A Conserved Mechanism for Post-Transcriptional Gene Silencing?

Eleanor M. Maine
Syracuse University

Follow this and additional works at: https://surface.syr.edu/bio

Part of the Biology Commons

Recommended Citation
Maine, Eleanor M., "A Conserved Mechanism for Post-Transcriptional Gene Silencing?" (2000). Biology. 8. https://surface.syr.edu/bio/8

This Article is brought to you for free and open access by the College of Arts and Sciences at SURFACE. It has been accepted for inclusion in Biology by an authorized administrator of SURFACE. For more information, please contact surface@syr.edu.
Minireview

A conserved mechanism for post-transcriptional gene silencing?
Eleanor M Maine

Address: Department of Biology, Syracuse University, Syracuse, NY 13244, USA.
E-mail: emmaine@syr.edu

Published: 13 September 2000

Genome Biology 2000, 1(3):reviews1018.1–1018.4

The electronic version of this article is the complete one and can be found online at http://genomebiology.com/2000/1/3/reviews/1018

© GenomeBiology.com (Print ISSN 1465-6906; Online ISSN 1465-6914)

Abstract

Proteins with homology to RNA-directed RNA polymerases function in post-transcriptional gene silencing: in quelling in the fungus Neurospora crassa, RNAi in the nematode Caenorhabditis elegans, and co-suppression in the mustard plant Arabidopsis thaliana. These findings are consistent with a conserved mechanism operating in these diverse species.

Post-transcriptional gene silencing (PTGS) is a general term for a variety of phenomena that repress gene expression by causing degradation of mRNA. PTGS was discovered 'by accident' in organisms that carried a transgene, were virally infected, or were treated with exogenous RNA. A form of PTGS triggered by transgenic DNA, called co-suppression, was initially described in plants [1,2], and a related phenomenon, termed quelling, was later observed in the filamentous fungus Neurospora crassa [3]. Co-suppression was first noticed when a transgenic petunia, expected to express a transgene involved in pigment formation at a high level, instead expressed neither the transgene nor related, endogenous genes [1,2]. Subsequent work indicated that viral infection can also trigger co-suppression in plants [4], leading to the hypothesis that the biological role of PTGS is as an anti-viral defense mechanism. Meanwhile, other experiments with the soil nematode Caenorhabditis elegans uncovered a phenomenon triggered by double stranded (ds) RNA, called RNA interference (RNAi), as well as transgene-induced co-suppression [5,6]. RNAi is an extremely valuable tool for 'reverse' genetic studies because it gives researchers a quick means to determine the loss-of-function phenotype for a gene. A wide variety of organisms have now been shown to respond to RNAi, including Drosophila and mouse (see, for example, [7-9]).

Because of the utility of PTGS for reverse genetic studies and its possible clinical uses, there is a great deal of interest in the underlying molecular mechanism(s). It has become apparent that different PTGS phenomena have common characteristics, and this realization has led to the speculation that PTGS in different organisms may be mediated by similar molecular mechanisms [6,10,11]. Recent genetic and molecular studies provide additional support for this hypothesis. Genes involved in PTGS have been identified in N. crassa (qde genes) [12], C. elegans (rde, mut, and ego-1 genes) [13-15], and the mustard plant Arabidopsis thaliana (sde, sgs genes) [16-18]. Intriguingly, related proteins function in PTGS in these organisms (Table 1), as would be expected if different forms of PTGS occur by similar mechanisms.

Among proteins associated with PTGS to date, the most widely conserved are those with homology to tomato RNA-directed RNA polymerase (RdRP) [19]: Neurospora QDE-1 [20], C. elegans EGO-1 [15], and Arabidopsis SGS-2/SGD-1 ([17,18]; Figure 1). The recent addition of Arabidopsis genes to this collection suggests that PTGS is a widely conserved, evolutionarily ancient means of gene regulation. Two additional protein families have been linked to PTGS in nematodes and Neurospora (Table 1) [13,14,21,22] but such a link has yet to be made in plants. The rde-1 and qde-2 genes are members of the piwi/sting family. Piwi/Sting proteins are related to eIF2C, a proposed translation factor (see [13,21]); several members of this family are known to have important developmental functions. The mut-7 and qde-3 genes encode members of the WRN (Werner’s syndrome) protein family, whose members include several RecQ DNA helicases; Werner’s syndrome is
Schematic alignment of tomato RdRP with proteins known to be involved in PTGS in fungus (QDE-1), nematodes (EGO-1), and plants (SGS2/SDE1). The region that is conserved among all four proteins is shaded. The total number of amino acids in each protein is listed to the right; amino acid positions delimiting the conserved regions are indicated. Within the shaded region, the percentage of RdRP amino-acid sequence identical to each related gene sequence is as follows: QDE-1, 17%; EGO-1, 25%; SDS2/SDE1, 41%. Sequence blocks of higher identity are scattered within the shaded region. Substantial.

Table 1

| Conserved proteins involved in PTGS |
|-----------------------------------|
| **Protein family** | **N. crassa** | **C. elegans** | **A. thaliana** |
| RdRP | QDE-1 | EGO-1 | SGS2/SDE1 |
| Piwi/Sting | QDE-2 | RDE-1 | ? |
| WRN protein | QDE-3 | MUT-7 | ? |

Gene names in full: EGO, enhancer of glp-1; MUT, mutator; QDE, quelling defective; RDE, RNAi defective; RdRP, RNA-directed RNA polymerase; SDE, silencing defective; SGS, suppressor of gene silencing; WRN, Werner’s syndrome.

Because co-suppression in plants can be triggered by viral infection and, in fact, is hypothesized to be a viral defense mechanism, both groups investigated the effects of viral infection on sgs2/sde1 mutants. Was virally induced PTGS defective? Were the mutants super-susceptible to viral infection? Dalmay and colleagues [18] found that PTGS triggered by tobacco mosaic virus and tobacco rattle virus is not defective in sde1 mutants. They interpret their data as meaning that SDE1 is not required for virally induced PTGS, but only for transgene-induced PTGS. They suggest that virally encoded RdRP activity can substitute for the putative RdRP activity of SDE1. In contrast, Mourrain and colleagues [17] found that sgs2 mutants had increased susceptibility to infection by certain viruses, such as a cucumovirus, but not others, such as a tobamovirus or a potyvirus. They interpret these results as indicating that PTGS indeed acts as a defense against at least some viruses. Interpretation of infection data is complicated by the fact that many viruses can inhibit PTGS: tobamovirus and potyvirus strongly inhibit PTGS, whereas cucumovirus inhibits it only weakly [17, 23]. Logically, the loss of a plant component of PTGS, such as SGS2/SDE1, will have no effect on a virus that fully blocks PTGS by itself, but would allow a higher level of infection by a virus that disables PTGS only partially or not at all. At any rate, these results suggest that the Dalmay et al. model is unlikely to be correct for all viruses; in at least some cases, viral RdRP cannot replace SGS2/SDE1.

**Arabidopsis RdRP-related genes**

Independent screens by the Vaucheret and Baulcombe laboratories for co-suppression-defective mutants in Arabidopsis have recovered mutations in a RdRP-related gene, named sgs2 (suppressor of gene silencing) [17] or sde1 (silencing defective) [18]. For the purposes of this review, the gene is referred to as sgs2/sde1. Mutants were isolated by screening for individuals defective in transgene-induced PTGS. Several other RdRP-related genes exist in Arabidopsis, but no mutations were recovered in those genes.

**The RdRP protein family**

RdRP activity has been known in plants for decades, although its physiological function has been unclear [24].
Many models for PTGS in plants postulate an RNA amplification step that could be accomplished by RdRP activity (for example in [25]), but it has yet to be shown definitively that RdRP is in fact involved in PTGS. In light of these models, it is intriguing that proteins related to the purified tomato RdRP have now been linked to PTGS in diverse organisms. It should be noted, however, that these proteins have not yet been shown to have RdRP activity. They contain large regions of sequence conservation with tomato RdRP, which may encode RdRP activity, but they also contain extensive regions of divergent sequences (see Figure 1) [15,17,18].

Analysis of genome sequence data has shown that *C. elegans* and *Arabidopsis* contain several RdRP-related genes. In *C. elegans*, for example, there are three *rrf* (RdRP family) genes in addition to *ego-1*. Thus far, six other RdRP-related genes have been found in the *Arabidopsis* genome in addition to *sgsz/sde1*. Genome sequencing has uncovered RdRP-related genes in many other organisms, including several plant species, such as wheat and petunia, and the fission yeast *Schizosaccharomyces pombe*. It is not yet clear, though, how many of these RdRP-related proteins actually function in PTGS. Some of them may have other cellular functions, perhaps in RNA metabolism. Indeed, *ego-1* was identified originally as being important in development of the *C. elegans* germ line, and was only later shown to function in RNAi; the connection between development and RNAi is not yet clear, but one possibility is that *ego-1* protein has different functions in the two processes. Since alleles of only one RdRP-related gene, *sgsz/sde1*, were recovered as suppressors of PTGS, perhaps the related genes in *Arabidopsis* do not function in PTGS. Alternatively, some or all of these genes may be redundant, so that simultaneous mutations in two or more of them would have to be induced in order to see a phenotype. In addition, if any RdRP-related gene is essential, it would not have been identified because the screens for silencing-defective mutants did not allow for recovery of lethal mutations.

RdRP-related genes are apparently absent from at least one organism that is susceptible to RNAi: *Drosophila melanogaster*. Genome sequence data are nearly complete for *Drosophila*, yet no gene with homology to either tomato or viral RdRP has been found. Since viral and cellular (for example, tomato) RdRP have little amino acid homology to each other, perhaps RdRP function in *Drosophila* is accomplished by an enzyme with yet a different amino acid sequence. Alternatively, RNAi in *Drosophila* may not require RdRP activity at all.

**SGS3**

Molecular characterization of another *Arabidopsis* *sgs* gene, *sgs3*, by Mourrain *et al.* [17] revealed that it encodes a novel protein. In general, *sgs3* mutants behave like *sgs2* mutants, including having an increased susceptibility to cucumovirus infection. Thus, it appears that SGS3 is as critical to PTGS as is SGS2/SDE1. No SGS3 relative has been found yet in any other organism, including those with fully sequenced genomes such as *C. elegans* and *Drosophila* and this result is consistent with SGS3 functioning in a plant-specific aspect of PTGS.

The extensive and growing genome sequence database is an important resource for studying the mechanics of PTGS and the role of RdRP-related genes in this and other cellular processes. Three protein families are now known to be important to PTGS. Genome sequence information has allowed researchers to identify paralogs and orthologs very quickly, and provides a focus for future experiments. For example, reverse genetic approaches can be used to generate deletion mutations in these related genes for use in studying their possible role in PTGS. We can expect a more complete molecular portrait of PTGS to be revealed in the near future.

**Acknowledgements**

The author thanks John Belote and M Kathryn Barton for helpful comments on the manuscript.

**References**

1. Napoli C, Lemieux C, Jorgensen R: *Introduction of a chimeric chalcone synthase gene into petunia results in reversible cosuppression of homologous gene in trans*. Plant Cell 1990, 2:179-289.
2. van der Krol AR, Mur LA, Beld M, Mol JNM, Stuitje AR: *Flavonoid genes in petunia: addition of a limited number of gene copies may lead to a suppression of gene expression*. Plant Cell 1990, 2:291-299.
3. Romano N, Macino G: *Quelling: transient inactivation of gene expression in Neurospora crassa by transformation with homologous sequences*. Mol Microbiol 1992, 6:3343-3353.
4. Ruiz MT, Voinnet O, Baulcombe DC: *Initiation and maintenance of virus-induced gene silencing*. Plant Cell 1998, 10:937-946.
5. Guo S, Kemphues KJ: *par-1*, a gene required for establishing polarity in *C. elegans* embryos, encodes a putative Ser/Thr kinase that is asymmetrically distributed. Cell 1995, 81:611-620.
6. Fire A, Xu S, Montgomery MK, Kostas SA, Driver SE, Mello CC: *Potent and specific genetic interference by double-stranded RNA in Caenorhabditis elegans*. Nature 1998, 391:806-811.
7. Kennerdell JR, Cartwright RW: *Use of ds-RNA-mediated genetic interference to demonstrate that frizzled and frizzled 2 act in the Wingless pathway*. Cell 1998, 95:1017-1026.
8. Forster E, Belote JM: *Temperature-dependent gene silencing by an expressed inverted repeat in Drosophila*. Genesis 2000, 26:240-244.
9. Wanney F, Sernicka-Goetz MW: *Specific interference with gene function by double-stranded RNA in early mouse development*. Nature Cell Bio 2000, 2:70-75.
10. Montgomery MK, Fire A: *Double-stranded RNA as a mediator in sequence-specific genetic silencing and co-suppression*. Trends Genet 1998, 14:255-258.
11. Fire A: *RNA-triggered gene silencing*. Trends Genet 1999, 15:358-363.
12. Cogoni C, Macino G: *Isolation of quelling-defective (qde) mutants impaired in posttranscriptional transgene-induced gene silencing in Neurospora crassa*. Proc Natl Acad Sci USA 1997, 94:10233-10238.
13. Tabara H, Sarkissian M, Kelly WG, Fleener J, Grishok A, Timmons L, Fire A, Mello CC: *The rde-1 gene, RNA interference, and transposon silencing in *C. elegans*. Cell 1999, 99:123-132.
14. Ketting RF, Haverkamp THA, van Luenen HGAM, Plasterk RHA: \textit{mut-7} of \textit{C. elegans}, required for transposon silencing and RNA interference, is a homolog of Werner syndrome helicase and RNaseD. \textit{Cell} 1999, 99:133-141.

15. Smardon A, Spoerke JM, Stacey SC, Klein ME, Mackin N, Maine EM: \textit{EGO-1} is related to RNA-directed RNA polymerase and functions in germline development and RNA interference in \textit{C. elegans}. \textit{Curr Biol} 2000, 10:169-178.

16. Elmayan T, Balzergue S, Beon F, Bourdon V, Daubremet J, Guenet Y, Mourrain P, Palausq JC, Vernhettes S, Vialle T et al.: \textit{Arabidopsis} mutants impaired in cosuppression. \textit{Plant Cell} 1998, 10:1447-1457.

17. Mourrain P, Beclin C, Elmayan T, Feuerbach F, Godon D, Morel JB, Jouette D, Lacombe AM, Nikic S, Picault N et al.: \textit{Arabidopsis} SGS2 and SGS3 are required for posttranscriptional gene silencing and natural virus resistance. \textit{Cell} 2000, 101:533-542.

18. Dalmay T, Hamilton A, Rudd S, Angell S, Baulcombe D: An RNA-dependent RNA polymerase gene in \textit{Arabidopsis} is required for posttranscriptional gene silencing mediated by a transgene but not by a virus. \textit{Cell} 2000, 101:543-553.

19. Schiebel W, Pelisser F, Riedel L, Thalmeir S, Schiebel R, Kempe D, Lottspeich F, Sanger HL, Wassenegger M: Isolation of an RNA-directed RNA polymerase-specific cDNA clone from tomato. \textit{Plant Cell} 1998, 10:2087-2102.

20. Cogoni C, Macino G: Gene silencing in \textit{Neurospora crassa} requires a protein homologous to RNA-dependent RNA polymerase. \textit{Nature} 1999, 399:166-169.

21. Catalanotto C, Assalin G, Macino G, Cogoni C: Gene silencing in worms and fungi. \textit{Nature} 2000, 404:245.

22. Cogoni C, Macino G: Posttranscriptional gene silencing in \textit{Neurospora} by a RecQ DNA helicase. \textit{Science} 1999, 286:2342-2344.

23. Voinnet O, Pinto YM, Baulcombe D: Suppression of gene silencing: a general strategy used by diverse DNA and RNA viruses of plants. \textit{Proc Natl Acad Sci USA} 1999, 23:14147-14152.

24. Astier-Manifacier S, Cornuet P: RNA-dependant RNA polymerase in \textit{Chinese Cabbage}. \textit{BBA} 1971, 232:484-493.

25. Wassenegger M, Pelisser T: A model for RNA-mediated gene silencing in higher plants. \textit{Plant Mol Biol} 1998, 37:349-362.