

## Accumulation of Pathogenesis-related Type-5 Like Proteins in Phytoplasma-infected Garland Chrysanthemum *Chrysanthemum coronarium*

Bo-Xiong ZHONG\* and Yan-Wei SHEN

Department of Bioresource Science, College of Animal Science, Zhejiang University, Hangzhou 310029, China

**Abstract** Soluble proteins extracted from leaves, apical shoots, axillary shoots, and stems of garland chrysanthemum plants infected by onion yellows phytoplasma were analyzed by two-dimensional gel electrophoresis. Computerized matching analysis revealed that at least six soluble proteins were accumulated specifically in phytoplasma-infected garland chrysanthemum. N-terminal amino acids sequences of these soluble proteins, determined by Edman degradation, shared high sequence similarities with those of pathogenesis-related type-5 (PR-5) proteins such as tobacco thaumatin-like protein. Accumulation of these six proteins was also found in garland chrysanthemum plants infected by other phytoplasmas. These results demonstrate that phytoplasmal infection induces the accumulation of PR-5 like proteins in garland chrysanthemum plants.

**Key words** phytoplasma; garland chrysanthemum *Chrysanthemum coronarium*; pathogenesis-related proteins; thaumatin; osmotin

Phytoplasmas, a group of cell wall-less, phloem-limited and uncultivable plant-pathogenic prokaryotes, which compose a genus in the class Mollicutes [1–3], are associated with diseases in several hundred species of plants [4]. In Japan, where phytoplasma was first observed then named as MLOs [5], a large number of phytoplasmal diseases in herbaceous crops such as vegetables, flowering plants, and medicinal herbs have occurred in various places. Furthermore most of these associated phytoplasmas are transmitted by either *Macrostelea striifrons* Anufriev or *Scleroracus flavopictus* Ishihara [6]. One group of phytoplasmas transmitted by *M. striifrons* (MS-phytoplasma) was classified as a member of the aster yellows group (16SrI), while the other group of phytoplasmas transmitted by *S. flavopictus* (SF-phytoplasma) was classified as a member of the X-disease group (16SrIII) on the basis of sequence and/or restriction analysis of 16S rDNA [7,8]. The host ranges of these two phytoplasmas are very wide and overlapped with each other. *Chrysanthemum coronarium* (garland

chrysanthemum), one of the common leafy vegetables, is highly susceptible to both phytoplasmas and is an attractive source of food for both species of leafhopper vectors.

Pathogenesis-related (PR) proteins [9] which accumulate in plants attacked by pathogens or treated with an inducer such as salicylate [10,11] or plant hormones [12] were first observed in tobacco varieties resistant to tobacco mosaic virus (TMV) and exhibited hypersensitive reaction with necrosis lesions against TMV infection [13, 14]. Since then, many and various kinds of PR proteins had been identified in many species of plants [9,15–18]. Van Loon et al proposed the classification of PR proteins into eleven families according to the similarity of amino acid sequences, serological relationships, and/or biological functions [19]. PR proteins related to phytoplasmal infection, however, have not been reported until now, whereas various plant pathogens including virus, viroids, bacteria, and fungi had been proved to induce PR protein accumulation in plants [20–25].

In this research, we report our analysis of several soluble proteins, considered PR-5 like proteins, accumulated specifically in garland chrysanthemum infected with phytoplasma.

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\*Corresponding author: Tel, 86-571-86971302; Fax, 86-571-86945417; E-mail, bxzhong@zju.edu.cn

## Materials and Methods

### Phytoplasma isolates

Phytoplasma isolates, onion yellows (OY) [26], spinach yellows (SY) [27], statice witches' broom 1 (SW1) [28], statice witches' broom 2 (SW2) [28], lettuce yellows 1 (LY1) [29] and lettuce yellows 2 (LY2) [29] were originally collected from naturally diseased plants in various places. These six isolates of MS-phytoplasma were similar in the biological characteristics, but LY2 on garland chrysanthemum was distinguished from others in symptoms [29]. Gentian witches' broom (GW), an isolate of SF-phytoplasma [30], was maintained and proliferated in garland chrysanthemum plants using viruliferous insects, which had fed on infected plants.

### Soluble protein extraction

Garland chrysanthemum seedlings were inoculated with viruliferous ("infected") or non-viruliferous insects ("pseudo-inoculated"). Thirty or 45 days after inoculation, young leaves, apical shoots, axillary shoots, and stems of infected or pseudo-inoculated garland chrysanthemum plants were excised for extracting the soluble proteins according to the method of Zhong *et al.* [31]. One gram of fresh plant tissue was homogenized with a mortar and a pestle on ice with 5 ml of chilled phosphate buffer (pH 8.0) containing 37 mM  $K_2HPO_4$ , 1.7 mM  $KH_2PO_4$ , and 400 mM NaCl. The homogenate was centrifuged at 12,000 *g* for 10 min. 100% trichloroacetic acid was added to the supernatant to achieve a final concentration of 10%, and the mixture was kept at 4 °C for 20 min. After centrifugation at 12,000 *g* for 10 min, the resulting precipitate was suspended in 1 ml of lysis buffer, sonicated for 2 min, adjusted to pH 7.0 with 2 M NaOH, and stored at -20 °C until use.

### Two-dimensional gel electrophoresis

Two-dimensional gel electrophoresis (2D-E) with isoelectric focusing (IEF) and sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) were carried out essentially as described by O'Farrell [32] with slight modifications [33]. Proteins were first separated by IEF in the tube gel containing 2% ampholine (the ratio of pH 5–8 vs. pH 3–10 is 1:1). IEF was run at 200 V for 1 h at first, then at 400 V for 16 h, and finally at 800 V for 1 h with disc gel unit (Marysol Industry Co., Ltd., Tokyo, Japan). Following the first-dimension electrophoresis, each tube gel was equilibrated in SDS-PAGE sample buffer for

30 min, then placed on top of 15% SDS-PAGE gel (with 5% stacking gel). SDS-PAGE was run at 25 mA per gel for approximately 4 h with dual vertical slab gel unit (Nihon Eido Co., Ltd., Tokyo, Japan).

### 2D-E gel image analysis

After 2D-E, the gels were stained with silver. 2D-E gel images were captured with a flatbed scanner and analyzed automatically with ImageMaster 2D elite software (Amersham Pharmacia Biotech Uppsala, Sweden). The isoelectric point and molecular weight of each protein was determined using isoelectric focusing and molecular weight calibration kit (Amersham Pharmacia Biotech Uppsala, Sweden).

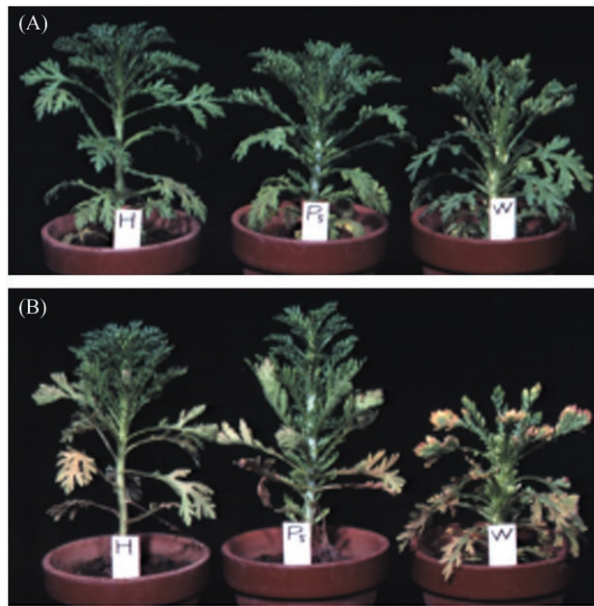
### N-terminal sequence analysis

Following separation by 2D-E, proteins were electroblotted onto PVDF membranes using semidry transfer unit (Nihon Eido Co., Ltd., Tokyo, Japan), and briefly stained with Coomassie Brilliant Blue R250 (CBB). Objective protein spots were then excised and applied for determination of their N-terminal amino acid sequences by automated Edman degradation with the 492 gas phase protein sequencer (PE Biosystems, Norwalk, CT). Amino acid sequence similarity was searched on the SWISS-PROT and PIR databases through the National Center for Biotechnology Information using BLAST program.

## Results

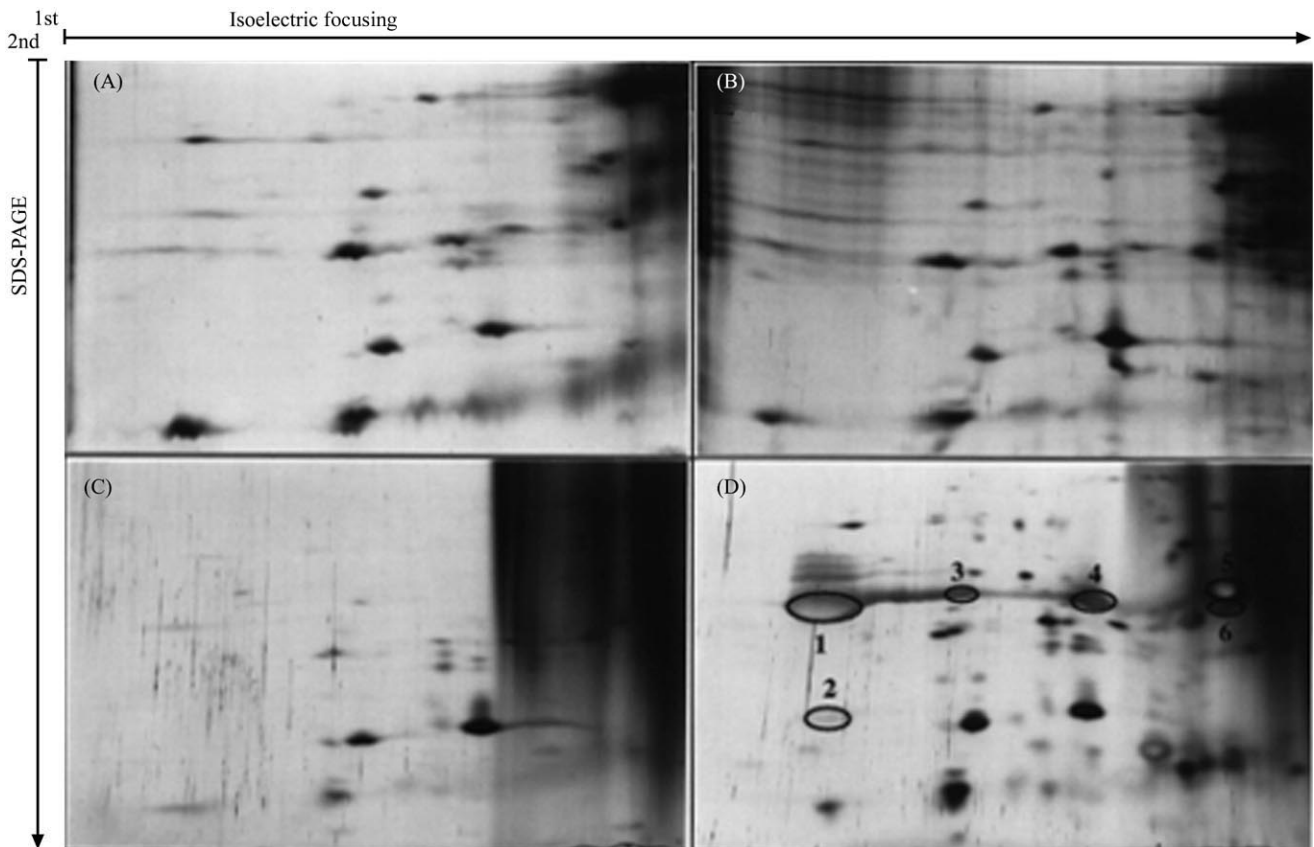
### The soluble proteins identified from garland chrysanthemum infected with phytoplasma

The OY-infected and pseudo-inoculated garland chrysanthemum plants did not change significantly in the appearance after 30 days inoculation, however, an early symptom about yellowing on newly emerged leaves was observed on OY-infected plants [Fig. 1(A)]. Few marked differences were found in both 2D-E separation patterns of soluble proteins extracted from newborn leaves [Fig. 2 (A,C)]. After 45 days inoculation, appearances of the two were considerably different. Typical and severe symptoms of stunting, yellowing and proliferation were observed on OY-infected plants, whereas only natural yellowing by leaf senescence were observed on pseudo-inoculated plants [Fig. 1(B)]. Specific accumulations of several soluble proteins were observed in OY-infected but not in pseudo-inoculated plant leaves by the comparison of 2D-E separation pattern [Fig. 2(B,D)]. Especially, six kinds of these



**Fig. 1** The development of the Garland chrysanthemum infected by the phytoplasma

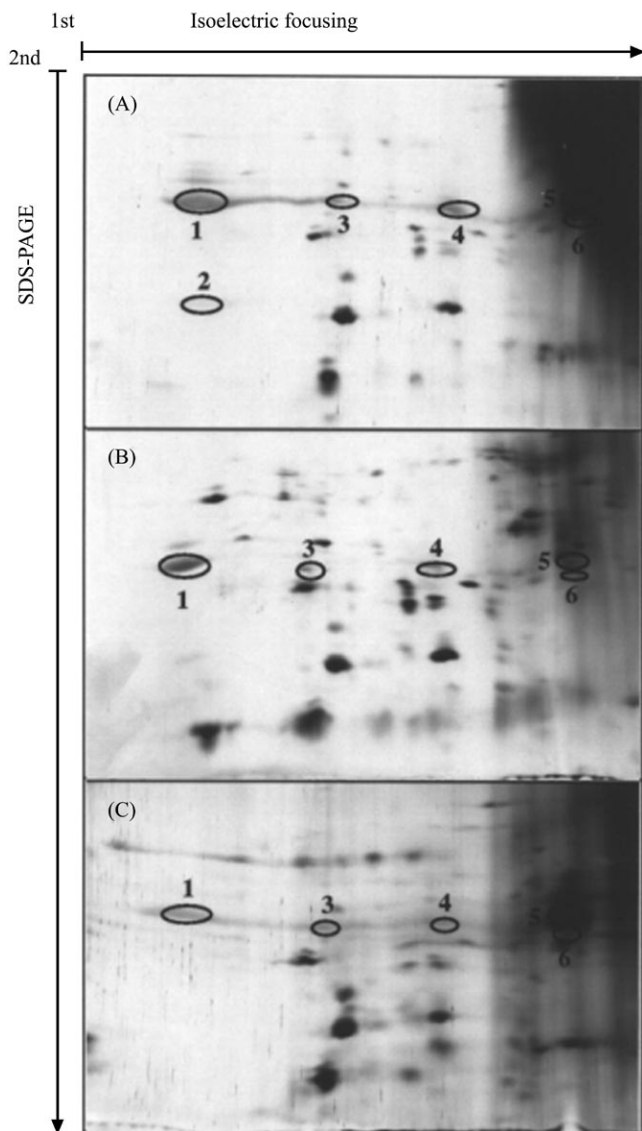
Garland chrysanthemum plants grown in green house at 25 °C for 30 days (A) and 45 days (B) after inoculation, which were not inoculated (H), pseudo-inoculated (Ps), and inoculated with OY-phytoplasma (W).



**Fig. 2** The 2D-E pattern of the soluble proteins from young leaves of the garland chrysanthemum infected by the OY-phytoplasma

2D-E pattern of the proteins from young leaves of pseudo-inoculated (A,B) and OY-infected (C,D) garland chrysanthemum plants 30 days (A,C) or 45 days (B,D) after inoculation.

soluble proteins, CTLP-1 (CTLP means traumatic-like protein in phytoplasma-infected *Chrysanthemum coronaries*) with pI 7.35 and MW 29.6 kD, CTLP-2 with pI 7.35 and MW 21.0 kD, CTLP-3 with pI 6.26 and MW 28.8 kD, CTLP-4 with pI 5.40 and MW 29.0 kD, CTLP-5 with pI 4.75 and MW 29.9 kD, and CTLP-6 with pI 4.75 and MW 27.6 kD were clearly observed in large quantities. As shown in Fig. 3, specific accumulations of



**Fig. 3** The 2D-E pattern of the soluble proteins from different organs and tissues of the Garland chrysanthemum infected by the OY-phytoplasma

2D-E pattern of the proteins extracted from axillary shoots (A), apical shoots (B), and stems (C) of the OY-infected garland chrysanthemum plants 45 days after inoculation.

these six CTLPs were also observed in axillary shoots, apical shoots, and stems of OY-infected garland chrysanthemum, but the accumulation of CTLP-2 was absent in apical shoots and stems.

#### N-terminal amino acid sequence of CTLPs

No N-terminals of any CTLPs were blocked. N-terminal amino acid sequences of CTLP-1, 2, 3, and 4 (CTLP-1–4) were completely identical with each other in residue 1–43. The search results for amino acid sequence similarity in protein databases revealed that the CTLPs' N-terminal amino acid sequences shared high similarity with those of PR-5 proteins reported previously (Fig. 4). N-terminal amino acid sequences of CTLP-1–4 with 43 residues also shared sequence similarities with thaumatin-like proteins from *Arabidopsis thaliana* [34], and *Prunus*

Protein	Amino acid sequence	Identity
(A)		
CTLP-1–4	AVFTVRNXXPYSIAPGVLTTGG–GAAA–STTGFQLAPGXSNVNV	
AT-PR5K	TNFTIENKCDYTVWPGFLTMT–TAVSLPTNGFSLKKGESRVINVP	41.9%
PA-TLP	ATISFKNPCPYVMWPGTLTSDQKPKQ–LSTTGFELASQASFQDTP	41.9%
AT-PR5	TDFTLRNNCPYTVWAGTLAQG–GPK–LGDGGFELTPGASRQLTAP	39.5%
AT-TLR	TVFTLQNSCAYTVWPGTLSGN–SIT–LGDGGFPLTPGASVQLTAP	37.2%
(B)		
CTLP-5	ANFDIINQXPYTVXAAASPGGGRRLETGQSXXLQVAPGTTXAAI	
AT-OLP	ATFEILNQCSYTVWAAASPGGGRRLDAGQSWRLDVAAGTKMARI	65.9%
NT-TLPe22	ATFDIVNKCTYTVWAAASPGGGRRLDGQSWWSINVNPGTVQARI	63.6%
NT-TLPe2	ATFDIVNQCTYTVWAAASPGGGRRQLNSGQSWWSINVNPGTVQARI	63.6%
CA-TLR	ANFEIVNCPYTVWAAASPGGGRRLDRCQTWNLWVWVWAGTSMARI	63.6%
(C)		
CTLP-6	AIFTIRNXXQQTVMXAGAVPVGGGQXLDXGQTXTLTD	
AS-TLR	ATFTITNCCGYTVWAAIPVGGGQQLDQGGQWTLN	62.9%
HV-PRS	ATFTVINKCQYTVWAAAVPAGGGQKLDAGQTSWISIX	57.1%
TA-TLP	ATFNKNNCPYTVWPAATPIGGGRQLNTGETWTLTD	51.4%
NT-OSM	ATIEVRNXXPYTVWAASTPIGGGRRLDRCQTXVIN	51.4%

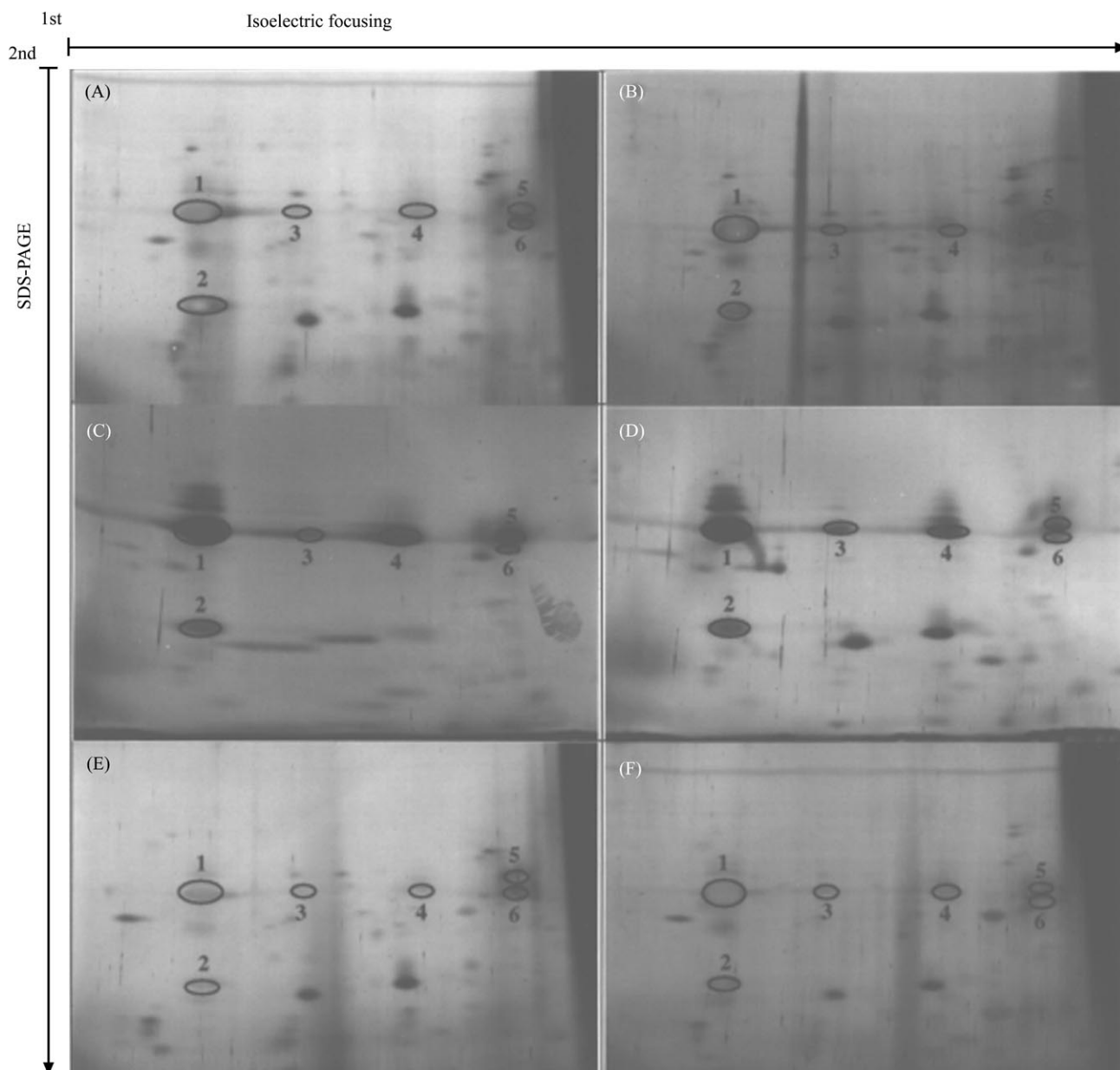
**Fig. 4** The homology analysis of the thaumatin-like proteins in the Garland chrysanthemum

Alignment of the N-terminal amino acid sequence of CTLP-1–4 (A), CTLP-5 (B), and CTLP-6 (C) and partial sequences of known PR-5 group proteins. AT-PR5K, PR5K of *A. thaliana* (ATU48698\_1, positions 26 aa to 68 aa); PA-TLP, thaumatin-like protein of *P. avium* (P50694, positions 24 aa to 67 aa); AT-PR5, PR-5 of *A. thaliana* (P28493, positions 24 aa to 66 aa); AT-TLP, thaumatin-like protein of *A. thaliana* (ATU83490\_1, positions 24 aa to 66 aa). AT-OLP, osmotin-like protein of *A. thaliana* (P50700, positions 23 aa to 66 aa); NT-TLPe22, thaumatin-like protein e22 of *N. tabacum* (P13046, positions 26 aa to 69 aa); NT-TLPe2, thaumatin-like protein e2 of *N. tabacum* (P07052, positions 26 aa to 69 aa); CA-TLP, thaumatin-like protein of *C. arietinum* (CAR010501\_1, positions 22 aa to 65 aa). AS-TLP, thaumatin-like protein of *A. sativa* (P50698, positions 22 aa to 56 aa); HV-PRS, PR-S of *H. vulgare* (P33045, positions 1 aa to 35 aa); TA-TLP, thaumatin-like protein of *T. aestivum* (TATHAUMLP\_1, positions 26 aa to 60 aa); NT-OSM, osmotin of *N. tabacum* (CAA64620, positions 22 aa to 56 aa).

*avium* [35]. The CTLP-5 with 44 residues shared similarity with tobacco thaumatin-like proteins from *Nicotiana tabacum* [36] and *Cicer aescinum*, and osmotin-like protein from *A. thaliana*. The CTLP-6 with 35 residues shared 80% similarities with thaumatin-like protein from *Avena sativa*, *Hordeum vulgare* [22] and *Triticum aestivum* [37], and the osmotin from *N. tabacum*.

### Accumulation of CTLPs in garland chrysanthemum plants infected with other phytoplasmas

As shown in Fig. 5, comparisons of 2D-E patterns revealed that CTLPs observed in OY-infected garland chrysanthemum plants also accumulated in leaves of garland chrysanthemum plants infected with SY, SW1, SW2, LY1,



**Fig. 5** The 2D-E pattern of the soluble proteins from young leaves of the Garland chrysanthemum infected by different types of the phytoplasma

2D-E pattern of the proteins from young leaves of garland chrysanthemum plants infected with SW1 (A), SW2 (B), LY1 (C), LY2 (D), SY (E), and GW (F) phytoplasma 45 days after inoculation.

LY2, and GW. The N-terminal amino acid sequence identity of these proteins with corresponding CTLPs was confirmed by a protein sequencer (data not shown).

## Discussion

2D-E analysis proved that CTLPs accumulated in OY-infected garland chrysanthemum plants accompanied the development of systemic symptoms. The accumulation was also recognized in garland chrysanthemum plants infected with other five isolates of the 16SrI and one of the 16SrII group phytoplasma. Accumulation of CTLPs did not induced by insect feeding or leaf senescence, because the accumulation was not observed in any pseudo-inoculated sample. Therefore, it was concluded that phytoplasmal infection induced the accumulation of CTLPs in garland chrysanthemum.

The N-terminal amino acid sequences of CTLP-1–4 were identical, but their pIs and molecular weights were different. One possible explanation is that genes encoding CTLP-1–4 constitute a group like a multi-gene family; the other possibility is that CTLP-1–4 originate from gene isoforms produced by post-translational modifications. Further analysis of the full sequence of CTLP-1–4 genes is necessary to clarify the relationships among CTLP-1–4.

CTLP-1–4 showing the highest sequence similarity to the N-terminal amino acid sequence of proteins which were known thaumatin-like proteins, and CTLP-5/6 also showing higher similarities to thaumatin-like or osmotin-like proteins were known as the PR-5 protein members. The determined molecular weights of CTLPs were within the range of known PR-5 proteins. Three isoforms, distinguished by their pIs (basic, neutral and acidic), of PR-5 proteins have been reported, and genes encoding them have been isolated in tobacco and *A. thaliana* [16,19,38]. In our case, CTLP-1–4 and CTLP-5/6 correspond to the neutral and acidic isoform of PR-5 proteins, respectively. These results show that CTLPs are member of the PR-5 protein group. Some PR-5 proteins have been known to possess antifungal activity [15,16,22,39,40], but CTLPs might not influence phytoplasmal infection or multiplication because their accumulation increase with the development of symptoms and no difference is recognized between the 2D-E pattern of LY1 and LY2.

It is interesting that phytoplasmal infection induces only PR-5 like proteins in garland chrysanthemum while TMV infection induces nine types of PR protein in tobacco [19]. No hypersensitive reaction was exhibited in

the appearances of phytoplasma-infected garland chrysanthemum plants, though cell necrosis was usually observed in the phloem [29]. The accumulation of CTLPs was assumed to be induced by the disturbance of the normal plant hormone balance or of regular translocation of substances through phloem, which were supposed to be caused by phytoplasmal infection, whose effects were similar to those of ethylene treatment or salt stress inducing PR-5 proteins in tobacco.

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