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The double-stranded RNA binding protein RDE-4 can act cell autonomously during feeding RNAi in *C. elegans*

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ABSTRACT

Long double-stranded RNA (dsRNA) can silence genes of matching sequence upon ingestion in many invertebrates and is therefore being developed as a pesticide. Such feeding RNA interference (RNAi) is best understood in the worm *Caenorhabditis elegans*, where the dsRNA-binding protein RDE-4 initiates silencing by recruiting an endonuclease to process long dsRNA into short dsRNA. These short dsRNAs are thought to move between cells because muscle-specific rescue of *rde-4* using repetitive transgenes enables silencing in other tissues. Here, we extend this observation using additional promoters, report an inhibitory effect of repetitive transgenes, and discover conditions for cell-autonomous silencing in animals with tissue-specific rescue of *rde-4*. While expression of *rde-4(+)* in intestine, hypodermis, or neurons using a repetitive transgene can enable silencing also in unrescued tissues, silencing can be inhibited wihin tissues that express a repetitive transgene. Single-copy transgenes that express *rde-4(+)* in body-wall muscles or hypodermis, however, enable silencing selectively in the rescued tissue but not in other tissues. These results suggest that silencing by the movement of short dsRNA between cells is not an obligatory feature of feeding RNAi in *C. elegans*. We speculate that similar control of dsRNA movement could modulate tissue-specific silencing by feeding RNAi in other invertebrates.

INTRODUCTION

Killing animals by feeding them double-stranded RNA (dsRNA) that matches an essential gene is a powerful way to control animal pests. For example, expression of long dsRNA in potato plants was recently used to kill Colorado potato beetle that feed on these plants (1). This approach to pest control relies on the ability of many insects and parasitic nematodes to process ingested long dsRNA and use it to silence genes of matching sequence through RNA interference (RNAi) (2,3, reviewed in 4). However, the mechanisms of gene silencing by ingested dsRNA are not well understood, making it difficult to anticipate resistance mechanisms and therefore design effective dsRNA pesticides.

Silencing of genes by feeding animals long dsRNA was first demonstrated in the nematode *Caenorhabditis elegans* (5), which remains the best animal model for understanding this process called feeding RNAi. In *C. elegans*, ingested dsRNA enters the animal through the intestine and can be delivered into the fluid-filled body cavity that surrounds all internal tissues without entry into the cytosol of intestinal cells (6–8). Entry into the cytosol of any cell requires a dsRNA-selective importer SID-1 (9)—a conserved protein with homologs in many insects (10). Upon entry into cells, silencing by dsRNA is thought to occur through the canonical RNAi pathway (reviewed in 11). Long dsRNA is first bound by the dsRNA-binding protein RDE-4, which recruits the endonuclease DCR-1 to generate short dsRNAs (12–14). One strand of this short dsRNA duplex is used as a guide by the primary Argonaute RDE-1 to identify mRNAs of matching sequence (12,15) and to recruit RNA-dependent RNA polymerases (RdRPs) to the mRNA. RdRPs then synthesize numerous secondary small RNAs (16–18) that are used for potent gene silencing within the cytosol by cytosolic Argonautes and/or within the nucleus by nuclear Argonautes (16–22). To infer whether any derivatives of long dsRNA generated within a cell also move between cells, components of the RNAi pathway were rescued in body-wall muscles using repetitive transgenes and silencing was assayed in other tissues (23) or in the next generation (24). These tissue-specific rescue experiments suggest that short dsRNAs could be transported from donor cells to initiate gene silencing independent of RDE-4 in recipient cells.

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Here, we demonstrate that expression from repetitive transgenes can inhibit silencing by feeding RNAi of some genes. Nevertheless, repetitive transgenes that express *rde-4(+)* under the control of additional tissue-specific promoters (intestine, hypodermis, or neurons) can enable silencing in multiple tissues. Finally, we show that single-copy transgenes that rescue RDE-4 in body-wall muscles or hypodermis can restrict silencing by feeding RNAi to the single rescued tissue.

MATERIALS AND METHODS

Worm strains

All strains were cultured on Nematode Growth Medium (NGM) plates seeded with 100 μl OP50 at 20°C and mutant combinations were generated using standard methods (25). All strains used are listed in Supplementary Material.

Balancing loci

Integrated transgenes expressing *gfp* were used to enable identification of mutant chromosomes in progeny of heterozygous animals. Animals were scored as homozygous mutants if they lacked both copies of the transgene. The *rde-4(ne301)* allele on Chr III was balanced by *juIs73*. About 99% (153/155) of the progeny of *rde-4(ne301)/juIs73* that lacked fluorescence were found to be homozygous *rde-4(ne301)* animals either by Sanger sequencing (n = 96) or by resistance to *pos-1* RNAi ($n = 59$).

Transgenesis

To make strains, N2 gDNA was used (unless otherwise specified) as a template to amplify promoter or gene regions. To amplify *gfp* to be used (unless otherwise specified) as a coinjection marker, a plasmid containing *gfp* sequence was used as a template. All PCRs were performed with Phusion Polymerase (New England Biolabs—NEB), unless otherwise specified, according to the manufacturer's recommendations. The final fusion products were purified using PCR Purification Kit (QIAquick, Qiagen).

Plasmids

The plasmid pJM6 (made by Julia Marré, Jose lab) was used to make *Si[Pnas-9::rde-4(+)::rde-4 3′UTR]*. The *nas-9* promoter (*Pnas-9*) was amplified using primers P48 and P49 and *rde-4(+)::rde-4 3′UTR* was amplified using primers P50 and P4. The two PCR products were used as templates to generate the *Pnas-9::rde-4(+)::rde-4 3′UTR* fusion product with primers P51 and P52. This fused product was purified and cloned into pCFJ151 using the SbfI and SpeI restriction enzymes (NEB) to generate pJM6.

The plasmid pPR1 was used to make *Si[Pmyo-3::rde-4(+)::rde-4 3′UTR]*. The *myo-3* promoter (*Pmyo-3*) was amplified using primers P77 and P78 and *rde-4(+)::rde-4 3′UTR* was amplified using primers P79 and P4. The two PCR products were used as templates to generate the *Pmyo-3::rde-4(+)::rde-4 3′UTR* fusion product with primers P80 and P81. This fused product was purified and cloned into pCFJ151 using the SbfI restriction enzymes (NEB) to generate pPR1.

The plasmid pYC13 (made by Yun Choi, Jose lab) is a derivative of pUC::unc-119_sgRNA with a different sgRNA (gift from John Calarco, Addgene plasmid #46169).

All other plasmids were as described earlier (pHC448 (23), pPD95.75 (gift from Andrew Fire, Addgene plasmid #1494), pBH34.21 (26), pCFJ151 (27), pCFJ601 (27), pMA122 (27), pGH8 (27), pCFJ90 (27), pCFJ104 (27), pL4440 (5), pHC183 (6) and pGC306 (a gift from Jane Hubbard, Addgene plasmid #19658)).

Genome editing

To generate *bli-1* null mutants, Cas9-based genome editing employing a co-conversion strategy was used (28). To prepare guide RNAs, the scaffold DNA sequence was amplified from pYC13 using primers P55 and P56 for *bli-1*, and primers P57 and P56 for the co-conversion marker *dpy-10*. The amplified DNA templates were purified (PCR Purification Kit, Qiagen), transcribed (SP6 RNA polymerase, NEB), and tested *in vitro* for cutting efficiency (Cas9, NEB). For injection into animals, homology template for repair (repair template) was amplified from N2 gDNA using Phusion polymerase and gene specific primers. P58 and P59 were used to amplify a region immediately upstream of the 5′ region of *bli-1* and P60 and P61 were used to amplify a region immediately downstream of the 3′ region of *bli-1* using Phusion Polymerase (NEB). The two PCR products were used as templates to generate the repair template with primers P62 and P63 using Phusion Polymerase (NEB) and the fused product was purified (PCR Purification Kit, Qiagen). Homology template for *dpy-10* was a single-stranded DNA oligo (P64). Wild-type animals were injected with 3.5 pmol/μl of *bli-1* guide RNA, 2.4pmol/μl of *dpy-10* guide RNA, 0.06 pmol/μl of *bli-1* homology repair template, 0.6 pmol/μl of *dpy-10* homology repair template and 1.6 pmol/μl of Cas-9 protein (PNA Bio Inc.). Resulting progeny animals were analyzed as described in Supplementary Figure S4.

Feeding RNAi

RNAi experiments were performed at 20°C on NGM plates supplemented with 1 mM IPTG (Omega Bio-Tek) and 25 μg/ml Carbenicillin (MP Biochemicals) (RNAi plates).

One generation or F1-only feeding RNAi. A single L4 or young adult (1 day older than L4) animal (P0) was placed on an RNAi plate seeded with 5 μl of OP50 *Escherichia coli* and allowed to lay eggs. After 1 day, when most of the OP50 *E. coli* was eaten, the P0 animal was removed, leaving the F1 progeny. 100 μl of an overnight culture of RNAi food (*E. coli* which express dsRNA against a target gene) was added to the plate. Two or three days later, the F1 animals were scored for gene silencing by measuring gene-specific defects (See Supplementary Table S1). All RNAi *E. coli* clones were from the Ahringer library (29) and generously supplied by Iqbal Hamza, with the exception of *unc-54* RNAi, which was made by inserting a fragment of *unc-54* DNA into pL4440 and transforming HT115(DE3) *E.*

coli cells with the resultant plasmid. Control RNAi by feeding *E. coli* containing the empty dsRNA-expression vector (pL4440), which does not produce dsRNA against any gene, was done in parallel with all RNAi assays.

Fluorescence intensity of L4 animals fed dsRNA against *gfp* was measured using ImageJ (National Institute of Health—NIH). Animals with an intensity of >6000 (a.u.) in a fixed area within the gut immediately posterior to the pharynx were considered not silenced. Based on these criteria, 91.7% of wild-type animals and a 100% of animals expressing *DsRed* in the muscle (*Ex[Pmyo-3::DsRed]*) showed silencing. In these silenced animals intensity of *gfp* was measured from below the pharynx to the end of the vulva and the background intensity for the same area was measured for each animal. The intensity of *gfp* after background subtraction was plotted for each worm (Supplementary Figure S2D).

Two generations or P0 & F1 Feeding RNAi. The experiments in all Figures (except Figure 2, Supplementary Figures S1B and C, S5A and B, and S6) were performed by feeding both the P0 and F1 generations, as described earlier (6). Control RNAi was done in parallel with all RNAi assays. Three or four days after P0 animals were subjected to RNAi, the F1 animals were scored for gene silencing by measuring gene-specific defects (See Supplementary Table S1).

In general, no difference in gene silencing was observed between F1-only feeding RNAi and P0 & F1 feeding RNAi for *rde-4* mutants with tissue-specific rescue (e.g. see 'F1 RNAi' and 'P0 & F1 RNAi' in Supplementary Figure S5). However, to test for inheritance of RDE-4 in Supplementary Figure S6, only F1 RNAi was used to avoid any inheritance of dsRNA that could occur when P0 & F1 RNAi is used (30).

For each RNAi experiment testing *rde-4* function, feeding of N2 and WM49 was performed alongside as controls. In the case of Supplementary Figure S7 (*act-5* feeding RNAi), L4 animals were scored a day after control L4 animals because these animals grew slower than control animals.

Scoring defects

For RNAi treatments, the proportions of animals that displayed the reported defects upon RNAi (see Supplementary Table S1) were scored as 'fraction silenced'. For *bli-1* defects upon RNAi and upon Cas9-based genome editing, the pattern of blister formation was scored. Each animal was partitioned into eight roughly equal sections (a to h) as shown in Figure 3C with the vulva being the mid-point of the animal. Sections with >50% of their length covered by a blister were marked black and sections with <50% of their length covered in a blister or with a discontinuous blister were marked grey. Wild-type animals subjected to *bli-1* feeding RNAi showed characteristic biases for blister formation – anterior more than posterior and dorsal more than ventral. Therefore, animals that did not follow the susceptibility pattern (a > b > c > d > e > f > g > h) were culled as variants for each genotype and the relative aggregate blister formation in each section among worms with altered susceptibility (Figure 3D, Supplementary Figure S4E–H) were computed using a score of black = 1.0 and gray = 0.5 for each section of every worm. The computed values for each section in all worms of a strain were summed and normalized to the value of the highest section for that strain. To compare multiple strains, these values for each strain were multiplied by the fraction of worms that showed a blister in that strain. Using these measures of normalized relative aggregate blister formation among animals with variant susceptibility, we generated heat maps (31), where black indicates highest frequency of blisters and white indicates the lowest frequency of blisters among the sections of all strains that are being compared.

Microscopy

Animals were immobilized in 5 μl of 3 mM levamisole, mounted on slides, and imaged using an AZ100 microscope (Nikon) at a fixed magnification under non-saturating conditions. Images being compared on any figure were adjusted identically using Adobe Photoshop (levels adjustment) for display. Images were identically inverted (i.e. *gfp* or *DsRed* expression = black) on Adobe Photoshop as per recent recommendations (e.g. (32)).

ImageJ (NIH) was used to generate merged images (Supplementary Figure S2A–C). To generate merged images, the LUT was set from 0 (white) to 127 (magenta) for DsRed and from 0 (white) to 127 (green) for GFP. One channel was then overlayed on the other with 50% opacity.

Statistical analyses

Error bars in all cases indicate 95% confidence intervals for single proportions calculated using Wilson's estimates with a continuity correction (Method 4 in (33)). Significance of differences between two strains or conditions was determined using pooled Wilson's estimates.

Data availability

All strains are available upon request.

RESULTS

Expression of a repetitive transgene in a tissue can inhibit RNAi in that tissue

Until recently, studies examining the function of *C. elegans* genes have relied on the use of repetitive transgenes often coupled with tissue-specific promoters (e.g. 34–36) and/or RNAi (e.g. 37–39). For example, rescue of *rde-4* or *rde-1* using the *myo-3* promoter to drive expression in body-wall muscles from an extrachromosomal repetitive transgene (*Ex[Pmyo-3::rde(+)]*) was employed to examine the systemic response to RNAi (23,24). While silencing in *rde-1(−)* animals with *Ex[Pmyo-3::rde-1(+)]* was observed only in body-wall muscles, silencing in *rde-4(−)* animals with *Ex[Pmyo-3::rde-4(+)]* was observed in both body-wall muscles and other tissues. We found that in both cases, silencing of one gene within body-wall muscle cells

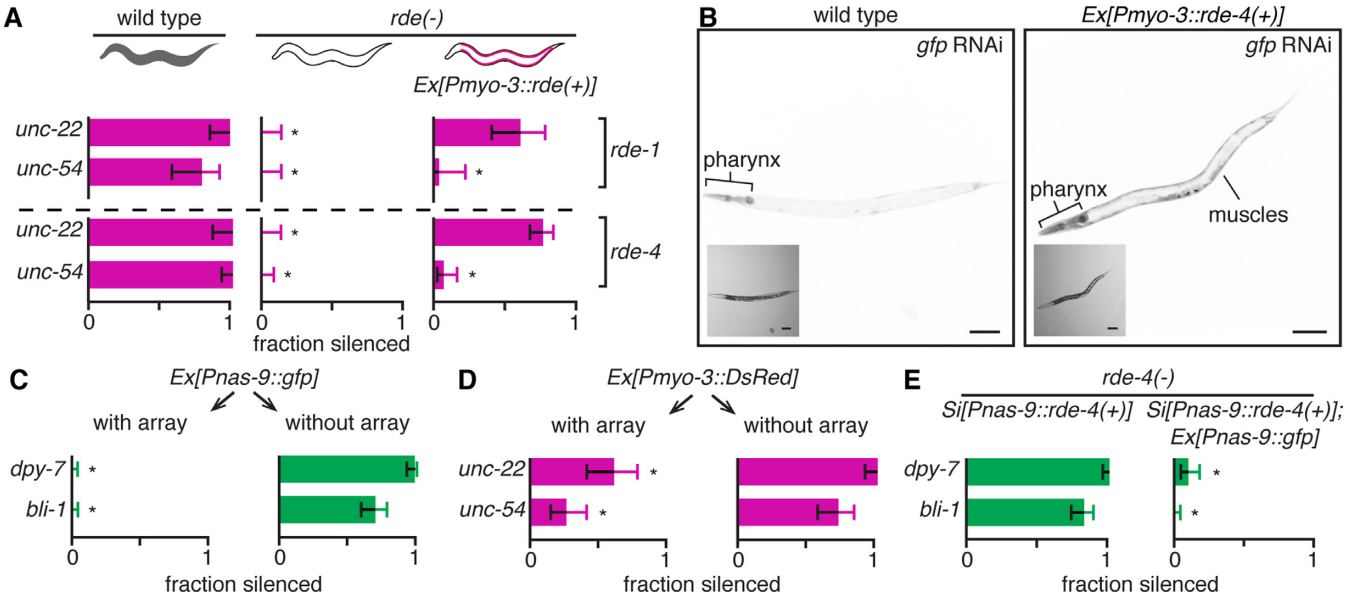

Figure 1. Expression of any repetitive transgene in a tissue can inhibit silencing by ingested dsRNA within that tissue. (**A**) Silencing by feeding RNAi of some endogenous genes is reduced in tissues expressing *rde-4(+)* or *rde-1(+)* from a repetitive transgene. Wild-type animals, mutant animals (*rde-1(−)*, top or *rde-4(−)*, bottom) or mutant animals with tissue-specific rescues in the body-wall muscles (*Ex[Pmyo-3::rde(+)]*) were fed dsRNA against *unc-22* or *unc-54* and the fractions of animals that showed silencing (fraction silenced) were determined. Asterisks indicate $P < 0.01$ (compared to wild-type animals). (**B**) Silencing of *gfp* in body-wall muscles that express RDE-4 from a repetitive transgene is reduced despite potent silencing in other *rde-4(−)* somatic tissues. Representative images of animals with *gfp* expression (black) in all somatic cells (*Peft-3::gfp*) in a wild-type background (left) or *rde-4(−)* background with *rde-4(+)* expressed in body-wall muscles (*Ex[Pmyo-3::rde-4(+)]*) (right) that were fed bacteria that express dsRNA against *gfp* (*gfp* RNAi) are shown. Tissues that show reduced silencing (pharynx, muscles) are labelled, insets are brightfield images, and scale bar = 50 μm. Also see Supplementary Figure S1B and C and methods for details on generation of the inverted grey-scale images presented in all figures. (**C** and **D**) Silencing of a gene by ingested dsRNA within a tissue can be inhibited by the expression of a repetitive transgene of unrelated sequence within that tissue. (C) Silencing of *bli-1* and *dpy-7* is inhibited by the expression of *gfp* from a repetitive transgene in the hypodermis. Wild-type animals that express *gfp* alone in the hypodermis (*Ex[Pnas-9::gfp]*) from extrachromosomal repetitive DNA (array) were fed dsRNA against hypodermal genes (*dpy-7* or *bli-1*, green). The fractions of animals either with or without the arrays that showed silencing (fraction silenced) were determined. (D) Silencing of *unc-22* and *unc-54* can be inhibited by the expression of *DsRed* from a repetitive transgene in body-wall muscles. Wild-type animals expressing *DsRed* in the body-wall muscle (*Ex[Pmyo-3::DsRed]*) from extrachromosomal repetitive DNA (array) were fed dsRNA against body-wall muscle genes (*unc-22* or *unc-54*, magenta). Silencing was determined as in (C). Asterisks indicate $P < 0.01$ (compared to animals without array). (**E**) Expression of RDE-4 from a single-copy transgene within a tissue does not inhibit feeding RNAi in that tissue. *rde-4(-)* animals that express RDE-4 in the hypodermis from a single-copy transgene (*Si[Pnas-9::rde-4(+)]*) or that additionally express *gfp* in the hypodermis (*Ex[Pnas-9::gfp]*) from a repetitive transgene were fed dsRNA against *dpy-7* or *bli-1* and were analyzed as in (C). Asterisks indicate $P < 0.01$ (compared to animals without *Ex[Pnas-9::gfp]*). Error bars indicate 95% confidence intervals (CI), $n > 23$ animals. Also see Supplementary Figures S1 and S2.

was substantially reduced compared to that in wild-type animals in response to feeding RNAi (compare *unc-22* silencing to *unc-54* silencing in Figure 1A. Also see Supplementary Table S1). Similar reduction in silencing was observed in hypodermal cells upon hypodermal rescue of *rde* genes (compare *dpy-7* silencing to *bli-1* silencing in Supplementary Figure S1A. Also see Supplementary Table S1). When a ubiquitously expressed target gene was tested in *rde-4(−); Ex[Pmyo-3::rde-4(+)]* animals, this reduction of silencing was observed only within body-wall muscles despite robust silencing in other tissues (*gfp* silencing in Figure 1B and Supplementary Figure S1B and C). The extent of gene silencing varied based on the specific promoter used (e.g. silencing of *dpy-7* when *wrt-2* promoter was used (Supplementary Figure S1A) was greater than when the *nas-9* promoter was used (Supplementary Figure S1D)). Thus, rescuing *rde-4* or *rde-1* using tissue-specific promoters and repetitive transgenes does not reliably restore tissue-restricted silencing of all genes.

To test if these cases of reduced silencing could be explained by insufficient levels of *rde* expression, we overexpressed RDE-4 in the hypodermis of wild-type animals (*Ex[Pnas-9::rde-4(+)]*) and examined silencing. Feeding RNAi of neither *bli-1* nor *dpy-7* resulted in detectable silencing (Supplementary Figure S1D), suggesting that the observed lack of silencing is not because there was insufficient *rde-4(+)* expression. An alternative possibility is that such lack of silencing for both tested genes could reflect co-suppression (40) of *rde-4* because of *rde-4(+)* expression from a repetitive transgene. However, this hypothesis cannot explain the differential susceptibility of *bli-1* and *dpy-7* that was observed when *rde-4(+)* was expressed under the *wrt-2* promoter. Alternatively, expression of any repetitive transgene could inhibit RNAi and the extent of inhibition could vary based on the promoter used and on the target gene being tested. To test these possibilities, we expressed *gfp* from a repetitive transgene in the hypodermis (*Ex[Pnas-9::gfp]*) and examined silencing of *bli-1* and of *dpy-7* by feeding RNAi. Surprisingly, no silencing was detected when *gfp* was expressed (Figure 1C), suggesting that inhibition of silencing is the result of expression from a repetitive transgene and not because of *rde-4* expression

or co-suppression. Similar inhibition of silencing of *unc-54*, *unc-22*, and *gfp* was also observed in body-wall muscles when we expressed *DsRed* from repetitive transgenes in body-wall muscles (Figure 1D, Supplementary Figure S2). Together, our results suggest that expression from repetitive transgenes in a tissue can interfere with silencing by ingested dsRNA within that tissue.

One explanation of these results could be that repetitive transgenes produce dsRNAs (41,42) that compete with ingested dsRNA for engaging the gene silencing machinery within a cell. Such competition between pathways is the reason silencing by feeding RNAi can be enhanced in animals that lack genes required solely for the processing of endogenous dsRNA (43,44, reviewed in 45). Consistent with this hypothesis, we found that loss of factors required for endogenous dsRNA production (the RdRP *rrf-3* or the endonuclease *eri-1*) but not loss of downstream Argonaute proteins (the primary Argonaute *ergo-1* or the secondary Argonaute *nrde-3*) overcame the inhibition of feeding RNAi (Supplementary Figure S3A, right). Because RRF-3 and ERI-1 are not required for the production of dsRNA from repetitive transgenes (46), these results suggest that silencing by feeding RNAi in the presence of expression from a repetitive transgene could be enabled by loss of dsRNA production at endogenous loci (see Supplementary Figure S9 in 47). While these results are consistent with competition between ingested dsRNA and dsRNA from repetitive transgenes, other underlying mechanisms are also possible (see Supplementary Discussion).

Certain genes appear to be more susceptible to inhibition by expression from repetitive transgenes. For example, *unc-54* was more susceptible than *unc-22* (Figure 1A) and *bli-1* was more susceptible than *dpy-7* (Supplementary Figure S1A). While the basis for these differences is unclear, we found silencing of *bli-1* and *unc-54* but not of *unc-22* showed a dependence on the secondary Argonaute NRDE-3 (Supplementary Figure S3B). Consistent with a role for the nuclear RNAi pathway in silencing these genes, we found that *bli-1* silencing by feeding RNAi also depended on components that act downstream of NRDE-3 (21,48) (Supplementary Figure S3C). This dependence on the nuclear RNAi pathway was also observed when *bli-1* was targeted for silencing by dsRNA expressed in neurons (Supplementary Figure S3D), suggesting that irrespective of the source of the dsRNA, NRDE-3 is required for silencing *bli-1*. Additional experiments are needed to establish mechanistic links, if any, between *nrde-3*-dependence and inhibition of RNAi by expression from repetitive transgenes.

Taken together, our analyses predict that the use of a single-copy transgene should eliminate the inhibition observed and enable silencing by RNAi. Accordingly, using a single-copy transgene to express *rde-4(+)* in the hypodermis (*Si[Pnas-9::rde-4(+)]*) enabled potent silencing of both *dpy-7* and *bli-1* by feeding RNAi (Figure 1E, left). Furthermore, this silencing could be inhibited by additionally expressing *Ex[Pnas-9::gfp]* (Figure 1E, right). Thus, expression of any repetitive transgene in a tissue can inhibit silencing of some genes within that tissue and using a single-copy transgene can avoid this problem.

Using repetitive transgenes to rescue *rde-4* in one somatic tissue can support RNAi within other somatic tissues

When repetitive transgenes were used to express the dsRNA-binding protein RDE-4 in body-wall muscles of *rde-4(−)* animals, silencing of genes that function in other somatic tissues was observed upon feeding RNAi (23). In contrast, when repetitive transgenes were used to express the Argonaute protein RDE-1 in body-wall muscles, silencing was restricted to body-wall muscles in *rde-1(−)* animals (23,49). These results were used to infer the possible intercellular movement of short dsRNAs generated downstream of RDE-4 but upstream of RDE-1. To test if this observation extended to other tissues (intestine, hypodermis, and neurons), we similarly used repetitive transgenes to perform tissue-specific rescues of *rde-1* and *rde-4*, and assessed silencing of genes expressed in somatic tissues (Figure 2A, Supplementary Table S1). In all cases, silencing by feeding RNAi was observed only in one RNAi-sensitive somatic tissue when RDE-1 was expressed in that somatic tissue (Figure 2A, top). In contrast, silencing was observed in all tested somatic tissues when RDE-4 was expressed in any one somatic tissue (Figure 2A, bottom). This silencing in *rde-4(−)* soma was also observed when a ubiquitously expressed gene (*Pgtbp-1::gtbp-1::gfp*) was targeted for silencing in *rde-4(−); Ex[Pmyo-3::rde-4(+)]* animals (Figure 2B). Together, these results are consistent with the interpretation that short dsRNAs are transported between somatic cells when long dsRNA is processed in one somatic tissue by RDE-4. Alternatively, it is formally possible that the RDE-4 protein or mRNA is transported between somatic tissues.

Rescue of *rde-4* in a somatic tissue from repetitive transgenes does not cause detectable silencing in the germline

If short dsRNAs are exported from a somatic tissue into the pseudocoelomic fluid, then they could be imported and used for silencing in all tissues, including the germline. Therefore, we tested if expression of RDE-4 in a somatic tissue (body-wall muscles, intestine, hypodermis or neurons) using repetitive transgenes was sufficient to enable silencing of genes expressed in the germline (*pos-1*, *par-1* or *par-2*) (See Supplementary Table S1). In contrast to the soma, no silencing was detectable within the germline in any case (Figure 2A). This lack of silencing in the germline was also observed when a ubiquitously expressed gene (*Pgtbp-1::gtbp-1::gfp*) was targeted for silencing in *rde-4(-); Ex[Pmyo-3::rde-4(+)]* animals (Figure 2B). These results suggest that the germline does not accumulate sufficient levels of short dsRNAs for gene silencing. Alternatively, all tested repetitive transgenes that express *rde-4(+)* could be broadly expressed within somatic tissues but not within the germline, which is known to have powerful mechanisms that silence repetitive transgenes (50). Such misexpression could be sufficient to explain the gene silencing observed for *rde-4* rescues but not for *rde-1* rescues despite both rescues using the same promoter if low levels of RDE-4 but not RDE-1 are sufficient for function.

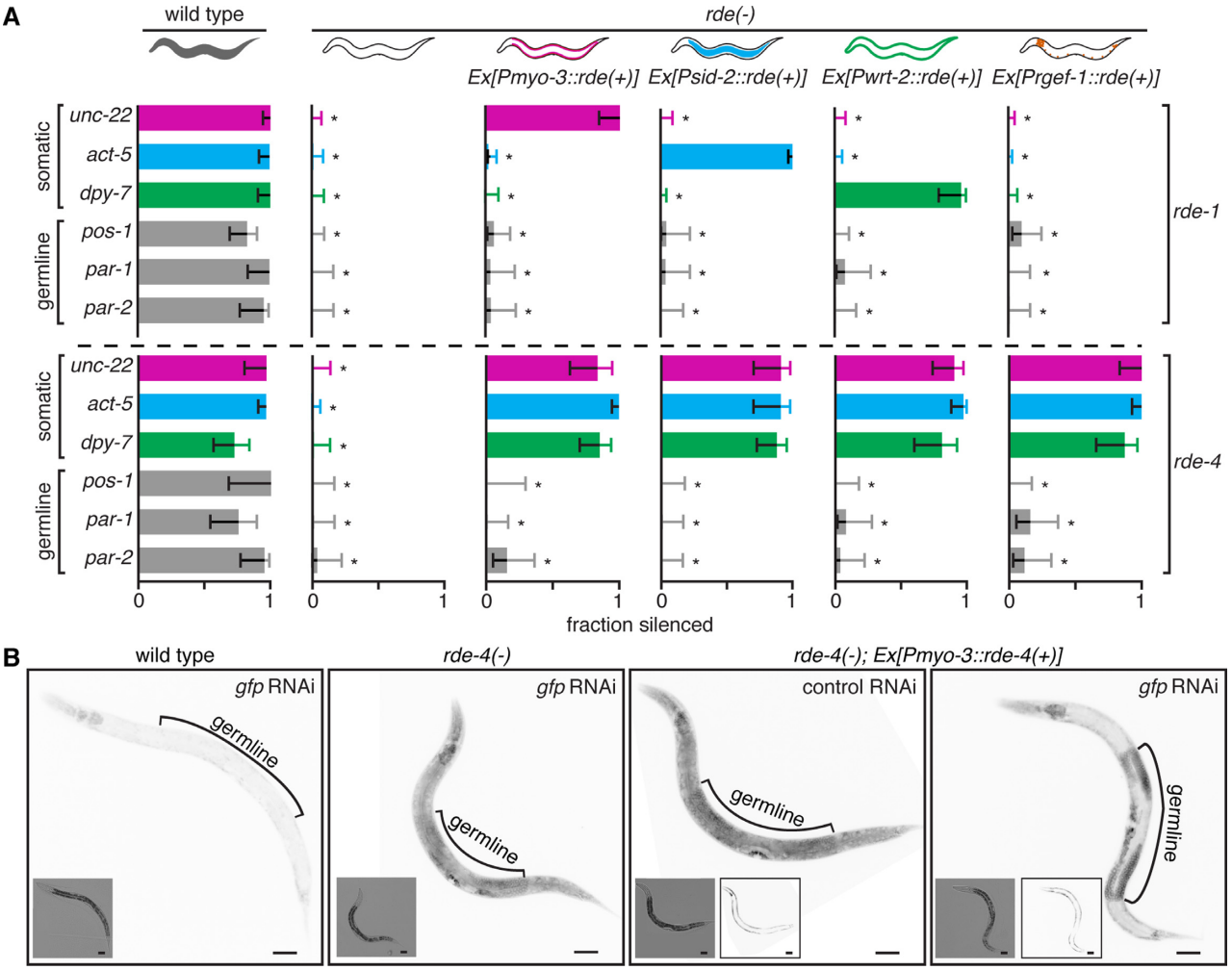

Figure 2. Tissue-specific rescues of RDE-4 from repetitive transgenes can enable silencing of genes in non-rescued somatic tissues. (**A**) Tissue-specific expression of RDE-4 but not RDE-1 from repetitive transgenes enables silencing of endogenous genes that function in mutant somatic tissues but not in mutant germline. Wild-type animals (gray), mutant animals (*rde-1(−)* or *rde-4(−)*, white), and mutant animals with tissue-specific rescues (colors within worms) of *rde-1* or *rde-4* were fed dsRNA against genes expressed in somatic tissues (the body-wall muscles (*unc-22*, magenta), intestine (*act-5*, blue), hypodermis (*dpy-7*, green)), or in the germline (*pos-1*, *par-1*, or *par-2*, gray) and the fractions of animals that showed silencing (fraction silenced) were determined. Wild-type genes (*rde-1* or *rde-4*) were expressed in the body-wall muscles (*Ex[Pmyo-3::rde(+)]*, magenta), in the intestine (*Ex[Psid-2::rde(+)]*, blue), in the hypodermis (*Ex[Pwrt-2::rde(+)]*, green), or in neurons (*Ex[Prgef-1::rde(+)]*, orange). Error bars indicate 95% CI and $n > 24$ animals. Also see Supplementary Table S1. Asterisks indicate $P < 0.01$ (compared to wild-type animals). (**B**) Tissue-specific rescue of *rde-4* enables silencing of *gfp* in *rde-4(−)* somatic tissue but not in *rde-4(−)* germline. Representative images of animals with *gfp* expression (black) in all somatic and germline cells (*Pgtbp-1::gtbp-1::gfp*) in a wild-type background, *rde-4(−)* background, or *rde-4(−)* background with *rde-4(+)* expressed in body-wall muscles (*Ex[Pmyo-3::rde-4(+)]*) that were fed control RNAi or *gfp* RNAi are shown. In all cases, 50 L4-staged animals were analysed and the majority phenotype (wild-type—100%, *rde-4(−)*—100%, *rde-4(−);Ex[Pmyo-3::rde-4(+)* control RNAi—100%, and *rde-4(−);Ex[Pmyo-3::rde-4(+) gfp* RNAi—68%) is shown. Insets are brightfield images and scale bar = 50 μm.

Spatial patterns of silencing vary with the promoters that drive tissue-specific rescue from repetitive transgenes

If transport of short dsRNAs, rather than misexpression in somatic tissues, is the reason for the observed silencing, then silencing could be more common in cells that are near the source of dsRNA. However, when an animal is only scored as silenced versus not silenced in response to feeding RNAi, such qualitative differences between animals are overlooked. Examination of such differences requires a target gene whose silencing in subsets of cells can be discerned in each animal. We found that null mutants of the hypodermal gene *bli-1* result in a fluid-filled sac (blister) along the entire worm (Figure 3A, Supplementary Figure S4A and B; (25)), and that blisters that form upon feeding RNAi in wild-type animals had a different pattern (Figure 3B). Specifically, upon *bli-1* feeding RNAi, anterior sections of the worm tended to be more susceptible to silencing when compared to posterior sections (Figure 3C, Supplementary Figure S4C, and see methods), resulting in a stereotyped pattern of relative susceptibility to blister formation (Figure 3C, bottom and Supplementary Figure S4D). This bias in the tendency to form blisters likely reflects the graded uptake of dsRNA from the anterior to the posterior in the intestine upon feeding RNAi. These characteristics of blister formation as a result of *bli-1* silencing enable examination of

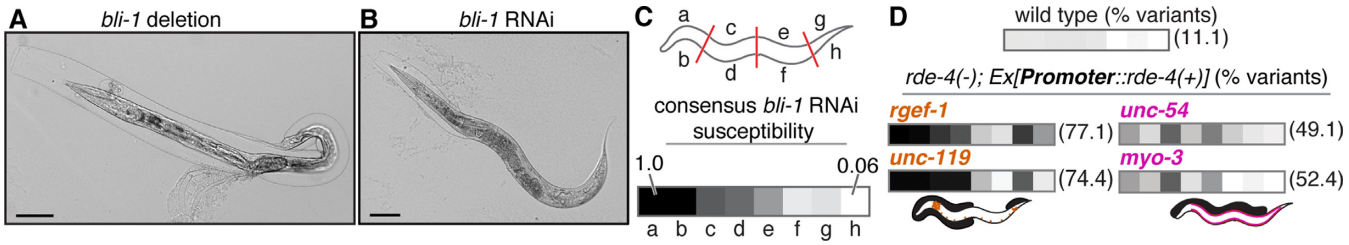

Figure 3. Repetitive transgenes expressing RDE-4 from different promoters enable different spatial patterns of *bli-1* silencing in *rde-4(−)* hypodermis. (**A**) A null mutation in *bli-1* results in blisters that cover the entire body. A representative image of a *bli-1* null mutant animal generated by Cas9-based genome editing is shown. Scale bar = 50 μm. (**B**) Feeding RNAi of *bli-1* in wild-type animals results in blisters that cover part of the body. A representative image of a wild-type animal fed dsRNA against *bli-1* (*bli-1* RNAi). Scale bar = 50 μm. (**C**) Susceptibility to *bli-1* feeding RNAi decreases from anterior to posterior hypodermis in wild-type animals. (top) Schematic of hypodermal sections (a through h) scored for blister formation. (bottom) Consensus relative frequency of blister formation in each hypodermal section of wild-type animals upon *bli-1* feeding RNAi. The frequency ranged from 1.0 (black, a) to 0.06 (∼white, h). (**D**) The patterns of blisters that result from silencing of *bli-1* in *rde-4(−)* hypodermis are different from the consensus blister pattern. Aggregate patterns of blister formation among animals that deviate from the consensus susceptibility order (consensus *bli-1* RNAi susceptibility in (C)) for each strain (variant susceptibility, % variants) are shown. All strains being compared were normalized together (black, section with highest frequency of blisters in all strains; white, section with the lowest frequency of blisters in all strains). Schematic of worms indicate locations of variant blisters (thick black shading) on worms with *rde-4(+)* expressed in neurons (orange) or in body-wall muscles (magenta). Also see Supplementary Figure S4.

qualitative differences, if any, between silencing in wild-type animals and in animals with tissue-specific *rde-4* rescue.

To systematically analyze such differences, we culled animals with a pattern of blister formation that differed from a consensus blister susceptibility pattern observed in most wild-type animals (see Materials and Methods). We found that unlike in wild-type animals, in animals with tissue-specific rescue of *rde-4* from repetitive transgenes, patterns of blisters that differed from the reference pattern were common (Figure 3D and Supplementary Figure S4E–H). Furthermore, the pattern of variant blister susceptibility differed depending on the promoter used for tissue-specific rescue (*rgef-1* or *unc-119* for neurons and *myo-3* or *unc-54* for body-wall muscles) (Figure 3D and Supplementary Figure S4G and H). Intriguingly, animals with different promoters that drive expression in the same tissue showed similar patterns of silencing. While these results could provide a case for the transport of short dsRNAs to nearby cells from the tissue where long dsRNA is processed by RDE-4, similar results would also be obtained if misexpression from each tissue-specific promoter occurred in subsets of hypodermal cells.

Using repetitive transgenes to express RDE-4 in one tissue and SID-1 in another tissue fails to provide support for the movement of short dsRNAs between cells

Consideration of the following observations on repetitive transgenes leaves open the possibility that misexpression of *rde-4(+)* in somatic tissues explains the silencing in all somatic tissues despite the use of tissue-specific promoters. First, the formation of a repetitive transgene can generate rearrangements that result in novel promoter elements (42,51,52) that could lead to misexpression despite the use of well-characterized tissue-specific promoters. In support of this possibility, animals expressing *gfp* in all somatic tissues (*Peft-3::gfp*) showed some silencing in non-muscle cells even in *rde-1(−); Ex[Pmyo-3::rde-1(+)]* animals (Supplementary Figure S5). Second, repetitive transgenes can be selectively silenced within the germline (50,53), potentially explaining the observed lack of silencing in the germline of animals with tissue-specific *rde-4* rescue (Figure 2). Third, because repetitive transgenes could be expressed at low levels within the germline (e.g. heat shock promoter (54)), and because feeding RNAi in all somatic tissues was observed in *rde-4(−)* progeny of heterozygous parents (30) we hypothesize that inherited RDE-4 from misexpression in the germline of parents could be responsible for feeding RNAi in progeny. While such silencing enabled by inherited RDE-4 was not detectable in most cases, it was detectable when *unc-22* silencing was examined in *rde-4(-)* progeny of animals with *rde-4* rescued using the *myo-3* promoter (Supplementary Figure S6).

We attempted to obtain additional evidence for the movement of short dsRNAs derived from ingested dsRNA. Tissues that express high levels of SID-1 act as sinks for dsRNA (7) and the entry of both long dsRNA and short dsRNAs generated upon processing by RDE-4 are expected to require SID-1. Therefore, if no silencing occurs when processing by RDE-4 is restricted to one tissue but import through SID-1 (9,55,56) is restricted to another tissue, it would provide strong support for the transport of short dsRNAs processed from ingested dsRNAs between tissues. We generated *sid-1(−); rde-4(−)* animals in which *rde-4* was rescued using the neuronal promoter *Prgef-1* and *sid-1* was rescued using the body-wall muscle promoter *Pmyo-3* (Figure 4A). We observed silencing in these animals upon feeding RNAi of the body-wall muscle gene *unc-54* (Figure 4B). Consistent with the restriction of SID-1-dependent dsRNA entry into body-wall muscle cells, we did not detect any silencing of the hypodermal gene *bli-1* upon feeding RNAi. However, these results leave open several possibilities. If misexpression occurred, then these results are consistent with either *rde-4(+)* misexpression in muscle cells or *sid-1(+)* misexpression in neurons but not the hypodermis. Misexpression of *rde-4(+)* implies that the direct entry of long dsRNA into each cell is sufficient to explain the observed silencing. Selective misexpression of *sid-1(+)* implies that entry of long dsRNA into neurons and subsequent production of short dsRNAs in neurons followed by their entry into the body-wall muscles caused silencing. Finally, even if there was no misexpression, the interpretation of results from this experiment

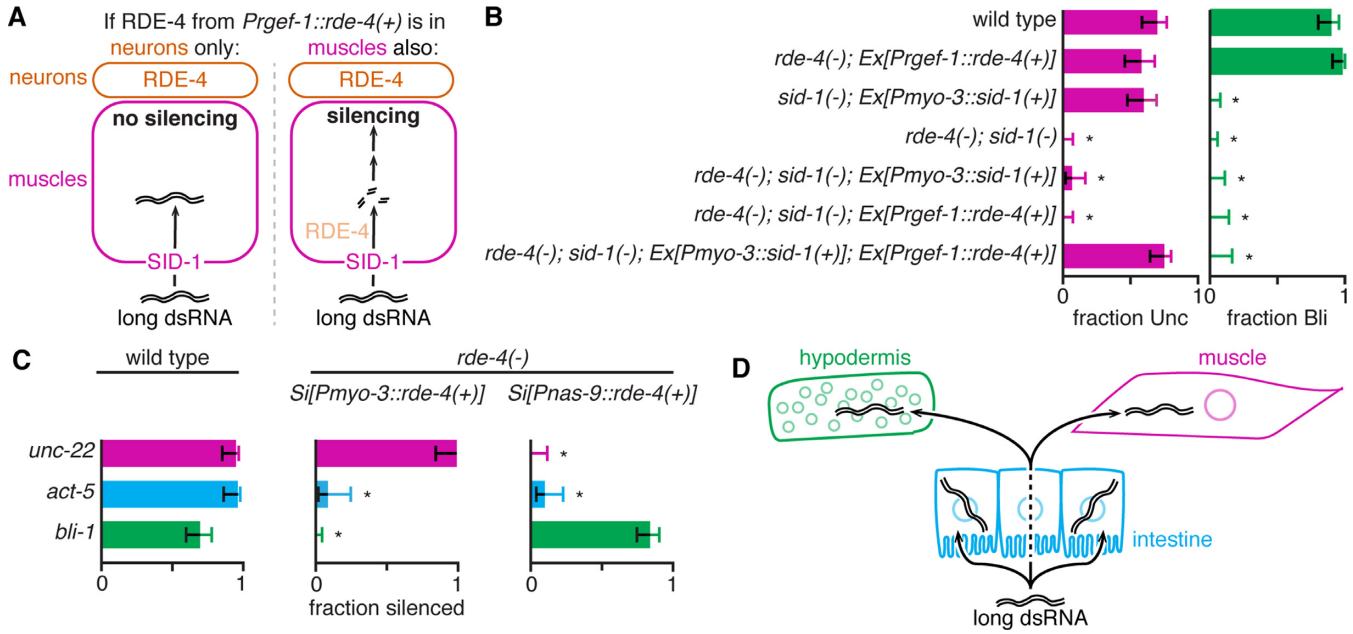

Figure 4. Expression of RDE-4 within a tissue can restrict silencing by feeding RNAi to that tissue. (**A**) Expected outcomes of test to distinguish movement of short dsRNAs from other possibilities (e.g. misexpression of RDE-4) in animals with tissue-specific rescue of RDE-4 from a repetitive transgene. (Left) If RDE-4 is expressed only in neurons from the *rgef-1* promoter (*Prgef-1::rde-4(+)*) in a *rde-4(−); sid-1(−); Ex[Pmyo-3::sid-1(+)]* background no silencing is expected in muscles, which can import dsRNA (have SID-1) but not process dsRNA (lack RDE-4). (Right) If RDE-4 is expressed in neurons and in muscles from the *rgef-1* promoter (*Prgef-1::rde-4(+)*) in a *rde-4(-); sid-1(−); Ex[Pmyo-3::sid-1(+)]* background silencing can occur in muscles, which can import dsRNA (have SID-1) and process dsRNA (have RDE-4). See text for additional possibilities. (**B**) RDE-4 could be present in muscles when expressed under the *rgef-1* promoter from a repetitive transgene. Wild-type animals, mutant animals (*rde-4(−)*, *sid-1(−)*, or *rde-4(-);sid-1(−)*) or mutant animals with *rde-4(+)* and/or *sid-1(+)* expressed from repetitive transgenes (as schematized in (A)) were fed dsRNA against a gene expressed in the body-wall muscle (*unc-54*) or in the hypodermis (*bli-1*) and the fractions of animals that showed silencing (fraction Unc or fraction Bli) were determined. Error bars indicate 95% CI, $n > 24$ animals and asterisks indicate $P < 0.01$ (compared to wild-type animals). (**C**) Expression of RDE-4 from a single-copy transgene reveals a requirement for RDE-4 within a tissue for silencing by ingested dsRNA in that tissue. Wild-type animals or *rde-4(−)* animals that express RDE-4 from a single-copy transgene in the body-wall muscle (*Si[Pmyo-3::rde-4(+)]*) or in the hypodermis (*Si[Pnas-9::rde-4(+)]*) were fed dsRNA against *unc-22* (magenta), *act-5* (blue) or *bli-1* (green). Silencing was scored as in Figure 2A. Error bars indicate 95% CI, $n > 24$ animals and asterisks indicate $P < 0.01$ (compared to wild-type animals). Also see Supplementary Figure S7. (**D**) Model: Silencing by entry of ingested long dsRNA into each tissue could account for tissue-restricted silencing in animals with single-copy rescue of RDE-4. See text for details.

could be complicated by unexpected interactions between the two repetitive transgenes used (also see Supplementary discussion).

Single-copy transgenes can restrict RDE-4 activity to specific somatic tissues

Because the formation of a repetitive transgene can generate rearrangements (42,51,52) that complicate interpretations, we used single-copy transgenes to re-examine if the expression of RDE-4 in one tissue could enable silencing in other somatic tissues. We expressed RDE-4 from a single-copy transgene using the *myo-3* promoter (*Si[Pmyo-3::rde-4(+)]*) or the *nas-9* promoter (*Si[Pnas-9::rde-4(+)]*) in *rde-4(−)* animals. In both cases, silencing was restricted to the intended tissue with RDE-4 expression (Figure 4C). These results suggest that upon expressing RDE-4 using a single-copy transgene short dsRNAs made in one tissue are not sufficient to cause silencing in another tissue. Furthermore, these results also do not support the possibility that RDE-4 protein or mRNA moves between cells, suggesting that RDE-4 can provide restricted function within the cells where it is made (Figure 4D). Thus the apparent intercellular transport of short dsRNAs seen in experiments using repetitive transgenes could be simply because of high levels of expression achieved using such transgenes or may have required some features of repetitive transgenes (see supplementary discussion, (57,58)).

DISCUSSION

We have shown that expression from repetitive transgenes within a tissue can selectively inhibit feeding RNAi in that tissue (Figure 1) and have generated single-copy transgenes that can restrict RDE-4 activity to specific tissues (Figure 4).

Efficiency of RNAi could be regulated by expression from repetitive DNA

Our discovery that expression from repetitive DNA within a tissue can interfere with silencing by feeding RNAi within that tissue (Figure 1) could impact studies that use RNAi to infer the function of a gene. For example, RNAi of a gene in strains that express fluorescent reporters within a tissue from a repetitive transgene could be specifically inhibited in that tissue. While many RNAi screens have successfully identified novel components of biological processes using strains that express repetitive transgenes (eg. (59–61)), it may be possible to identify additional components if our

results are also taken into account in the design of future screens.

The efficiency of feeding RNAi differs between tissues and is a concern for the application of feeding RNAi to combat animal pests (4). For example, in *C. elegans*, genes expressed in neurons are relatively refractory to silencing by feeding RNAi (noted in (62)). One reason for such reduced silencing could be that neurons have high levels of expression from endogenous repetitive DNA. Consistent with this possibility, both silencing in tissues with expression from repetitive DNA (Supplementary Figure S3A) and silencing in neurons are enhanced upon loss of the exonuclease ERI-1 (63) or the RdRP RRF-3 (64). Similarly, tissue-specific expression from endogenous repetitive DNA could explain differential sensitivity to RNAi among insect tissues.

Silencing by feeding RNAi can be restricted to a tissue with RDE-4

The ability of dsRNA expressed in one cell to cause SID-1-dependent silencing in other cells (6,9) revealed that dsRNA or its derivatives can be exported from cells, and be imported into cells, in *C. elegans*. Observations with repetitive transgenes presented here (Figures 2 and 3) and in previous studies (23,24) are consistent with a 'transit' model for feeding RNAi where dsRNA first enters the cytosol of a cell, is subsequently processed within the cytosol of that cell, and finally exported for silencing in distant cells. However, results from strains with single-copy rescues of *rde-4* that we have generated suggest that in some cases cell-autonomous processing of long dsRNA by RDE-4 could be sufficient to account for silencing upon feeding RNAi (Figure 4). Specifically, because dsRNA can be transported across intestinal cells without entry into the cytosol (6–8) and reach the pseudocoelomic fluid that bathes all *C. elegans* tissues, the direct entry of dsRNA into all cells that show silencing and subsequent processing by RDE-4 in each cell could be sufficient to explain the systemic response to feeding RNAi in these strains.

Taken together with recent studies, our results suggest that several characteristics of feeding RNAi in many insects and parasitic nematodes (see 4,65,66 for reviews) could be similar to those in *C. elegans*. First, long dsRNA (>60 bp) is preferentially ingested (67) and realization of this preference was crucial for developing plastid expression as an effective strategy to deliver long dsRNA into crop pests (1). Second, dsRNA can be detected in intestinal cells and in internal tissues upon feeding RNAi (68). Third, with the exception of dipteran insects, most invertebrates have homologs of the dsRNA importer SID-1 (10). Finally, silencing initiated by feeding RNAi can persist for multiple generations (69). These similarities suggest that insights gleaned using the tractable animal model *C. elegans* are likely to be applicable to many invertebrates, including agronomically important insect and nematode pests.

AVAILABILITY

All strains are available upon request.

SUPPLEMENTARY DATA

Supplementary Data are available at NAR Online.

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