-ucp3-peh-1 (簡稱 ucp 片段)。為了確認 NTPase 片段是否只存在於 XCC，分別以 PCR 及 Southern hybridization 檢測，結果發現 NTPase 片段只存在於 XCC，而其他 Xanthomonas 屬細菌則缺乏此片段，進一步測試 XCC 不同菌株，除均含有 NTPase 片段外，此片段也均位於 mrdB- peh-1 兩基因之間，顯示此 NTPase 片段可能經由水平基因轉移方式，移入 XCC 之共同祖先，而成為 XCC 菌株所共有。針對 NTPase 片段內的 chp 基因，設計 PCR 引子對 XCCchp-F/ XCCchp-R1，發現所測試的 XCC 菌株皆可擴增出 443-bp 大小的 DNA 片段，而其他 Xanthomonas 屬或非 Xanthomonas 屬植物病原細菌，除 X. campestris pv. aberrans 及 X. bromi 外，均無法擴增出任何的 DNA 片段，因此 XCCchp-F/ XCCchp-R1 之 PCR 引子對，可用於對十字花科黑腐病菌進行專一性的檢測之用。此外，將 XCC 細菌與甘藍種子混合培養 48 小時後，可利用 XCC 專一引子自混合培養液中擴增出目標片段。同樣地，針對 XOO 獨有的 ucp 片段中之 ucp2 基因設計 PCR 引子對 Xo-ucp-F/ Xo-ucp-R，僅 XOO 菌株可擴增出 643-bp 大小的 DNA 片段，因此可用於對 XOO 的專一性檢測。利用 mrdB 與 peh-1 二基因專一性引子探針及跨基因引子對 Xanthomonas 屬不同菌株進行測試，得知它們皆具有此二基因，但其間序列長短情形有差異。以 mrdB-peh-1 跨基因引子 mrdB-F2L/ Xpeh-R 分別將 Xanthomonas 屬內 11 個種的菌株 mrdB-peh-1 間序列選殖出並定序比對，依結果可分為 A~H 八種類型，其中除了 X. campestris pv. syngonii 有一 IS 插入，其餘菌株在此部份並沒有任何功能基因存在。利用此處的序列差異，分別將 A~G 七種類型菌株所特有的核酸序列以 PCR 方式擴增出並製成探針，發現各探針對相對應類型的菌株具有專一性，因此可利用此 mrdB-peh-1 間序列對 Xanthomonas 屬細菌進行初步鑑定。除了 mrdB-peh-1 為可能的水平轉移區域外，本實驗室也在另外一段區域發現了類似的情形。先前在研究 Xanthomonas 代謝 quinate 的能力時，發現僅 X. arboricola 擁有此能力，其後進一步自 X. arboricola pv. juglandis XJC5 菌株中將相關基因 qumA-qumB 選殖出，經定序分析結果得知，qumA-qumB 基因兩側尚有具相同轉錄方向的 unknown 與 pep 基因，基因排列順序由 5’ 端開始依序為 unknown-qumA-qumB-pep。比對已知的 Xanthomonas 基因體序列 XCC ATCC33913、XAC 306 以及 XOO KACC 10331，發現此處基因排列順序皆為 unknown-pep，缺少 qumA-qumB 約 4.4-kb 的片段，因此推測 qumA-qumB 也是經由水平基因轉移的方式移入 X. arboricola 的共同祖先。以 unknown-pep 跨基因引子 UN-F6/ pep-R7 分別將 Xanthomonas 屬內 12 個種的菌株 unknown-pep 間序列選殖出並定序比對，依結果可分為七種類型，其中 X. campestris pv. zantedeschiae 與 X. arboricola 同樣具有 qumA-qumB 片段，而 X. oryzae pv. oryzicola、X. hortorum pv. pelargonii 有 IS 插入，其餘菌株在此部份沒有任何功能基因存在。將此分類結果與 mrdB-peh-1 基因間序列的分類結果進行比較，推測 XCC 的 NTPase 片段、XOO 的 ucp 片段以及 X. arboricola 的 qumA-qumB 片段可能分別經由水平基因轉移移入 Xanthomonas 中。
摘要 (英)	The study on insertion sequence IS1404 of Xanthomonas campestris pv. campestris XCC1-1 led to a discovery of NTPase gene which is interrupted by IS1404. Based on whole genome sequences of X. campestris pv. campestris

	ATCC33913 (XCC ATCC33913), X. axonopodis pv. citri 306 (XAC 306), and X. oryzae pv. oryzae KACC10331 (XOO KACC10331), it was found that an IS1404 is located inside the NTPase of XCC ATCC33913, but XAC 306 and XOO KACC10331 do not contain NTPase gene. In addition, the three Xanthomonas spp. have different gene content in this region. In XCC ATCC33913, the order of genes is mrdB-NTPase-chp-hp-peh-1 (NTPase fragment), whereas XAC 306 is mrdB-peh-1, and XOO KACC10331 is mrdB-ucp1-hp-ucp2-ucp3-peh-1 (ucp fragment). To determine weather NTPase fragment exists only in XCC, PCR and Southern hybridization are used to test different Xanthomonas species and XCC strains. The results indicated that NTPase fragment only existed in XCC strains and was located between mrdB and peh-1 in all XCC strains tested. However, two flanking genes, mrdB and peh-1 were highly conserved and widely distributed in Xanthomonas spp., Indicating that NTPase fragment was acquired by XCC through horizontal gene transfer. A specific primer set XCCchp-F/ XCCchp-R1 for chp gene of NTPase fragment was designed and could amplify a 443-bp DNA fragment from all XCC strains, but not from non-XCC strains (except X. campestris pv. aberrans and X. bromi) or non-Xanthomonas plant pathogenic bacteria in PCR tests. The primer set was used to detect the presence of XCC in artificially inoculated cabbage seeds. The same strategy was applied to XOO, a specific primer Xo-ucp-F/ Xo-ucp-R for ucp2 gene of ucp fragment was designed and could only amplify a 643-bp DNA fragment from all XOO strains tested, but not from other Xanthomonas spp. The mrdB-peh-1 intergenic region of other species of Xanthomonas were amplified using primer mrdB-F2L/ Xpeh-R and sequenced. Based on sequence analysis, the regions could be seperated into eight different types. The nucleotide sequence of each type was used as a DNA microarray probe to identify different species of Xanthomonas. In addition to the region of mrdB-peh-1, we also found another DNA region which was probably acquired by horizontal gene transfer. In previous study, X. arboricola has qumA and qumB involved in quinate metabolism, which were absent in other Xanthomonas spp. The flanking genes of qumA and qumB in X. arboricola pv. juglandis XJC5 is unknown-qumA-qumB-pep. Based on whole genome sequences of XCC ATCC33913, XAC 306, and XOOKACC 10331, these Xanthomonas spp. have unknown and pep, but do not contain 4-kb qumA-qumB DNA frament. Amplification and sequencing of twelve different species of Xanthomonas showed variable nucleotide sequences in unknown-pep intergenic region. The regions could be separated into seven different types. The studies on mrdB-peh-1 and qumA-qumB allowed us to find specific DNA fragments of XCC and XOO, respectively, and to group Xanthomonas spp. by these two intergenic nucleotide sequences.
論文目次	

	果 mrdB-peh-1 cluster： 在 Xanthomonas 中之 mrdB-peh-1 cluster 內基因種類與坐落位置的分析 mrdB 與 peh-1 二基因的序列分析 XCC 之 chp 基因在 Xanthomonas 或其它屬植物病原細菌的存在情形 利用 XCC 的 chp 基因專一性引子檢測甘藍菜種子內之 XCC XOO 之 ucp2 基因在 Xanthomonas 中的存在情形 mrdB-peh-1 cluster 在非 XCC、XOO 的 Xanthomonas 中排列情形 mrdB-peh-1 間序列分析與分子類型區分 以 Dot blot 的方式區分不同類型的 Xanthomonas 利用 mrdB-peh-1cluster 建立演化關係樹 unknown-pep cluster： 在 Xanthomonas 中之 unknown-pep cluster 內基因種類與坐落位置的分析 unknown 與 pep 二基因在 Xanthomonas 中的存在情形與序列分析 unknown-pep 間序列分析與分子類型區分 利用 unknown-pep cluster 建立演化關係樹 討論 參考文獻 表 圖
參考文獻	李永安. 2002. Xanthomonas 屬病原菌及甘蔗流膠病之診斷鑑定技術. 植物重要防檢疫疫病診斷鑑定技術研習會專刊: 135-159. 李永安. 2003. Xanthomonas 屬植物病原細菌之診斷鑑定觀念及系統之研發. 重要防檢疫植物病原細菌綜合管理研討會專刊:15-21. 胡智國. 1999. 十字花科黑腐病菌基因組內插入序列 IS1404 座落位置分析. 輔仁大學生物學研究所碩士論文. 周淑玲. 2002. 對 Xanthomonas arboricola 具專一性的 qumA-qumB gene cluster 序列及座落位置分析. 輔仁大學生物學研究所碩士論文. 曾義雄. 2001. Comparative genomics suggests horizontal gene transfer between Xanthomonas campestris and Xylella fastidiosa mediated by filamentous phages. 東華大學分子生物科技研討會專刊:48-53. 劉雅惠. 2003. 十字花科黑腐病菌 virD4 同源基因功能分析、存在情形及其應用. 輔仁大學生命科學研究所碩士論文. 羅千惠. 2004. Xanthomonas 屬病原細菌 qum-pep cluster 之結構分析與應用. 輔仁大學生命科學研究所碩士論文. Alvarez, A. M., and Lou, K. 1985. Rapid identification of Xanthomonas campestris pv. campestris by ELISA. Plant. Dis. 69:1082-1086. Baggesen, D. L., Sandvang, D. and Aarestrup, F. M. 2000. Characterization of Salmonella enterica serovar typhimurium DT104 isolated from Denmark and comparison with isolates from Europe and the United States. J. Clin. Microbiol. 38:1581-1586. Bouzar, H., Jones, J. B., Somodi, G. C., Stall, R. E., Daouzli, N., Lambe, R. C., Felix-Gastelum, R., and Trinidad-Correa, R. 1996. Xanthomonas campestris pv. vesicatoria race variation in tomato and pepper fields of Mexico. Can. J. Plant. Pathol. 18:75-77. Brenner, D. J., Staley, J. T., and Krieg, N. R. 2001. Classification of prokaryotic organisms and the concept of bacterial speciation. In Bergey's Manual of Systematic Bacteriology (2nd ed.) Vol. 1. (Staley, J. T., Boone, D. R., Brenner, D. J., Castenholz, R. W., Garrity, G. M., Goodfellow, M., Krieg, N. R., Rainey, F. A., and Schleifer, K. -H eds) pp. 27-38. Springer-Verlag, New York. Burkholder, W. H., and Starr, M. P. 1948. The generic and specific characters of phytopathogenic species of Pseudomonas and Xanthomonas. Phytopathology 38:494-502. Capage, M., and Hill, C. W. 1979. Preferential unequal recombination in the glyS region of the Escherichia coli chromosome. Phytopathology 52:726. Chitarra, L. G., Langerak, C. J.,Bergervoet, J. H. W., and van den Bulk, R. W. 2002. Detection of the plant pathogenic bacterium Xanthomonas campestris pv. campestris in seed extracs of Brassica sp. applying fluorescent antibodies and flow cytometry. Cytomety. 47:118-126. Chun,

W. W. C., and Alvarez, A. M. 1983. A starch-methionine medium for isolation of Xanthomonas campestris pv. campestris from plant debris in soil. Plant. Dis. 67:632-635. Clewley, J. P. 2004. A role for arrays in clinical virology: fact or fiction? J. Clin. Virol. 29:2-12. Cohan, F. M. 1994. Genetic exchange and evolutionary divergence in prokaryotes. Trends. Ecol. Evol. 9:175-180. Cohan, F. M. 1996. The role of genetic exchange in bacterial evolution. ASM News. 62:631-636. Dewettnick, T., Hulsbosch, W., Van Hege, K., and Verstraete, W. 2001. Molecular fingerprinting of bacterial populations in ground-water and bottled mineral water. Appl. Microbiol. Biotechnol. 57:412-418. Domen, H. Y., and Alvarez, A. M. 1978. Dection of Xanthomonas campestris in soil using a direct immunofluorescent technique. In. Proc. 4th Int. Conf. Plant Pathog. Bact., Angers, France, pp. 301-305. Dowson, W. J. 1939. On the systematic position and generic names of the Gram negative bacterial plant pathogens. Zentralbl. Bakteriol. Parasitenkd. Infektionskr. Hyg. Abt. 2 100: 177-193. Dye, D. W. 1962. The inadequacy of the usual determinative tests for the identification of Xanthomonas spp. N. Z. J. Sci. Technol. 5:393-416. Dye, D. W. 1963. Comparative study of the biochemical reactions of additional Xanthomonas spp. N. Z. J, Sci. Technol. 6:483-486. Dye, D. W. 1966. Cultural and biochemical reactions of additional Xanthomonas spp. N. Z. J, Sci. Technol. 9:913-919. Dye, D. W., and Lelliott, R. A. 1974. Genus II. Xanthomonas Dowson 1939. In Bergey's Manual of Determinative Bacteriology (Buchanan R. E., and Gibbons, N. E. eds.), 8th ed. pp. 243-249. The Williams & Wilkins Co., Baltimore. Fox, G. E., Wisotzkey J. D., and Jurtshuk, Jr., P. 1992. How close is close: 16S rRNA sequence identity may not be sufficient to guarantee species identity. Int. J. Syst. Bacteriol. 41:166-170. Frost, L. S., Leplae, R., Summers, A. O., and Toussaint, A. 2005. Mobile genetic elements: the agents of open source evolution. Nat. Rev. Microbiol. 3:722-732. Franken, A. A. J. M. 1992. Comparision of immunofluorescence microscopy and dilution-plating for the detection of Xanthomonas campestris pv. campestris in crucifer seeds. Fukui, R., Arias, R., and Alvarez, R. 1994. Efficacy of four semiselective media for recovery of Xanthomonas campestris pv. campestris from topical soils. J. Appl. Bacteriol. 77:534-540. Gabriel, D. W. 1999. Why do pathogens carry avrulence genes? Physiol. Mol. Plant. Pathol. 55:205-214. Gonn?alves, E. R., and Rosato, Y. B. 2002. Phylogenetic analysis of Xanthomonas species based upon 16S-23S rDNA intergenic spacer sequences. 52:355-361. Goodfellow, M., Manfio, G. P. and Chun, J. 1997. Towards a practical species conpect for cultivable bacteria. In Species: the Units of Biodiversity, pp 25-59. Edited by M. F. Claridge, H. A. Dawah and M. R. Wilson. London: Chapman Hall. Gough, C. L., Genin, S., Zischek, C., Boucher, C. A. 1992. hrp genes of Pseudomonas solanacearum are homologous to pathogenicity determinants of animal pathogenic bacteria and are conserved among plant pathogenic bacteria. Mol. Plant. Microbe. Interact. 5:384-389. Gray, M. W., Sankoff, D., and Cedergren, R. J. 1984. On the evolutionary descent of organisms and organelles: a global phylogeny based on a highly conserved structural core in small subunit ribosomal RNA. Nucleic Acid Res. 12:5837-5852. Hall, R. M., and

Collis, C. M. 1995. Mobile gene cassettes and integrons: capture and spread of genes by site-specific recombination. Mol. Microbiol. 15:593-600. Hauben, L., Vauterin, L., Swings, J., and Moore., E. R. B. 1997. Comparison of 16S ribosomal DNA sequences of all Xanthomonas species. Int. J. Syst. Bacteriol. 47:328-335. Haubold, B., and Rainey, P. B. 1996. Genetic and ecotypic structure of a fluorescent Pseudomonas population. Mol. Ecol. 5:747-761. Harrel, L. J., Andersen, G. L., and Wilson, K. H. 1995. Genetic variability of Bacillus anthracis and related species. J. Clin. Microbiol. 33:1847-1850. Hayward, A. C. 1993. The host of Xanthomonas In Xanthomoans (Swings, J. G., and Civerolo, E. L. eds). Chapman & Hall Inc. Boundary Row, London. pp. 1-120. Hill, C. W., Sandt, C. H., and Vlazny, D. A. 1994. Rhs elements of Escherichia coli population structure. Genetics. 141:15-24. Jaenecke, S., de Lorenzo, V., Timmis, K. N. and Diaz, E. 1996. A stringently controlled expression system for analyzing lateral gene transfer between bacteria. Mol. Microbiol. 21:293-300. Jackson, P. J., Walthers, E. A., Kalif, A. S., Richmond, K. L., Adair, D. M., Hill, K. K., Kuske, C. R., Andersen, G. L., Wilson, K. H., Hugh-Jones, M. E., and Keim, P. 1997. Characterization of the variable-number tandem repeats in vrrA from different Bacillus anthracis isolates. Appl. Environ. Microbiol. 63:1400-1405. Janse, J. D., Rossi, M. P., Gorkink, R. F. J., Derks, J. H. J., Swings, J., Janssens, D., and Scortichini, M. 2001. Bacterial leaf blight of strawberry (Fragaria (×) ananassa) caused by a pathovar of Xanthomonas arboricola, not similar to Xanthomonas fragariae Kennedy & King. Description of the casual organism as Xanthomonas arboricola pv. fragariae (pv. nov., comb. nov.). Plant. Pathol. 50:653-665. Johansson, M. L., Molin, G., Pettersson, B. Uhlen, M., and Ahrne, S. 1995. Characterization and species recognition of Lactobacillus plantarum strains by restriction fragment length polymorphism (RFLP) of the 16S rRNA gene. J. Appl. Bacteriol. 79:536-541. Jonasson, J., Olofsson, M., and Monstein, H.-J. 2002. Classification, identification and sobtyping of bacteria based on pyrosequencing and signature matching of 16S rDNA fragments. APMIS 110:263-272. Jones, J. B., Bouzar, H., Stall, R. E., Almira, E. C., Roberts, P. D., Bowen, B. W., Sudberry, J., Strickler, P. M. and Chun, J. 2000. Systematic analysis of xanthomonads (Xanthomonas spp.) associated with pepper and tomato lesions. Int. J. Syst. Evol. Microbiol. 50:1211-1219. Kudva, I. T., Eveans, P. S., Perna, N. T., Barrett, T. J., DeCASTRO, G. J., Ausubel, F. M., Blattner, F. R., and Calderwood, S. B. 2002. Polymorphic amplified typing sequences provide a novel approach to Escherichia coli O157:H7 strain typing. J. Clin. Microbiol. 40:1152-1159. Lan, R., and Reeves, P. R. 1996. Gene transfer is a major factor in bacterial evolution. Mol. Biol. Evol. 13:47-55. Lazo, G. R., Roffey, R., and Gabriel, D. W. 1987. Pathovars of Xanthomonas campestris are distinguishable by restriction fragment length polymorphism. Int. J. Syst. Bacteriol. 37:214-221. Lee, B. -M., Park, Y. -J., Park, D. -S., Kang, H. -W., Kim, J. -G., Song, E. -S., Park, I. -C., Yoon, U. -H., Hahn, J. -H., Koo, B. -S., Lee, G. -B., Kim, H., Park, H. -S., Yoon, K. -O., Kim, J. -H., Jung, C. -H., Koh, N. -H., Seo, J. -S., and Go, S. -J. 2005. The genome sequence of Xanthomonas oryzae pathovar oryzae KACC10331, the bacterial

blight pathogen of rice. Nucleic. Acids. Res. 33:577-586. Lee, Y. -A., and Chiu, S. -P. 1995. A repetitive sequence widely distributed in Xanthomonas campestris is an insertion sequence belonging to IS3 family. Plant Pathol. Bull. 4: 201 (Abstract). Lee, Y. -A., and Chiu, S. -P. 1998. IS1403 and IS1404: analysis and distribution of two new insertion sequences in Xanthomonas campestris. Bot. Bull. Acad. Sin. 39: 231-239. Lee, Y. -A., and Chou, S. L. 2003. Quinate metabolism and utilization as phenotypic properties to identify Erwinia cypripedii and E. rhapontici. Plant Pathology Bulletin 12:242-246. Letowski, J., Brousseau, R., and Masson, L. 2004. Designing better probes: effect of probe size, mismatch position and number on hybridization in DNA oligonucleotide microarrays. J. Microbiol. Methods. 57:269-278. Leyns, F., De Cleene, M., Swings, J. -G., and De Ley, J. 1984. The host range of the genus Xanthomonas. Bot. Rev. 50: 308-356. Lima, W. C., Van Sluys, M. A., and Menck, C. F. 2005. Non-gamma-proteobacteria gene islands contribute to the Xanthomonas genome. OMICS. 9:160-172. Lin, R. J., Capage, M., and Hill, C. W. 1984. A repetitive DNA sequence, rhs, responsible for duplications within the Escherichia coli K-12 chromosome. J. Mol. Biol. 177:1-18. Lorenz, M. G. and Wackernagel, W. 1994. Bacterial gene transfer by natural genetic transformation in the environment. Microbiol. Rev. 58:563-602. Louws, F. J., Fulbright, D. W., Stephens, C. T., and de Bruijn, F. J. 1994. Specific genomic fingerprints of phytopathogenic Xanthomonas and Pseudomonas pathovars and strains generated with repetitive sequences and PCR. Appl. Environ. Microbiol. 60:2286-2295. Ludwig, W., Amann, R.I., Martinez-Romero, E., Sch?nhuber, W., Bauer, S., Neef, A., and Schleifer. K. H. 1998. rRNA based identification and detection systems for rhizobia and other bacteria. Plant Soil 204:1-19. Marmur, J., and Doty., P. 1961. Thermal renaturation of DNA. J. Mol. Biol. 3:584-594. Mazel, D., Dychinco, B., Webb, V. A., and Davies, J. 1998. A distinctive class of integron in the Vibrio cholerae genome. Science. 280:605-608. McClelland, M., Arensdorf, H., Cheng, R., and Welsh, J. 1994. Arbitrarily primed PCR fingerprints resolved on SSCP gels. Nucleic. Acids. Res. 22:1770-1771. Michael, L., Kotewicz, E. W., Brown, J., LeClerc, E., and Cebula, T. A. 2003. Genomic variability among enteric pathogens: the case of the mutS-rpoS intergenic region. Trends. Microbiol. 11:2-6. Muyzer, G., De Waal, E. C., and Uitterlinden , A. G. 1993. Profiling of complex microbial populations by denaturing gradient gel electrophoresis analysis of polymerase chain reaction-amplified genes coding for 16S rRNA. Appl. Environ. Microbiol. 59:695-700. Nembaware, V., Seoighe, C., Sayed, M., and Gehring, C. 2004. A plant natriuretic peptide-like gene in the bacterial pathogen Xanthomonas axonopodis may induce hyper-hydration in the plant host: a hypothesis of molecular mimicry. BMC Evol. Biol. 4:10. Ochiai, H., Inoue, Y., Takeya, M., Sasaki, A., and Kaku, H. 2005. Genome sequence of Xanthomonas oryzae pv. oryzae suggests contribution of large numbers of effector genes and insertion sequences to its race diversity. JARQ. 39:275-287. Patel, J. B. 2001. 16S rRNA gene sequencing for bacterial pathogen identification in the clinical laboratory. Mol. Diagn. 6:313-321. Patil, P. B., and Sonti, R. V. 2004. Variation suggestive of

horizontal gene transfer at a lipopolysaccharide (lps) biosynthetic locus in Xanthomonas oryzae pv. oryzae, the bacterial leaf blight pathogen of rice. BMC Microbiol. 4:40. Peplies, J., Glockner, F. O., and Amann, R. 2003. Optimization strategies for DNA microarray-based detection of bacteria with 16S rRNA-targeting oligonucleotide probes. Appl. Environ. Microbiol. 69:1397-1407. Pfunder, M., and Frey, J. E. 2005. Dissociation analysis in polymerase chain reaction and 1×SSC buffer as a prerequisite for selection of 13mer microarray probe sets with uniform hybridization behavior. Mol. Biotechnol. 29:1-10. Qian, W., Jia, Y., Ren, S. -X., He, Y. -Q., Feng, J. -X., Lu, L. -F., Sun, Q, Ying, G., Tang, D. -J., Tang, H., Wu, W., Hao, P., Wang, L., Jiang, B. -L., Zeng, S., Gu, W. -Y., Lu, G., Rong, L., Tian, Y., Yao, Z., Fu, G., Chen, B., Fang, R., Qiang, B., Chen, Z., Zhao, G. -P., Tang, J. -L., and He, C. 2005. Comparative and functional genomic analyses of the pathogenicity of phytopathogen Xanthomonas campestris pv. campestris. Genome. Res. 15:757-767. Roberts, S. J., and Koenraadt, H. 2003. ISTA-PDC Technical report: Revised for detection of Xanthomonas campestris pv. campestris in Brassica seed. ISTA Method Validation Reports. 1:1-9. Rudi, K., Nogva, H. K., Moen, B., Nissen, H., Bredholt, S., Moretro, T., Naterstad, K., and Holck, A. 2002. Development of nucleic acid-based technologies for microbial community analyses in foods. Int. J. Food Microbiol. 78:171-180. Sadosky, A. B., Davidson, A., Lin, R. – J., and Hill, C. W. 1989. rhs gene family of Escherichia coli K-12. J. Bacteriol. 171:636-642. Sagerstr?m, C. G., Sun, B. I., and Sive, H. L. 1997. Subtractive cloning: past, present, and future. Annu. Rev. Biochem. 66:751-783. Sakthivel, N., Mortensen, C. N., and Mathur, S. B. 2001. Detection of Xanthomonas oryzae pv. oryzae in artificially inoculated and naturally infected rice seeds and plants by molecular techniques. Appl Microbiol Biotechnol. 56:435-441. Schaad, N. W., and Donaldson, R. C. 1980. Comparison of two methods for detection of Xanthomonas campestris ininfected crucifer seeds. Seed Sci. Technol. 8:383-391. da Silva. A. C., Ferro, J. A., Reinach, F. C., Farah, C. S., Furlan, L. R., Quaggio, R. B., Monteiro-Vitorello, C. B., Van Sluys, M. A., Almeida, N. F., Alves, L. M., do Amaral, A. M., Bertolini, M. C., Camargo, L. E., Camarotte, G., Cannavan, F., Cardozo, J., Chambergo, F., Ciapina, L. P., Cicarelli, R. M., Coutinho, L. L., Cursino-Santos, J. R., El-Dorry, H., Faria, J. B., Ferreira, A. J., Ferreira, R. C., Ferro, M. I., Formighieri, E. F., Franco, M. C., Greggio, C. C., Gruber, A., Katsuyama, A. M., Kishi, L. T., Leite, R. P., Lemos, E. G., Lemos, M. V., Locali, E. C., Machado, M. A., Madeira, A. M., Martinez-Rossi, N. M., Martins, E. C., Meidanis, J., Menck, C. F., Miyaki, C. Y., Moon, D. H., Moreira, L. M., Novo, M. T., Okura, V. K., Oliveira, M. C., Oliveira, V. R., Pereira, H. A., Rossi, A., Sena, J. A., Silva, C., de Souza, R. F., Spinola, L. A., Takita, M. A., Tamura, R. E., Teixeira, E. C., Tezza, R. I., Trindade dos Santos, M., Truffi, D., Tsai, S. M., White, F. F., Setubal, J. C., and Kitajima, JP. 2002. Comparison of the genomes of two Xanthomonas pathogens with differing host specificities. Nature 417:459-463. Sneath, P. H. A. 1993. Evidence from Aeromonas for genetic crossing-over in ribosomal sequences. Int. J. Syst. Bacteriol. 43:626-629. Southern, E., Mir, K., and Shchepinov, M. 1999.

Molecular interactions on microarrays. Nat. Genet. 21:5-9. Stackebrandt, E., and Goebel, B. M 1994. Taxonomic note: a place for DNA-DNA reassociation and 16S rRNA sequence analysis in the present species definition in bacteriology. Int. J. Syst. Bacteriol. 44:846 – 849. Stall, R. E., Beaulieu, C., Egel, D. S., Hodge, N. C., Leite, R. P., Minsavage, G. V., Bouzar, H., Jones, J. B., Alvarez, A. M., and Benedict, A. A. 1994. Two genetically diverse groups of strains are included in Xanthomonas campestris pv. vesicatoria. Int. J. Syst. Bacteriol. 44:47-53. Stenger, D. A., Andreadis, J. D., Vora, G. J., and Pancrazio, J. J. 2002. Potential applications of DNA microarrays in biodefense-related diagnostics. Curr. Opin. Biotechnol. 13:208-212. Str?tz, M., Mau, M., and Timmis, K. N. 1996. System to study horizontal gene exchange among microorganisms without cultivation of recipients. Mol. Microbiol. 22:207-215. Sullivan, J. T., and C. W. Ronson. 1998. Evolution of rhizobia by acquisition of a 500-kb symbiosis island that integrates into a phe-tRNA gene. Proc. Natl. Acad. Sci. USA. 95:5145-5149. Syvanen, M. 2002. On the occurrence of horizontal gene transfer among an arbitrarily chosen group of 26 genes. J. Mol. Evol. 54:258-266. Tegli, S., Sereni, A., and Surico, G. 2002. PCR-based assay for the detection of Curtobacterum flaccumfaciens pv. flaccumfaciens in bean seeds. Lett. Appl. Microbiol. 35(4):331-337. Thieme, F., Koebnik, R., Bekel, T., Berger, C., Boch, J., Buttner, D., Caldana, C., Gaigalat, L., Goesmann, A., Kay, S., Kirchner, O., Lanz, C., Linke, B., McHardy, A. C., Meyer, F., Mittenhuber, G., Nies, D. H., Niesbach-Klosgen, U., Patschkowski, T., Ruckert, C., Rupp, O., Schneiker, S., Schuster, S. C., Vorholter, F. J., Weber, E., Puhler, A., Bonas, U., Bartels, D., and Kaiser, O. 2005. Insights into genome plasticity and pathogenicity of the plant pathogenic bacterium Xanthomonas campestris pv. vesicatoria revealed by the complete genome sequence. J. Bacteriol. 187:7254-7266. Ticknor, L. O., Kolst, A. -B., Hill, K. K., Keim, P. Laker, M. T. Tonks, M., and Jackson, P. J. 2001. Fluorescent amplified fragment length polymorphism analysis of Norwegian Bacillus cereus and Bacillus thuringiensis soil isolates. Appl. Environ. Microbiol. 67:4863-4873. Tobler N. E., Pfunder, M., Herzog, K., Frey, J. E., and Altwegg, M. 2005. Rapid detection and species identification of Mycobacterium spp. using real-time PCR and DNA-Microarray. J. Microbiol. Methods. In press. Trad, S., Allignet, J., Frangeul, L., Davi, M., Vergassola, M., Couve, E., Morvan, A., Kechrid, A., Buchrieser, C., Glaser, P., and El-Solh, N. 2004. DNA macroarray for identification and typing of Staphylococcus aureus isolates. J. Clin. Microbiol. 42:2054-2064. Tr?baol, G., Gardan, L., Manceau, C., Tanguy, J. -L., Tirilly, Y., and Boury, S. 2000. Genomic and phenotypic characterization of Xanthomonas cynarae sp. nov., a new species that causes bacterial bract spot of artichoke (Cynara scolymus L.). Int. J. Syst. Evol. Microbiol. 50:1471-1478. Vauterin, L., Swings, J., Kersters, K., Gillis, M., Mew, T. W., Schroth, M. N., Palleroni, N. J., Hildebrand, D. C., Stead, D. E., Civerolo, E. L., Hayward, A. C., Maraite, H., Stall, R. E., Vidaver, A. K. and Bradbury, J. F. 1990. Towards an improved taxonomy of Xanthomonas. Int. J. Syst. Bacteriol. 40:312-316. Vauterin, L., Swings, J., and Kersters, K. 1991. Grouping of Xanthomonas campestris pathovars by SDS-PAGE of proteins. J.

	Gen. Microbiol. 137:1677-1687. Vauterin, L., Hoste, B., Kersters, K., and Swings, J. 1995 Reclassification of Xanthomonas. Int. J. Syst. Bacteriol. 45:472-489. Volokhov, D., Chizhikov, V., Chumakov, K., Rasooly, A. 2003. Microarray-based identification of thermophilic Campylobacter jejuni, C. coli, C. lari, and C. upsaliensis. J. Clin. Microbiol. 41:4071-4080. Wakker, J. H. 1883. Vorl?ufige Mitteilungen ?ber Hyacinthenkrankheiten Bot. Centralbl. 14:315-317. Wang, Y. D., Zhao, S., and Hill, C. W. 1998. Rhs elements comprise three subfamilies which diverged prior to acquisition by Escherichia coli. J. Bacteriol. 180:4102-4110. Ward, D. M., Weller, R., and Bateson, M. M. 1990. 16S rRNA sequences reveal numerous uncultured microorganisms in a natural community. Nature 345:63-65. Waterhouse, R. N., and Glover, L. A. 1993. Identification of prokaryotic repetitive DNA suitable for use as fingerprinting probes. Appl. Environ. Microbiol. 59:1391-1397. Wilderman, P. J., Vasil, A. I., Johnson, Z., and Vasil, M. L. 2001. Genetic and biochemical analyses of a eukaryotic-like phospholipase D of Pseudomonas aeruginosa suggest horizontal acquisition and a role for persistence in a chronic pulmonary infection model. Mol. Microbiol. 39:291-303. Williams, P. H. 1980. Black rot: a continuing threat to world crucifers. Plant. Dis. 64:736-734. Woese, C. R. 1987. Bacterial evolution. Microbiol. Rev. 51:221-271. Yang, P., Vauterin, L., Vancanneyt, M., Swings, J., and Kersters, K. 1993. Application of fatty acid methyl esters for the taxonomic analysis of the genus Xanthomonas. Syst. Appl. Microbiol. 16:47-71. Young J. M. 2001. Implication of alternative classifications and horizontal gene transfer for bacterial taxonomy. Int. J. Syst. Evol. Microbiol. 51:945-953.
論文頁數	150
附註	
全文點閱次數	
資料建置時間	
轉檔日期	
全文檔存取記錄	
異動記錄	M admin Y2008.M7.D3 23:17 61.59.161.35