Silencing of a viral RNA silencing suppressor in transgenic plants

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Introduction

RNA silencing is a host defence mechanism targeted against invasive or mobile RNA elements, such as viruses or transposable retro-elements, leading to sequence-specific RNA degradation (reviewed by Baulcombe, 1999; Chicas & Macino, 2001; Matzke et al., 2001; Vance & Vaucheret, 2001; Waterhouse et al., 2001). It is highly conserved in plants and animals and known as post-transcriptional gene silencing (PTGS) in plants. RNA silencing was discovered in transgenic plants expressing transgenes from strong promoters, e.g., the 35S promoter of Cauliflower mosaic caulimovirus (CaMV), and which produce stable (polyadenylated) mRNAs. In such plants, the highly expressed mRNA can be inactivated in a sequence-specific manner in the cytoplasm (van der Krol et al., 1990; Napoli et al., 1990).

Plant viruses encode proteins able to suppress RNA silencing, probably to facilitate virus replication and systemic movement (Anandalakshmi et al., 1998; Brigneti et al., 1998; Kasschau & Carrington, 1998; Mallory et al., 2001; Voinnet et al., 1999, 2000). Virus silencing suppressors have been valuable tools for dissecting RNA silencing pathway(s), consisting of initiation, maintenance and propagation (signalling) phases (reviewed by Carrington et al., 2001). Initiation of RNA silencing is dependent on the presence of dsRNA and results in establishment of a silent state for targeted genes or RNAs. The maintenance phase is associated with homology-dependent transgene methylation of unknown significance. The propagation phase of silencing is manifested by the spread of silencing from the initially silenced cells to non-silenced cells, tissues and different parts of the plant. The putative signal is transported systemically similarly to viruses and photo-assimilates (Palauqui et al., 1997; Voinnet & Baulcombe, 1997; Citovsky & Zambryski, 1999). Short (21–26 nt) sense and antisense RNAs complementary to the targeted RNA...
silencing and re-establish transgene expression (Brigneti et al., 2001a). PCR was carried out as described by Wang et al. (1993) to check the T1 progeny for possible non-transgenic segregants, which were discarded.

**Potato virus A (PVA) isolates, inoculation and virus detection.** PVA isolates used in this study have been described (Rajamaki et al., 1998; Kekarainen et al., 1999). Concentrations of PVA and HCpro in leaves were estimated by ELISA using rabbit polyclonal antibodies (courtesy of F. Rabenstein, BAFZ, Aschersleben, Germany), as described previously (Savenkov & Valkonen, 2001a).

**RNA extractions and RNA gel blot analysis.** Total RNA was extracted from ~100 mg of plant tissue (Verwoerd et al., 1989). Total RNA (10–30 μg) was electrophoresed through 2:2 M formaldehyde–agarose gels and blotted onto Hybond-N+ membranes (Amersham). PCR with HCpro gene-specific primers was used to generate [32P]dCTP-labelled deoxyribozyme probes. The primer sequences were (5′ forward primer) 5′ TCACATCGAGGTTATTAACTC3′ and (3′ primer) 5′ GAATACAGTGACTGCCATCAT3′. Filters were hybridized in hybridization buffer (5 X Denhardt’s solution, 6 X SSC, 0.5% SDS and 0.5 mg/ml boiled herring sperm DNA) overnight at 65 °C and washed twice with a final solution of 2 X SSC (1 X SSC contains 0.15 M NaCl and 0.015 M sodium citrate) for 10 min each and once with 2 X SSC supplemented with 0.1% SDS for 30 min at 70 °C. The filters were exposed to PhosphorImager screens for image detection (Molecular Dynamics). RNA size markers (GibcoBRL) were used to determine the size of the transgene mRNA and genomic viral RNA.

**Methylation analyses.** Total genomic DNA was isolated from individual plants of the experimental line ab34 using a DNAeasy Plant Mini kit (Qiagen). Equal amounts of total DNA (~100 ng) were digested for 14 h at 37 °C with 20 units of Clal or NotI restriction endonucleases (Fermentas). Primers flanking the Clal or NotI restriction sites were designed. The sequence of the 3′ reverse primer (R1) used for all PCR analyses was 5′ GAATACGATGGAGTGCCATCAT3′. The sequences of the three forward primers used in our experiments were: (F1) 5′ CTGGCGAGGATTCAATCGAAC3′; (F2) 5′ TCACATCGAGGTTATTAACTC3′; and (F3) 5′ CAAGACCTTCCTTATATAAG3′. The F1/R1 primer pair amplified a 89 kb fragment, indicative of methylation at the Clal site, when Clal-digested samples were used for PCR amplification (see Fig. 6). This same primer pair served for amplification of the short control fragment from NotI-digested samples. The F2/R1 primer pair amplified a 0.60 kb control band for Clal-digested samples. The F3/R1 primer pair amplified a 13 kb fragment, indicative of methylation at the NotI site, when NotI-digested samples were used for PCR amplification.

The samples of total DNA (either undigested or digested with Clal or NotI) were subjected to PCR amplification using the appropriate primer pair. At least two plants were tested at each time-point and for each PVA isolate. The PCR conditions were as follows: the hot-start represented a 4 min denaturing step at 94 °C, followed by 35 cycles consisting of denaturation (1 min at 94 °C), primer annealing (1 min at 58 °C) and strand elongation (1 min at 72 °C). PCR products were separated by size in 1% agarose gels containing ethidium bromide.

**Results**

**Main properties of the transgenic N. benthamiana plants**

In a previous study, several transgenic lines of N. benthamiana (ab12, -13 and -34) expressing the PVA HCpro were produced, characterized and self-pollinated for production of T1 progeny (Savenkov & Valkonen, 2001a). The transgenic lines and T1 progeny plants expressed high levels of...
of HC<sup>pro</sup> mRNA, as shown by Northern blot analysis (Fig. 1), and HC<sup>pro</sup>, as measured by ELISA using antibodies to HC<sup>pro</sup> (Savenkov & Valkonen, 2001a). The T1 progeny of line ab34 was chosen for this study and the seeds grown for experiments. Controls included the T1 progeny of a line of <i>N. benthamiana</i> transformed with the PVA coat protein (CP) gene and the T1 progeny of another transgenic line (GUS1) expressing the GUS marker gene. These transgenic lines and their transgene constructs and the transgenic lines are summarized in Table 1.

**Responses to challenge inoculation with the homologous PVA isolate B11**

Responses of the HC<sup>pro</sup>-transgenic and wt <i>N. benthamiana</i> plants to PVA infection were initially tested by mechanical inoculation with PVA isolate B11, the isolate from which the HC<sup>pro</sup> and CP transgenes were derived. Similar severe symptoms of mosaic and malformation of leaves were observed in the HC<sup>pro</sup>-transgenic and wt <i>N. benthamiana</i> plants at 14 days p.i. Virus titres were also similar, as estimated by ELISA, in the systemically infected leaves (HC<sup>pro</sup>-transgenic plants: 39 µg/g leaf, n = 26; wt control plants 37-7 µg/g leaf, n = 18). Thus, HC<sup>pro</sup> expression in the transgenic plants had no detectable effect on PVA accumulation and disease phenotype at an early stage of systemic infection.

However, at 21–28 days p.i. with PVA isolate B11, a peculiar phenotype was observed in the expanding sixth (position +6) and seventh (position +7) leaf above the inoculated leaf (position 0) in the HC<sup>pro</sup>-transgenic plants. These leaves had an elongated, narrow leaf tip that was chlorotic (yellow) (Fig. 2A). All new leaves above those with the LLT phenotype developed without symptoms. The inoculated leaves (position 0) and all leaves above the inoculated leaves (positions 1–10) from several HC<sup>pro</sup>-transgenic plants and PVA-infected control plants were tested for PVA by ELISA at 21 days p.i. Only the inoculated leaves and the upper leaves at positions 1–5 were PVA-infected for the HC<sup>pro</sup>-transgenic plants, whereas the symptomless leaves at positions 8–10 were virus-free, as determined by ELISA and Northern blot analysis (Fig. 3). In contrast, all leaves at positions 0–10 were virus-infected in the GUS1 and wt control plants, showed severe symptoms and no LLT phenotype was observed. The response of all HC<sup>pro</sup>-transgenic lines (ab12, -13 and -34) was similar. These data indicate recovery of the HC<sup>pro</sup>-transgenic plants from PVA infection (sensu Lindbo et al., 1993).

Distribution of PVA and the steady-state levels of transgene mRNA expression were examined in different parts of the leaves displaying the LLT phenotype. The leaves from positions +6 and +7 on 10 recovered HC<sup>pro</sup>-transgenic plants and leaves from similar positions on a few healthy HC<sup>pro</sup>-transgenic plants (controls) were harvested and each leaf was divided into three parts (Fig. 2). The samples were

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**Table 1. Main characteristics of the N. benthamiana plants transformed with the HC<sup>pro</sup> or CP-encoding sequences of PVA**

<table>
<thead>
<tr>
<th>Transgenic line</th>
<th>Gene</th>
<th>35S promoter</th>
<th>Translational enhancer*</th>
<th>Plant intron</th>
<th>RT–PCR</th>
<th>Northern blot</th>
<th>Protein assay†</th>
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<tr>
<td>ab34</td>
<td>HC&lt;sup&gt;pro&lt;/sup&gt;</td>
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<td>Yes</td>
<td>No</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
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<tr>
<td>ab10</td>
<td>CP</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>GUS1</td>
<td>GUS</td>
<td>Yes</td>
<td>No</td>
<td>Yes</td>
<td>NT</td>
<td>NT</td>
<td>Yes</td>
</tr>
</tbody>
</table>

* PVA leader (5’ UTR) sequence.
† In case of the GUS1 line, expression was tested by β-glucuronidase histochemical assay.

nt, Not tested.
Fig. 2. For legend see facing page.
analysed by ELISA and Northern blot (Fig. 2). Readily detectable amounts of the PVA CP antigen (Fig. 2B,C), transgene mRNA and PVA genomic RNA (Fig. 2D) were detected in the tips of the leaves showing the LLT phenotype. In contrast, the other parts of these leaves contained very low or undetectable amounts of the virus and transgene mRNA (Fig. 2B–D). The symptomless leaves at position +8 and above did not contain detectable amounts of the virus or transgene mRNA (Fig. 2D) were detected 28 days p.i. due to degradation by the RNA silencing mechanism. The amount of RNA (~30 µg) loaded per lane was verified by ethidium bromide staining of ribosomal RNAs (bottom panel).

Responses to infection with different isolates of PVA

Three additional PVA isolates (Ali, TamMV and U), differing in their HCpro and CP sequences compared to isolate B11 (Kekarainen et al., 1999), were used for inoculation of the HCpro-transgenic plants. Also, a mutant of PVA isolate B11 (B11-DAG), bearing two nucleotide substitutions in the CP gene and accumulating to ca. 10-fold lower titres than B11 in tobacco plants (N. tabacum cv. Samsun) (Andrejeva et al., 1999), was included in the experiments. Accumulation of these PVA isolates in N. benthamiana was first tested in wt and GUS-transgenic plants and found to be different. Isolate B11 (37-7 µg/g leaf, n = 18) had very high titres. Isolate Ali (6-86 µg/g, n = 13) had moderately high titres, TamMV (3-0 µg/g, n = 15) and B11-DAG (2-76 µg/g, n = 13) had low titres and isolate U (0-35 µg/g, n = 21) had very low titres, as estimated by ELISA on at least 13 inoculated plants per isolate. These differences in virus accumulation were consistent with the differences observed in tobacco plants (Rajamäki et al., 1998; Andrejeva et al., 1999; Valkonen et al., 2002). The T1 progeny plants of the CP-transgenic line were shown previously to be resistant to all these PVA isolates, probably due to a PTGS-based resistance mechanism, as proposed previously (Table 1) (Savenkov & Valkonen, 2001b). In this study, these plants were compared to the HCpro-transgenic plants for their response to infection with the aforementioned PVA isolates and the mutant B11-DAG. No infection with any of these viruses was detectable in inoculated or upper non-inoculated leaves in any of nine plants per virus tested in two experiments (data not shown). Thus, the CP-transgenic plants expressed extreme resistance to a range of PVA isolates showing as low as 86-9% sequence identity to the transgenic (CP-encoding region; the 5’ UTR sequences of TamMV and B11 are only 68-9% identical) (Kekarainen et al., 1999).

Fig. 3. Northern blot analysis of accumulation of the HCpro transgene mRNA (asterisk) in leaves at position –1 before PVA inoculation (sample 0; lanes 1, 3, 5, 7, 9 and 11) and by 28 days p.i. (sample 1; lanes 2, 4, 6, and 8 in the recovered symptomless leaves at position +8 and in a mock-inoculated plant (lanes 13 and 14). Note that PVA genomic RNA was not detected 28 days p.i. due to degradation by the RNA silencing mechanism. The amount of RNA (~ 30 µg) loaded per lane was verified by ethidium bromide staining of ribosomal RNAs (bottom panel).
were compared for accumulation of transgene mRNA and PVA RNA (Fig. 5). A few leaves at position +9 from plants inoculated with isolate B11 or B11-DAG were included as well. No transgene mRNA or viral RNA was detected in the symptomless leaves, whereas transgene mRNA and viral RNA were detected in all symptomatic leaves (Fig. 5). Thus, isolate U induced a delayed recovery from infection, which was observed in only a few plants and was devoid of the LLT phenotype, in contrast to B11, B11-DAG and Ali. No recovery was observed in plants infected with TamMV. The data suggest that the PVA isolates showing higher sequence similarity with the transgene (B11, B11-DAG and Ali versus U and TamMV) and/or accumulating to higher titres (B11 and Ali versus U and TamMV) were more likely to induce recovery in the HCpro-transgenic plants.

Methylation of the HCpro-transgene DNA

Methylation of the HCpro transgene during recovery of plants from PVA infection was tested using a PCR-based technique employing methylation-sensitive endonucleases and subsequent PCR amplification (Ingelbrecht et al., 1994; Guo et al., 1999; Mallory et al., 2001). Total DNA was isolated from young leaves before PVA inoculation and from the upper leaves at positions +7 and +8 above the inoculated leaf by 28 and 38 days p.i., respectively. DNA from young seedlings 5 days post-germination was used as a control for the methylation test. Two enzymes were used to provide two sets of independent reference digestions (Fig. 6A). To amplify three partially overlapping portions of the HCpro transgene, four primers were designed and used. The reverse primer complementary to the 3′ proximal part of the transgene was used in combination with three forward primers (Fig. 6A). If the Clal (Nofl) sites in an analysed transgene were methylated, then it would be expected that the enzymes would not be able to cut the genomic DNA and both a 0.89 kb (1.2 kb in the case of Nofl site) and a 0.6 kb (0.89 kb) PCR product would be amplified. However, if the DNA was not methylated at those sites, then the enzymes would cut and only the small fragments of 0.6 kb (0.89 kb) would be amplified.

Results of the analysis for methylation within the transgene DNA indicated that of the Clal (Nofl)-digested DNA samples from young seedlings, from plants prior to PVA inoculation and from the recovered leaves at 28 days p.i., produced the pattern predicted for unmethylated DNA, since the large fragments were not amplified (Fig. 6B, panels I and IV), whereas the small fragments (Fig. 6B, panels II and V) as well as the expected fragment from undigested DNA (Fig. 6B, panels III) were amplified.

At 38 days p.i., the pattern predicted for methylated DNA was observed for recovered leaves of plants inoculated with PVA isolates B11 or B11-DAG but not in the recovered leaves of plants inoculated with isolate U (Fig. 6B, panels I and IV) (plants inoculated with isolate U showed recovery by 38 days
p.i., 10 days later than the plants inoculated with B11 or B11-DAG). Methylation of the \( HC^{\text{pro}} \) transgene was not detected in the plants inoculated with isolates U or TamMV and which did not undergo recovery but showed disease symptoms in the upper leaves by 38 days p.i.

A single plant among the over one hundred T1 plants of line ab34 tested in our experiments showed a unique phenotype. Recovery of the upper leaves started 1 week earlier than in other plants and chlorotic vein banding in lower leaves as well as the LTT phenotype developed in this plant. In addition, the steady-state levels of \( HC^{\text{pro}} \) mRNA (Fig. 3, lane 11) were somewhat lower than in other plants prior to PVA inoculation. We found that \( Ca1l \) (NotI)-digested DNA produced the pattern of amplification predicted for methylated DNA at all three time-points: amplification of both the long (Fig. 6B; panels I and IV, lanes 3–5) and the short (Fig. 6B; panels II and V, lanes 3–5) fragments was observed.

Taken together, these results suggest that these particular \( Ca1l \) and NotI sites located 300 nt from each other were not methylated during the initiation and the early maintenance stage of silencing (recovery) but became methylated to some extent at the later maintenance stage. Isolates unable to induce recovery and silencing of the transgene failed to induce methylation of the homologous sequence within a transgene. On the other hand, early methylation of the coding sequence of the transgene was associated with a distinct rare recovery phenotype (‘chlorotic vein banding’ sample; Fig. 6B, lanes 3–5).

**Discussion**

RNA silencing constitutes a natural defence mechanism against viruses in plants (Covey et al., 1997; Ratcliffe et al., 1997; Al-Kaff et al., 1998). Thus, it is conceivable that transgenic plants expressing an RNA silencing suppressor, such as the potyvirus \( HC^{\text{pro}} \), would be compromised for virus resistance and converted to hypersusceptibility to virus infection. Indeed, expression of the \( P1/HC^{\text{pro}} \) polyprotein of *Tobacco etch potyvirus* (TEV) in transgenic tobacco plants enhances accumulation of unrelated viruses in these plants (Vance et al., 1995). Also, the titre of *Potato leafroll potexvirus* is significantly increased in the PVA \( HC^{\text{pro}} \)-transgenic *N. benthamiana* plants (Savenkov & Valkonen, 2001a). However, it was of particular interest to investigate how transgenic plants overexpressing an RNA silencing suppressor would respond to infection with viruses homologous to the transgene. In such plants, the anti-silencing force conferred together by the transgenic product and the silencing suppressor produced from the replicating virus would be encountered by a silencing induction force created by dsRNA, a potent inducer of RNA silencing (Chicas & Macino, 2001) produced during virus replication (virus-induced gene silencing, VIGS) (Baulcombe, 1999). Our study shows that the force of VIGS overcomes the silencing suppression potential conferred by the combined production of \( HC^{\text{pro}} \) from the transgene and replicating PVA in the plants used in this study. Interestingly, only brief, transient recovery was observed in another recent study in which *N. benthamiana* plants transformed with the \( HC^{\text{pro}} \) gene of *Cuphea aphid-borne mosaic potyvirus* were challenged with the homologous virus (Mlotshwa, 2001).

The \( HC^{\text{pro}} \)-transgenic *N. benthamiana* plants used in this study express high levels of \( HC^{\text{pro}} \) (300–900 ng \( HC^{\text{pro}} \) per gram of leaf, as compared to 500–1700 ng/g accumulating in wt plants infected with PVA isolate B11) (Savenkov & Valkonen, 2001a). No spontaneous silencing of the \( HC^{\text{pro}} \) transgene has been observed in any of the several hundred T1 progeny plants examined from several transgenic lines. Also, all examined plants were initially susceptible to PVA infection. The \( HC^{\text{pro}} \)-transgenic plants of this study showed no morphological abnormalities, in contrast to another study on TEV \( HC^{\text{pro}} \) transgenic plants (Anandalakshmi et al., 2000), possibly due to differences in the viruses or transgene constructs used.

Replication of PVA following systemic spread to newly developing tissues results in a rapid increase of the PVA RNA...
Fig. 6. Analysis of transgene methylation in PVA HCpro-transgenic plants upon infection with four PVA isolates. (A) Schematic representation of the HCpro transgene. The HCpro gene is flanked by the CaMV 35S promoter fused with the PVA 5’ UTR and the nopaline synthase gene terminator sequence (nos). Restriction sites for NotI and ClaI are indicated. Sizes of the PCR products amplified following digestion with NotI/ClaI are shown and the positions of PCR primers in relation of the transgene sequence are indicated with arrows. One reverse primer and three forward primers were used, of which the forward primer used for amplification of the 0–89 kb fragment was the same for digestions with both NotI/ClaI. (B) Agarose gel electrophoresis of the PCR products amplified from ClaI-digested (panels I and II), NotI-digested (panels IV and V) or non-digested (panel III) samples of total DNA. The digested DNA was amplified by two pairs of primers, in which the forward primer was located upstream (panels I and IV) or downstream (panels II and V) of the restriction site. Uncut DNA (panel III) was amplified using the forward primer, also used to amplify the 0–89 kb fragment. The reverse primer was the same for all PCR amplifications. The HCpro-transgenic plants were inoculated with four PVA isolates (B11, B11-DAG, U and TamMV). Upper leaves were analysed prior to PVA inoculation (lanes 3, 6, 9, 12, 15 and 18) and the leaves at positions +9 and +10 above the inoculated leaf were analysed by 28 (lanes 4, 7, 10, 13, 16 and 19) and 38 (lanes 5, 8, 11, 14, 17 and 20) days p.i. The recovery phenotypes are indicated on the top (see text for detailed description). A DNA sample from young seedlings (5 days post-germination) of the HCpro-transgenic plants was included as a control (lane 2). Lane 1 in each panel shows the λ EcoRI/HindIII molecular mass marker, of which the sizes of two marker bands are indicated.
concentration in the cells. However, meristematic tissues that lack functional plasmodesmal connections and very young leaf primordia which lack veins and phloem tissues supportive to virus transport and unloading (Roberts et al., 1997) cannot be systemically infected following phloem-dependent virus transport from other parts of the plant (Oparka & Santa Cruz, 2000). The initiation of recovery (LLT phenotype) was consistently observed in two successive new leaves, in which the tips were found to be virus-infected but the rest of the leaf was symptomless and virus-free. The tip is developmentally the oldest part of the leaf (Roberts et al., 1997). Thus, it seems likely that RNA silencing is initiated in close proximity to the meristematic tissues. Indeed, meristems do not undergo RNA silencing (Beclin et al., 1998; Voinnet et al., 1998) and potyviruses do not access the meristem (Jones et al., 1998b).

A spatial pattern of RNA silencing resembling the LLT phenotype observed in this study is induced by infection with a homologous virus in transgenic pea plants expressing Nlb, the potyviral RNA-dependent RNA polymerase derived from PShMV (Jones et al., 1998b). Recovery from PShMV infection was first observed in the pea leaves at positions +3 and +4 above the inoculated leaf, similar to leaves at positions +6 and +7 in our study, and was characterized by a restriction of symptoms and virus accumulation to the distal part of the leaf. Furthermore, the leaf at position +5 and the subsequent new leaves, similar to the leaf +8 and the subsequent new leaves in our study, were resistant to mechanical inoculation with PShMV (Jones et al., 1998b). In the PShMV Nlb-transgenic pea plants and the PVA HCP-pro-transgenic N. benthamiana plants, the rest of the leaf lamina showed recovery. However, the leaves of N. benthamiana plants transformed with the Nb gene of Plum pox potyvirus (Guo & Garcia, 1997) show an irregular pattern of dark green islands ('bubbles') within otherwise chlorotic leaf lamina, indicating a sporadic induction of RNA silencing in the leaf lamina (Moore et al., 2001).

Once recovered, the new top leaves did not become systemically infected with VPA transported from the lower, full-grown, PVA-infected source leaves. However, six leaves of the 29 recovered leaves mechanically inoculated with the homologous PVA isolate B11 were infected, showing that the recovered leaves were not completely protected against PVA infection. Apparently, mechanical inoculation of PVA can circumvent the mechanism that prevented infection via systemic, phloem-dependent virus transport from the lower leaves. These data are consistent with the hypothesis that RNA silencing may be hyperactive in phloem cells that control phloem-loading and/or phloem-unloading of viruses (Marathe et al., 2000). Thus, effective degradation of viral RNA upon infection of the phloem cells could inhibit systemic infection, whereas in the mechanically inoculated leaves, the gatekeeper function of the phloem cells would be circumvented.

A threshold model of RNA silencing predicts that the concentration of silencing target RNA is reduced to just below a threshold level in leaves where silencing has been initiated (Meins, 2000). It is intriguing in this regard that in the lamina of +6 leaves, PVA accumulated at greatly reduced but detectable titres, which are, in quantitative terms, similar to the titres of PVA-U, an isolate that was able to induce only delayed recovery in some of the infected plants. These findings suggest that viruses replicating to only low titres and/or accumulating low amounts of replicative intermediates (dsRNA) do not reach a threshold level and can evade and/or do not induce the plant RNA surveillance system. However, because no virus and no transgene mRNA were detected in the leaves at position +8 or higher, our data suggest that another mechanism independent of the threshold level contributes to the propagation and maintenance phases of silencing.

Our data indicate that the level of sequence homology between the transgene and the infecting virus constitutes an important factor in induction of recovery. Isolates B11 and B11-DAG are identical to the transgene sequence and induced recovery to the same rate regardless of a more than 10-fold difference in the level of virus accumulation. However, isolate TamMV with a low nucleotide sequence identity to the transgene (81-3 % or, more specifically, 68-9% for the 5’ UTR and 83-2% for the HCP pro-cistron) (Kekarainen et al., 1999) and an accumulation level similar to isolate B11-DAG induced no recovery (Fig. 4). Isolate U accumulated to titres ca. 10-fold lower than B11-DAG and TamMV, but it induced a delayed recovery in 47-4% of infected plants, probably due to its high levels of sequence similarity with the transgene (97-5%) (Fig. 4). In contrast to the HCPpro-transgenic plants, the CP-transgenic plants were resistant to all five PVA isolates tested and no infection was observed. The sequence identity between TamMV and the CP transgene is 86-9%, which is slightly higher than the identity between TamMV and the HCPpro transgene. Taken together, our data suggest that higher levels of virus accumulation and sequence similarity with the transgene both represent factors of great importance for RNA silencing induction by a virus (VIGS).

Methylation of the transgene is often found to be associated with the maintenance phase of RNA silencing (Jones et al., 1998b, 1999; Guo et al., 1999). In order to address the possible role of transgene methylation on RNA silencing in the HCPpro-transgenic plants, methylation was assayed at two restriction sites located ca. 300 nt apart at different times after infection with five PVA isolates. No indication of methylation was apparent at the time when many leaves of the plants had recovered from PVA infection. Even though methylation of the transgene was later observed in recovered leaves, its appearance at a late stage of recovery indicated no significant role in the initiation phase of recovery but rather a possible significance in the maintenance stage of transgene silencing (Jones et al., 1999).

The results of our study are consistent with the previous observations that many viruses encoding functional suppressors of RNA silencing will, nevertheless, trigger RNA silencing during infection (Carrington et al., 2001) and are,
therefore, both suppressors and targets of the silencing (Voinnet et al., 1999).

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