

木瓜畸葉嵌紋病毒台灣品系病害調查、親緣性分析與具感染力轉錄體之構築

許婷婷、江主惠

E-mail: 321901@mail.dyu.edu.tw

摘要

木瓜輪點病毒(Papaya ringspot virus, PRSV)為主要危害台灣木瓜栽種的病毒，造成嚴重的經濟損失，近年來在田間也發現有木瓜畸葉嵌紋病毒(Papaya leaf distortion mosaic virus, PLDMV)之感染，所以本研究針對 PRSV 及 PLDMV 在台灣的感染情形進行調查。採集來自10個縣市之木瓜樣本，包含來自網室及非網室材料共768個樣本，利用酵素免疫分析法進行病毒偵測，其中有374個樣本(49%)單獨感染 PRSV、27個樣本(4%)單獨感染 PLDMV、134個樣本(17%)為複合感染，剩餘233個樣本(30%)為未感染此兩種病毒之材料。當以酵素免疫分析無法判定其是否感染病毒時，利用多重引子對反轉錄聚合 γ 鎖反應方式(multiplex RT-PCR)進行偵測，即可依增幅出來的 DNA 片段大小判定其感染病情。另外，本研究也選殖了15個來自不同地區之 PLDMV 分離株的病毒鞘蛋白基因，利用 NCBI 進行比對，此15個 PLDMV 鞘蛋白選殖株彼此間的核 γ 藹 C與台灣其他分離株(TW-DL、TW-TD及TW-WF)比較有很高的相同度，為94.9%-99%；與日本分離株(J56P及J179P)有93.7-95.2%相同度，但與瓜類分離株 J199C 相比只有85.1-86.4%。根據 PLDMV 鞘蛋白核 γ 藹 C進行演化樹分析，則可發現本次所選殖得到的台灣分離株和 TW-TD、TW-KS 及日本之 PLDMV 歸屬於不同群組。另外，為了測試台灣 PLDMV 木瓜分離株是否也能感染瓜類，分別將來自農試所試驗田及大里之 PLDMV 接種於胡瓜及刺角瓜中，並以酵素免疫分析法及西方墨點法偵測病毒感染，結果發現 PLDMV 均無法感染胡瓜，感染刺角瓜的比例只有8.8%且無明顯病徵。之前本實驗室已將大部分 PLDMV 大里分離株(TW-DL)的基因體解序完成，但最5'端之序列仍然未知，因此本研究再利用5'RACE 來獲得 PLDMV-DL 5'端序列，並將其全長度及5'UTR 之核 γ 藹 C與網路 PLDMV TW-KS 及 J56P 進行比對，結果全長度基因體之相同度約為95%，而5'UTR 序列為84%-87%。在 PLDMV 具感染力轉錄體的構築方面，選殖七個互相重疊可以涵蓋整個 PLDMV 基因體的質體，分別為 p35S-5PL426、p5PL-2764、pPL2680Narl-4361、pPL4247-6604、pPL5761-8298、pPL8150-9810及 pPL9528-PolyA-NotI。目前已完成 p35SPL2711-9779NotI 之構築，此質體中的35S 啟動子後面接有 PLDMV 第1到第2711個核 γ 藹 P第9779至3'端 poly A 的 DNA 片段，只需再將第2680-9810的片段剪切黏合，即可完成 PLDMV 全長度之構築。

關鍵詞：木瓜畸葉嵌紋病毒、感染力轉錄體、多重引子對反轉錄聚合 γ 連鎖反應、酵素免疫分析法

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