A forward genetic screen reveals essential and non-essential RNAi factors in *Paramecium tetraurelia*

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ABSTRACT

In most eukaryotes, small RNA-mediated gene silencing pathways form complex interacting networks. In the ciliate *Paramecium tetraurelia*, at least two RNA interference (RNAi) mechanisms coexist, involving distinct but overlapping sets of protein factors and producing different types of short interfering RNAs (siRNAs). One is specifically triggered by high-copy transgenes, and the other by feeding cells with double-stranded RNA (dsRNA)-producing bacteria. In this study, we designed a forward genetic screen for mutants deficient in dsRNA-induced silencing, and a powerful method to identify the relevant mutations by whole-genome sequencing. We present a set of 47 mutant alleles for five genes, revealing two previously unknown RNAi factors: a novel *Paramecium*-specific protein (Pds1) and a Cid1-like nucleotidyl transferase. Analyses of allelic diversity distinguish non-essential and essential genes and suggest that the screen is saturated for non-essential, single-copy genes. We show that non-essential genes are specifically involved in dsRNA-induced RNAi while essential ones are also involved in transgene-induced RNAi. One of the latter, the RNA-dependent RNA polymerase RDR2, is further shown to be required for all known types of siRNAs, as well as for sexual reproduction. These results open the way for the dissection of the genetic complexity, interconnection, mechanisms and natural functions of RNAi pathways in *P. tetraurelia*.

INTRODUCTION

Small RNA pathways have greatly diversified in function during the evolution of eukaryotes (1,2) but generally rely on the production of 21–28 nt short RNAs (sRNAs) from single- or double-stranded RNA precursors. Once loaded onto Argonaute-containing effector complexes, sRNAs can target complementary transcripts and silence homologous sequences by diverse mechanisms, such as posttranscriptional or transcriptional inhibition or even DNA elimination (1,3). In RNA interference (RNAi), short interfering RNAs (siRNAs) are produced by endonucleases of the Dicer family from long double-stranded RNA (dsRNA) (4,5). The initial dsRNA triggers may be products of RNA-dependent RNA polymerases (RdRPs), enzymes that also act at downstream steps in some organisms to amplify the silencing response through the synthesis of secondary siRNAs (6,7).

Different small RNA pathways often coexist in a single organism, involving distinct types of sRNAs. In plants, animals and fungi, miRNAs and endogenous siRNAs regulate the expression of somatic and germline-specific genes, and specific endogenous siRNAs control transposons in somatic cells (2,3). Various organisms can also respond to environmental dsRNA, for instance some nematode and insect species that process dsRNA ingested within food bacteria or entering cells by endocytosis (8). Exogenously induced RNAi pathways were shown in several species to mediate antiviral defense (9–12). Despite the diversity of trigger molecules and sRNA responses, the different pathways involved can be interconnected by sharing some protein factors (3).

In ciliates, a phylum characterized by nuclear dimorphism, a meioisis-specific class of small RNAs (scRNAs) targets the elimination of specific sequences during development of the somatic micronucleus (MAC) from the germline micronucleus (MIC) (13–17). As a result, the MAC genome is cleared of transposable elements and derived single-copy internal eliminated sequences (IESs) (18; for review see 19). In addition, siRNA pathways are active throughout the life cycle, as shown in *Tetrahymena thermophila* (20,21) and *Paramecium tetraurelia* (15,22,23).
In *P. tetraurelia*, experimental induction of gene silencing revealed that different trigger molecules recruit different RNAi factors and produce different classes of sRNAs. It was first discovered that transformation of the MAC with high-copy transgenes lacking the 3' UTR results in aberrant transcripts on both strands (22,24) and silencing of homologous endogenous genes (24,25). Transgene-induced silencing requires the Dicer protein Dcr1 (15), the Piwi proteins Ptiwi13 and Ptiwi14 (23), and the RdRP Rdr3 (22). Although Rdr3 appears to be catalytically inactive, it was implicated in the regulation of surface antigen gene expression and in the accumulation of endogenous siRNAs of unknown function (22). Transgene-induced siRNAs are 5' monophosphate and modified at the 3' end, presumably by 2'-O-methylation (22).

A second pathway, which allows *Paramecium* to process exogenous dsRNA, was found to involve a distinct but overlapping set of RNAi factors. Feeding cells with *Escherichia coli* bacteria engineered to produce dsRNA, equivalent to the ‘feeding’ technique in *Caenorhabditis elegans* (26,27), induces silencing of endogenous genes homologous to the dsRNA (28). In this pathway, Dcr1 (15) and the two RdRPs Rdr1 and Rdr2 (22) are required for accumulation of two types of siRNAs: primary siRNAs, predominantly 23 nt in length and produced from the original dsRNA trigger, and secondary siRNAs, presumably produced from the target mRNA (15). In contrast to the primer-independent, 5' triphosphate secondary siRNAs produced by direct RdRP activity in *C. elegans* (29–31), *P. tetraurelia* dsRNA-induced siRNAs are 5' monophosphate. Three Piwi proteins (Ptiwi13, Ptiwi12 and Ptiwi15) appear to be involved in this pathway (23).

The MIC genome of *P. tetraurelia* has undergone at least three whole genome duplications (WGDs), resulting in ∼40,000 genes in the MAC genome, which is responsible for all gene expression. 68% of genes still retain their duplicates from the most recent WGD (WGD1), and the conservation of protein sequences suggests that most duplicate pairs are functionally redundant (32). WGDs may explain in part the large number of genes encoding core RNAi factors: eight Dicer- and Dicer-like genes (including one WGD1 duplicate pair), 17 Piwi genes (two unpublished) (six WGD1 pairs) and four RdRP genes (no WGD1 duplicate). Only a few of these genes have been assigned any function, making *P. tetraurelia* a very interesting model to study the genetic and mechanistic complexity of small RNA-mediated pathways. Due to the lack of an established method to transform the MIC genome, however, reverse genetics approaches have been restricted to RNAi thus far, providing only limited possibilities for the functional analysis of genes involved in RNAi. Targeting a gene involved in its own silencing (recursive RNAi (33)) is a self-defeating process which cannot be completed, and is not conclusive when no effect is observed.

In this study, we describe the outcome of a forward genetic screen for mutants deficient in dsRNA-induced silencing, based on lethal dsRNA ‘feeding’, which was expected to yield loss-of-function alleles for genes that do not have functionally redundant paralogs. A combined strategy, including the development of a powerful method to identify mutations by whole-genome resequencing, allowed us to characterize 71 RNAi-deficient mutants and yielded a total of 47 alleles for three known and two previously unknown genes. Analyses of allelic diversity revealed a non-essential dsRNA processing machinery but provided evidence for an essential RNAi function during the life cycle, and suggested that the screen is saturated for non-essential, single-copy genes. The dsRNA- and transgene-induced RNAi pathways are further shown to share essential protein factors.

### MATERIALS AND METHODS

#### *Paramecium* strains, cultivation and genetic analyses

Mutagenesis and other experiments were carried out with wild-type strain 51 of *P. tetraurelia*, mating type E. RNAi mutants were back-crossed either with strain 51 or with strains carrying the nd7–1 mutation (34) as a genetic marker (after three rounds of back-cross into strain 51). Unless otherwise specified, cells were grown at 27°C in wheat grass powder (Pines International Co., Lawrence, KS, USA) suspension medium bacterized with *Klebsiella pneumoniae* the day before use and supplemented with 0.8 µg/ml β-sitosterol. Genetic analyses of mutants were carried out according to standard procedures (35). F1 phenotypes were recorded for each of the two karyonides resulting from the two exconjugants of at least two conjugating pairs, and at least 30 F2 clones resulting from autogamy of F1 heterozygotes were studied.

#### Random mutagenesis and screening for RNAi-deficient mutants

UV mutagenesis (254 nm) was carried out on several independent batches of 200,000 pre-autogamous cells, according to Cohen (36), with a modified dose of 650 J/m². Cells were allowed to undergo two divisions before autogamy was triggered by starvation to make MIC mutations homozygous in the MICs and MACs of progeny. Three batches in which autogamy reached >90% of the cells, and showing a post-autogamous survival rate of 75–80%, were selected for screening. To isolate mutants deficient in dsRNA-induced RNAi, post-autogamous cells were first fed with three volumes of *Klebsiella* medium (~1–2 vegetative divisions) and starved again to eliminate fragments of the old MAC (monitored by DAPI staining), which would otherwise complement mutations in the new MAC. Cells were then washed and transferred to three volumes of *N. sitosterol*. Each clone was replicated for storage and further experiments. RNAi deficiency was verified by feeding each clone with dsRNAs from the unrelated genes *ND7* and *ND169* (34,37) both required for trichocyst discharge, a quantitative phenotype that allows to distinguish full and partial RNAi deficiencies (see below).

#### Induction of RNAi and phenotypic analyses

Production of dsRNA in *E. coli* strain HT115DE3, feeding to *Paramecium* cells, transgene-induced silencing of *ND169* and monitoring of trichocyst discharge phenotypes were
tire open reading frame and flanking sequences, including the endogenous promoter, cloned into the pUC18 plasmid vector. For details of all plasmid constructs see Supplementary Table S1. For re-sequencing of known genes, coding sequences including flanking regions were amplified by polymerase chain reaction using a proof-reading polymerase (Phusion® High Fidelity, Thermo Fisher Scientific, Waltham, MA, USA). Products were purified by phenol extraction and polyethylene glycol 8000 precipitation (7.5% final) and sequenced with marginal and internal primers (oligonucleotide sequences on request).

**Purification of MAC DNA, whole-genome sequencing and identification of SNPs**

RNAi mutants carrying an unknown mutation were backcrossed to wild type and one karyonide of each exconjugant F1 clone was brought to F2 by autogamy. Thirty F2 clones were isolated and tested for RNAi deficiency by feeding of *ND169* or *NSF* dsRNA. Mutant clones showing silencing deficiency were raised to large cultures. Immediately prior to DNA extraction, vegetative mutant cultures of both mating types were fused and MAC DNA was extracted from this pool (∼3 Mio cells) according to the protocol used for DNA purification from developing MACs (18). Briefly, cells were concentrated, washed, supplemented with three volumes of lysis buffer (0.25 M sucrose, 10 mM MgCl₂, 10 mM Tris pH 6.8, 0.2% Nonidet P-40) and lysed at 4°C with a Potter–Elvehjem homogenizer, allowing cell—but not MAC lysis. MACs were collected and purified from bacteria and cell debris by ultracentrifugation through a 2.1 M sucrose cushion. Recovered MACs were lysed and DNA was extracted as described (39). 5 μg of RNaseA-treated genomic DNA were used for library construction. DNA was sequenced by single-end (75 bp read length) or paired-end (50 or 100 bp read length) strategies using Illumina GAII and HiSeq next-generation sequencers (for overview of sequencing output for each mutant F2 pool, see Supplementary Table S2). The reads were mapped to the reference *P. tetraurelia* strain 51 genome (18, 32) using the Burrows-Wheeler Alignment tool (BWA) (40) with default parameters and the mapping indexed with SAMtools (41). Custom Perl scripts and the SAMtools mpileup function were used to identify positions where at least 80% of the calls differed from the reference genome, at positions with at least 10-X coverage and less than 300-X coverage. The list of single nucleotide polymorphisms (SNPs) was then curated to identify candidate mutations for experimental validation.

**Small RNA analysis by northern blot**

Total RNA extraction and small RNA northern blots were carried out as described (22). As previously, two adjacent 50 nt sense oligonucleotide probes matching to the dsRNA region were used to detect *ND169* siRNAs, as most of the produced siRNAs are antisense to the target transcript. Similarly, endogenous cluster22 siRNAs were detected with two adjacent 50 nt oligonucleotide probes, complementary to the top strand (relative to transcription of the 5' marginal open reading frame).

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**Plasmid constructs and re-sequencing of known genes**

To induce silencing of *NSF* and of *ND169* by dsRNA feeding or by transgene (pTI-) plasmid constructs produced previously (22, 28) were used. For silencing of *PDS1* and *CID1*-like genes, fragments of the coding region were cloned into the plasmid L4440 and dsRNA was synthesized in *E. coli* HT115 DE3 (Supplementary Figure S1). Complementation of mutants was achieved by microinjection of the end-
RESULTS

Lethal dsRNA feeding allows isolation of Mendelian mutants fully or partially deficient in RNAi

To isolate mutants of the dsRNA-induced silencing pathway, we first treated wild-type cells with UV light to induce random mutations in the MIC genome. Cell populations were then allowed to undergo autogamy, a self-fertilization sexual process in which only one of the parental MIC alleles is retained, and made homozygous in the MICs and MACs of progeny (Figure 1A). Cultures were then screened by feeding them an *E. coli* strain producing dsRNA homologous to *NSF*, an essential gene involved in exocytosis and membrane traffic (42,43). *NSF* dsRNA feeding rapidly kills the wild-type (28), so that only mutant cells deficient in dsRNA-induced RNAi would be able to survive. One hundred and fifty surviving cells were isolated, and the RNAi-deficient phenotypes were confirmed by dsRNA feeding targeting different genes (*NSF*, *ND7* and *ND169*, two single-copy, unrelated genes involved in the exocytosis of secretory granules called trichocysts (34,37); for details, see below, Figure 7B). After sorting out non-viable, false positive or strongly hypomorphic clones, a set of 79 RNAi-deficient cell lines was established (detailed outcome of the screen in Supplementary Table S3).

Seventy-one lines were further analyzed. Of these, 64 were fully deficient in RNAi, showing normal growth rates in *NSF* feeding medium and wild-type levels of trichocyst discharge upon *ND7* and *ND169* feeding. Seven lines were only partially compromised in RNAi, suggesting hypomorphic mutations. We reasoned that feeding cells with a smaller amount of dsRNA would be more sensitive to partial defects in the RNAi machinery. Consistently, diluting the silencing trigger (e.g. *ND169* dsRNA bacteria in a 1:5 ratio with bacteria producing dsRNA from *ICL7a*, which encodes a non-essential centrin (25)) revealed stronger phenotypes in hypomorphic mutants, comparable to the full RNAi deficiency, although this still led to complete silencing in wild-type cells.
Back-crossing selected lines to the wild type confirmed that RNAi phenotypes were due to Mendelian and recessive loss-of-function mutations: F1 heterozygotes showed a wild-type phenotype, and F2 homozygotes obtained by autogamy of the F1s showed the expected 1:1 segregation of wild-type and mutant phenotypes upon dsRNA feeding (Supplementary Table S4A). Although these segregation analyses would not be sufficient to dissociate closely linked mutations, the total number of UV-induced mutations in the genome was later estimated to be ~30 per irradiated cell on average after autogamy (Supplementary Table S5A; for mutations, see Supplementary Table S5B), indicating that in most cell lines the RNAi deficiency is due to a single mutation.

The mutant screen reveals known and new genes involved in dsRNA-induced RNAi

To identify the mutations in RNAi-deficient lines, we developed a whole-genome sequencing procedure to distinguish the mutation causing the phenotype from other, irrelevant UV-induced mutations, after a single round of backcross to the wild type (Figure 1B). Briefly, F1 heterozygotes were taken through autogamy, and sets of ~30 homoygous F2 clones were tested for their capacity to respond to dsRNA feeding. Deep sequencing of MAC DNA from pools of ≥15 independent RNAi-deficient F2s will identify the RNAi mutation as being present in 100% of reads, while other, unlinked mutations show up only in 50% of reads on average. This strategy was used in combination with complementation tests and resequencing of genes previously implicated in the pathway to identify candidate mutations in all 71 lines. 45 of them contained mutations in previously identified genes involved in RNAi (Table 1), confirming the role of these genes in dsRNA-induced RNAi.

The remaining 26 lines were found to carry mutations in either of two new genes, for which one allele was initially identified by the whole-genome sequencing procedure. The missense mutation 1.8 (Figure 2; Supplementary Figure S2) resulted in an RNAi-deficient phenotype. We conclude that CIR1 and PDS1 are required for dsRNA-induced silencing.

All sequenced species of the Paramecium genus, allowing identification of conserved amino acids (Figure 3A; Supplementary Figure S4). Deduced from its specificity for dsRNA-induced RNAi (see below), we named this gene PDS1. These candidate mutations were shown to co-segregate with the RNAi-deficient phenotype in each of the F2 clones included in the genome-sequencing pools, and microinjection of the cloned wild-type genes into MAC of mutant cells rescued the RNAi deficiency (data not shown). In addition, depletion of these proteins by recursive RNAi experiments (see below, Figure 7D) resulted in an RNAi-deficient phenotype. We conclude that CIR1 and PDS1 are required for dsRNA-induced silencing.

The RNAi response to dsRNA from food bacteria is not essential for viability

Our screen for RNAi-deficient mutants was unlikely to reveal genes with functionally redundant WGD1 ohnologs, unless disruption of one copy led to a dosage effect. For single-copy genes, we could expect null alleles of non-essential genes and hypomorphic alleles of essential genes. Unambiguous null alleles were here defined as those containing nonsense mutations or frameshifts resulting in premature stop codons, due to indels or mutations in intron splice sites (48), except in cases where the best part of the protein is conserved and where there is experimental evidence for a partial RNAi deficiency. An allele was categorized as hypomorphic if the RNAi deficient phenotype was only partial and/or dsRNA feeding-induced siRNAs were reduced, but still detectable on northern blots. Indeed, the diversity of alleles obtained for each of the genes hit appeared to reflect their importance for cellular viability (Fig-
Table 1. Mutants obtained in a screen for dsRNA-induced RNAi deficiency

<table>
<thead>
<tr>
<th>Mutants</th>
<th>Alleles</th>
<th>Function</th>
<th>Homologs</th>
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<tr>
<td>RDR1</td>
<td>41</td>
<td>RdRP</td>
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<tr>
<td>RDR2</td>
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<tr>
<td>DCR1</td>
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<tr>
<td>CID1*</td>
<td>16</td>
<td>nucleotidyl transferase</td>
<td>Tt, At, Ce, Sp, Dm, Mn, Hs</td>
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<tr>
<td>PDS1*</td>
<td>10</td>
<td>unknown</td>
<td>Paramecium</td>
</tr>
</tbody>
</table>

The first alleles to be discovered for the two new genes (*) CID1 and PDS1 were identified by whole-genome sequencing of pooled F2 clones (see Figure 1).

Figure 4. Abolished siRNA accumulation in RNAi mutants. (A) Northern blot analysis of ND169 siRNAs revealed failure or strong reduction of accumulation of exogenously induced siRNAs in all mutants, consistent with previous findings from depletion of Dcr1, Rdr1 and Rdr2 by RNAi (15,22,23). This suggests a role of these RNAi factors upstream or within siRNA biosynthesis or stabilization. It is of note that silencing efficiencies can vary from one dsRNA feeding experiment to another, possibly due to contamination by traces of the standard food bacterium Klebsiella (showing partial Ampicillin resistance) which overgrows dsRNA-producing E. coli. This may explain differences in the total level of dsRNA-induced siRNAs in different wild-type cultures. The ND169 probe corresponds to a 100 bp region of the dsRNA and is sense oriented, as antisense siRNAs represent the predominant fraction of siRNAs in the dsRNA region (22). (B) Detection of endogenous siRNAs from an intergenic region of scaffold 22 (cluster22) revealed that rdr2 mutants are unable to accumulate these siRNAs. The probe is complementary to the predominant fraction of siRNAs (top strand) of this region. The lower panel shows hybridization to glutamine tRNA as a loading control.

Figure 5. Saturation of the screen for non-essential single-copy genes involved in dsRNA-induced RNAi. Gene sizes of non-essential RNAi factors (A) plotted against the number of identified mutant alleles obtained (B). Extrapolation by linear regression determined the mutation frequency to 1 in 172 bp of coding sequence.

Figure 2): 41 rdr1 mutants were found, representing 26 different alleles. Among these were eight putative null alleles (e.g. rdr1–5.28 or rdr1–5.7). Missense alleles were mostly non-conservative substitutions in conserved residues, two of which in the putative catalytic core region (rdr1–1.4 D1021N and rdr1–3.16 D1021Y) (49–51) (Supplementary Table S6). Similarly, the 10 alleles obtained for PDS1 included null alleles, suggesting that this gene, like RDR1, is not required for viability. Although no unambiguous null allele was found among the seven cid1 alleles, some of the mutations changed highly conserved amino acids (cid1–3.4 D68N and cid1–1.6 D70N) shown to be required for uridylyl transferase activity (47,52). In all putative null mutants tested, a complete loss of dsRNA-induced siRNAs was observed on northern blots (Figure 4A and Supplementary Figure S6). RNAi-deficient rdr1, pds1 and cid1 null mutants are fully viable throughout the life cycle (vegetative growth and sexual events), and no other phenotypic anomaly was observed. Furthermore, the F2 (Supplementary Table S4B) and F3 generations of an rdr1–3.1/cid1–1.8 double homozygote showed normal vegetative growth in standard conditions and at high temperature (34°C). We conclude that the capacity to synthesize siRNAs from dsRNA ingested with food is not essential in laboratory conditions.

Nevertheless, the dsRNA-induced RNAi pathway appears to be highly conserved in the Paramecium genus, since tblastn searches identified at least one copy of the RDR1, CID1 and PDS1 genes in all sequenced species of the P. aurelia complex, as well as in P. multimicronucleatum and P. caudatum (Supplementary Figure S5). Essential factors playing a role in this pathway in P. tetraurelia (see below) are also highly conserved (not shown). This suggests that the pathway may fulfill an important function required for long-term survival of these species in their natural environment.
The screen is saturated for non-essential single-copy genes

The large numbers of alleles obtained for three non-essential, single-copy genes suggest that the screen is saturated for this category of genes. For RDR1, PDS1 and CID1, the number of alleles is roughly proportional to the length of the gene; the relationship indicates that, with the number of mutant lines analyzed here, one mutation was obtained for every 172 bp of coding sequence on average (Figure 5). Thus, there may not be any other non-essential, single-copy gene involved in the dsRNA-induced RNAi pathway.

Essential genes may be involved in dsRNA-induced RNAi

In contrast to RDR1, CID1 and PDS1, only two alleles of RDR2 were identified. rdr2–3.7 is an amino acid substitution (E859K) within a less conserved region of the RdRP domain, and rdr2–1.24 retains an intragenic IES (MIC-specific) located downstream of the conserved RdRP domain region, due to a T-to-A mutation in one of the TA boundaries that are required for excision during macronuclear development (53) (Supplementary Figure S8B). Both alleles are hypomorphic, as indicated by partial RNAi deficiency and by partial loss of siRNAs upon dsRNA feeding (Figure 4A and Supplementary Figure S6). The greater reduction in siRNA levels in rdr2–1.24 was paralleled by a weaker silencing of the ND169 target using dilute dsRNA trigger (not shown). Similarly, for DCR1 only two hypomorphic missense alleles were identified. Interestingly, the mutations are located within the N-terminal helicase (dcr1–5.5 E87K) or helicase C domains (dcr1–5.27 H622D). Dcr1–5.5 shows a stronger RNAi deficiency than dcr1–5.27, judging from both phenotypes and siRNA levels (Figure 4A and Supplementary Figure S6). These findings suggest that the helicase and helicase C domains play a role in the biosynthesis of dsRNA-derived siRNAs, unlike the helicase domain of C. elegans’ Dcr-1, which is only required for a subset of endo-siRNAs (54). The fact that RDR2 and DCR1 are only represented in the mutant collection by a small number of hypomorphic alleles suggests that they are essential genes for which null alleles would lead to lethality. Thus, RNAi may fulfill essential functions in P. tetraurelia.

Another, putatively essential nucleotidyl transferase is involved in dsRNA-induced silencing

Whereas no other PDS1-related gene could be identified in the P. tetraurelia genome, 22 Cid1-like non-canonical poly(A)-polymerases were found (Supplementary Table S7). According to phylogenetic analyses (Supplementary Figure S2), five of them, including Cid1, fall in a common branch with Rdn1 and Rdn2 of T. thermophila (Figure 6A). None of them is an ohnolog to another. To analyze their function in dsRNA-induced RNAi, we used a recursive RNAi approach, i.e. we silenced each of them by dsRNA feeding, simultaneously with ND169 as a reporter (22). Apart from CIDI, targeting CID2 also prevented silencing of ND169 by dsRNA feeding (Figure 6B). This was correlated with a reduced accumulation of ND169 siRNAs (Figure 6C). It is of note that silencing of a gene involved in its own silencing has only limited efficiency, explaining the partial impairment of ND169 silencing and siRNA accumulation. The results indicate that, like CID1, CID2 is involved in dsRNA-induced RNAi. Although it is a single-copy gene, our screen did not yield a mutant allele, raising the hypothesis that CID2 is essential for viability.
Putatively essential RNAi factors are shared with the transgene-induced silencing pathway

Although transgene-induced siRNAs are biochemically different from dsRNA-induced siRNAs, Dcr1 and Ptiwi13 are shared between these two pathways. Like DCR1, PTIWI13 is possibly an essential gene, as mutants were not obtained in our screen, probably due to inefficient recovery of hypomorphic mutants. Rdr3, a factor specifically involved in transgene-induced silencing, also seems to be essential, as its silencing results in a reduced vegetative growth rate (22). To test whether the newly identified genes are also involved in transgene-induced silencing, we induced silencing of ND169 by injecting a transgene construct (pTI-) truncated at the 3' end of the coding sequence (Figure 7A), as previously described (22). Candidate genes were then silenced in injected clones by dsRNA, and the ND169 silencing phenotype was monitored (recursive RNAi, as described previously (22)). To increase the sensitivity of the silencing response to depletion of potentially involved factors, we used injected clones that showed only moderate ND169 silencing efficiency (tric+/−) (Figure 7B). Cells showed a strong decrease in silencing efficiency upon CID2 silencing and, as expected, upon RDR3 and PTIWI13 silencing (Figure 7C).

Surprisingly, using this experimental setup we were also able to detect a significant reduction of transgene-induced silencing efficiency when RDR2 was co-silenced, which had not been observed previously on strongly silenced clones using the same RDR2 silencing construct (22). In contrast, targeting CID1, PDS1 or RDR1 did not result in reduced silencing of the ND169 transgene, although dsRNA-induced RNAi was inhibited in control experiments (Figure 7D). This suggests that these genes are not involved in the transgene-induced RNAi pathway. The involvement of the putative essential gene DCR1 in silencing induced by the ND169 transgene construct (as well as ND169 dsRNA) could also be confirmed (not shown), as previously shown for a promotor-less transgene (15). We conclude that RDR1, CID1 and PDS1 are specific for the dsRNA-induced pathway, while genes hypothesized to be essential according to the above criteria (RDR2, CID2, DCR1, PTIWI13) are involved in both dsRNA- and transgene-induced RNAi pathways.
Rdr2 mutants are compromised in endogenous siRNA accumulation and show reduced viability after sexual reproduction

Factors of the transgene-induced RNAi pathway may have essential functions in any phase of the life cycle, including vegetative growth, sexual events and development. We checked whether mutants are impaired in the accumulation of a cluster of endogenous siRNAs of unknown function (cluster22) which are produced throughout the life cycle from an intergenic locus (15). Northern blot analysis revealed that their accumulation was completely suppressed in the rdr2–1.24 mutant (Figure 4B). Signal quantification (Supplementary Figure S6) showed only a slight, if any, reduction for the rdr2–3.7 allele, consistent with its strongly hypomorphic nature. Tested mutations in RDR1, CID1 and PDS1 had little or no effect. Surprisingly, dcr1 mutants showed only slight (if any) reduction in cluster22 siRNA levels as well, as also observed after targeting DCR1 by dsRNA-induced RNAi (not shown). Similarly, targeting CID2 did not result in any detectable reduction (Figure 6C), though this may be due to inefficient depletion by recursive RNAi. Despite the molecular phenotype evidenced here, the rdr2 mutants did not differ from the wild type in viability or growth rate during vegetative growth.

In contrast, rdr2 mutants showed a range of defects during sexual reproduction. Survival of homozygotes for the stronger allele rdr2–1.24 was found to be affected by a long starvation period (≥3 days), but only when this immediately followed autogamy, and not when the same starvation was experienced by vegetative clones that had already undergone 7–8 divisions (Supplementary Figure S7). New MAC development nevertheless appeared to be cytologically normal, as judged from DAPI staining, and the reason for this post-autogamous defect remains unknown.

Conjugation was also impaired in both rdr2 mutants. After a cross to the wild type, the F1 clones derived from one or both parents were unviable for 35% (18/51) of conjugating pairs and the frequency of proper formation of heterozygous new MACs seemed reduced (Supplementary Figure S8A, Table S4A). The most striking effect was that autogamy of the viable, heterozygous F1s most often (9/10; P = 0.01) gave rise to F2 progeny in which close to 100% of clones were unviable or showed regeneration of the F1 MAC (Supplementary Figure S8, Table S4A). This was observed for F1s deriving from both parents and suggests a dominant-negative maternal effect of the heterozygous F1 MAC with incomplete penetrance, because the rare cases where the F2 progeny survived gave the expected 1:1 segregation of rdr2 and wild-type F2 homoyzogotes, and both types of clones survived equally well. The reason why post-autogamous lethality is much stronger for heterozygotes than for rdr2 homozygotes, and the nature of the cellular process affected, remain unclear. Testing excision of some IESs in post-autogamous, newly developed MACs (rdr2–1.24) did not reveal any DNA rearrangement defect for maternally controlled (scnRNA-dependent) or non-maternally controlled IESs (data not shown). Nevertheless, our observations indicate that RDR2 has essential functions during sexual reproduction. A similar phenotype was not observed in any other RNAi mutant.

DISCUSSION

A whole-genome sequencing method to identify mutations potentiates a powerful screen

In this study, we have used a powerful and straightforward mutagenesis screen to identify genes required for the RNAi response to dsRNA feeding in *P. tetraurelia*: dsRNA homologous to the essential gene NSF efficiently kills the wild type, and can be fed to large populations of cells. Mutational studies have long benefited from the easy genetics and short generation time of this organism (55–59), but the identification of mutations relied on functional complementation and sib-selection sorting of an indexed library (60,61), a time-consuming method ill-suited for large mutant collections. We have designed an efficient procedure to identify phenotype-causing mutations after a single round of back-cross to the wild type. Other, unlinked mutations segregate independently among F2 homozygotes, so that whole-genome sequencing of pools of phenotypically mutant and wild-type F2s will show the RNAi mutation in 100% and 0% of reads, respectively, while most irrelevant mutations should be present in 50% of reads from both
Mutations causing full or partial RNAi deficiency identify known and new genes

Mutations were identified in 71 RNAi-deficient cell lines, yielding a total of 47 different alleles for only five genes (Figure 8). Three of them (RDR1, RDR2 and DCR1) were previously implicated in dsRNA-induced RNAi on the basis of recursive RNAi experiments. The two new genes included the nucleotidyl transferase CID1 and the Paramecium-specific gene PDS1. Among the 47 alleles, 14 were isolated more than once; in three cases the same alleles were recovered from different mutagenized cultures and thus originated from different mutation events. This suggests that our analysis provides a rather exhaustive view of the genes and alleles that can be identified by the experimental scheme used.

The latter allowed recovery of some hypomorphic alleles (seven out of 47) causing only partial RNAi deficiencies, as confirmed by functional tests using dilute dsRNA trigger. The rather low frequency of such alleles may be due to the ~7 vegetative divisions allowed for fully resistant mutants in NSF dsRNA feeding medium, before cell isolation: although hypomorphic mutants were able to survive that step, their growth rate was probably greatly reduced. The experimental scheme would thus have to be modified to yield a higher frequency of hypomorphic alleles, the only ones that can be obtained for essential genes.

The dsRNA- and transgene-induced RNAi pathways share essential genes

Analysis of the diversity of alleles obtained for each of these five genes showed that they fall in two groups. For RDR1, CID1 and PDS1, the many alleles recovered included unambiguous null ones such as nonsense mutations and/or non-conservative changes of conserved residues, which all abolished accumulation of siRNAs upon dsRNA feeding. Although these mutants were completely deficient in the silencing response to dsRNA, they did not show any other phenotype at any stage of the life cycle, indicating that the capacity to synthesize siRNAs from dsRNA ingested as food is not required for short-term viability in laboratory conditions. In contrast, only two alleles were obtained for each of DCR1 and RDR2 and these were hypomorphic, only partially impairing the silencing response and siRNA accumulation. This strongly suggests that these are essential genes in which null mutations would be lethal at some stage of the life cycle. In particular, these results establish a clear distinction between RDR1 and RDR2, two RdRPs which could not be distinguished in previous recursive RNAi tests applied during the vegetative phase (22).

Strikingly, these two groups of genes also differ in the specificity of their involvement in RNAi pathways (Figure 8). We confirmed that DCR1 is also required for transgene-induced silencing and showed that the same is true of RDR2, although this had not been seen previously. Here, recursive RNAi tests (by dsRNA feeding) were made more sensitive by using a transformed clone showing only moderate silencing of the ND169 reporter (as proposed in a model for recursive RNAi dynamics (33)). In the same conditions, recursive silencing of RDR1, CID1 and PDS1 did not affect transgene-induced silencing. Thus, the only essential genes uncovered by our screen are those also involved in transgene-induced RNAi. Two more genes likely belong to this group. By testing close paralogs of CID1, we found that CID2 is involved in both pathways, as previously shown for PTWI113. The fact that no mutation was recovered in these genes is consistent with the idea that they are also essential.

A third, presumably non-catalytic RdRP gene previously implicated in transgene-induced silencing, RDR3, is further required for normal vegetative growth rate and accumulation of cluster22 endogenous siRNAs. The latter differ from transgene-induced siRNAs in that they lack a modification of the terminal ribose, and interestingly, were also absent or reduced in the hypomorphic rdr2 mutants. RDR2 thus appears to be required for all known types of siRNAs in Paramecium (Figure 8). However, the wild-type growth rate of the mutants suggests that its putative essential function may not be needed during the vegetative phase.

In contrast to rdr2, no effect was observed in dcr1 mutants or CID2 knock down cells on cluster22 siRNAs. Although we cannot completely exclude a false-negative result due to the hypomorphic nature of the dcr1 alleles and the inefficient knock down of CID2, this may indicate that these endogenous siRNAs are not dependent on all components of the transgene-induced pathway and are thus produced by a different pathway (Figure 8). This is supported by the observation that they do not carry a 3’ modification.

RDR2 is involved in sexual reproduction

The crosses of rdr2 mutants to the wild type revealed defects in sexual reproduction. F1s showed a high lethality rate and occasional failure of the formation of heterozygous MACs. However, it is unclear whether this was significant in F1s deriving from the wild-type parent (which would point to defects in pre-zygotic stages such as karyogamy). More striking was the frequent unviability of most or all F2 clones produced by autogamy of some—though not all—viable heterozygotes, regardless of F2 genotype or F1 parental origin. The stochastic nature of the effect raises the possibility that it is due to defects in maintenance of the germline in mutant homozygotes, such as defects in chromosome segregation during MIC mitosis, which would have no impact on vegetative growth of mutants, but would lead...
to aneuploidy in the F1 and therefore lethality in the F2. Such defects have been observed for instance in RNAi mutants in *S. pombe*, including the RdRP Rdp1 (64,65) and the nucleotidylic transferase Cid12 (66), which are both essential for pericentromeric heterochromatin formation (45,67). Stochastic loss of MIC chromosomes during vegetative growth would make each mutant clone potentially unique in its ability to foster viable F2 progeny.

The genetic complexity of the dsRNA-induced RNAi pathway

Previous studies have probed the genetic complexity of RNAi pathways (68–72). In *C. elegans*, a genome-wide RNAi screen for genes involved in silencing induced by RNA hairpin expression identified 90 genes, 54 of which are essential for viability (69). In our study, the screen RNAi expression identified 90 genes, 54 of which still have their WGD1 duplicate (32). Such may be the case for essential, single-copy genes, all three of which are specifically involved in dsRNA-induced silencing pathways (Rdf1 and Rdf2 are not conserved in the *P. tetraurelia* genome). The reason why two RdRCs should be required for dsRNA-induced silencing, however, will remain puzzling until their precise functions are identified. They may have distinct roles in the production of primary and secondary siRNAs (15,22). The present work opens the way for an analysis of siRNAs and their precursors in each mutant, which is likely to provide insight into the processing mechanisms.

SUPPLEMENTARY DATA

Supplementary Data are available at NAR Online, including: Supplementary Figures S1–S8 and Supplementary Tables S1–S7 including Supplementary References (79–81).

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REFERENCES


