Molecular dissection of Penelope transposable element regulatory machinery

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ABSTRACT

Penelope-like elements (PLEs) represent a new class of retroelements identified in more than 80 species belonging to at least 10 animal phyla. Penelope isolated from Drosophila virilis is the only known transpositionally active representative of this class. Although the size and structure of the Penelope major transcript has been previously described in both D. virilis and D. melanogaster transgenic strains, the architecture of the Penelope regulatory region remains unknown. In order to determine the localization of presumptive Penelope promoter and enhancer-like elements, segments of the putative Penelope regulatory region were linked to a CAT reporter gene and introduced into D. melanogaster by P-element-mediated transformation. The results obtained using ELISA to measure CAT expression levels and RNA studies, including RT–PCR, suggest that the active Penelope transposon contains an internal promoter similar to the TATA-less promoters of LINEs. The results also suggest that some of the Penelope regulatory sequences control the preferential expression in the ovaries of the adult flies by enhancing expression in the ovary and reducing expression in the carcass. The possible significance of the intron within Penelope for the function and evolution of PLEs, and the effect of Penelope insertions on adjacent genes, are discussed.

INTRODUCTION

Retrotransposons are generally regarded as being of one or other of two classes, either long terminal repeat (LTR) retrotransposons, or non-LTR retrotransposons, also known as LINEs. These classes are distinguished on the basis of their general organization and mode of transposition (1,2). Penelope-like elements (PLEs) do not fit easily into either class, however. Active Penelope elements were originally isolated from Drosophila virilis after hybrid dysgenesis was first described in this species (3,4). This phenomenon is observed when females from strains lacking Penelope are crossed with males carrying multiple active copies (4). Other transposable elements belonging to different classes are mobilized during this form of hybrid dysgenesis but it is the activation of Penelope that is responsible for such cross-mobilization (3,5,6). Penelope elements have been found in all species of the virilis group that have been studied so far. They are probably inactive except in D. virilis itself and have an unusually complex and highly variable organization (3). Database searches and analyses of genomic DNAs have detected PLEs in genomes of crustaceans, echinoderms, fish, amphibians, flatworms, roundworms and rotifers (7–10). These elements code for a protein that represents a fusion between a reverse transcriptase and a GIY-YIG endonuclease (11).

The majority of PLEs in D. virilis and bdelloid rotifers contain introns in different regions of the element, and RT–PCR analysis has confirmed that these can be correctly spliced (8). The ability to retain an intron during transposition, their peculiar structural organization and

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The authors wish it to be known that, in their opinion, the first two authors should be regarded as joint First Authors

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a distinct placement in the phylogeny of RT-containing elements lead us to conclude that the PLE clade is clearly different from both LTR and non-LTR retrotransposons and constitutes a third, and probably ancient, class of eukaryotic retroelements (8,12), which is supported by analysis of the amino acid sequence of the reverse transcriptase encoded by Penelope. This indicates that PLEs form a clade that is distinct from that of both LTR-retrotransposons and non-LTR retrotransposons (8).

The partial-tandem organization characteristic of active copies of Penelope from D. virilis includes ‘pseudo-LTRs’ (Figure 1B) (3,13). These appear to result from tandem insertions of Penelope and have one or two copies of a 34–37-bp repeat sequence (the 34 bp repeat) at their 3’ end. Copies of Penelope without terminal repeats have been found in the genome of D. virilis. These are flanked by a target site duplication and have therefore transposed without pseudo-LTRs, indicating that these are not generated by reverse transcription. This organization is also observed in several copies of Poseidon/Xena PLEs from Tetraodon nigroviridis (14), and in many other PLEs (I.A., unpublished data). The tandemly repeated PLEs that are often observed may be needed to create a functionally active transcriptional unit, in a way mechanistically similar to that described for Drosophila melanogaster HeT-A elements (15). Indeed, the 2947-nt Penelope transcript initiates within the upstream ‘LTR’ (7).

The experiments reported herein have been performed to identify the sequences required for full activity of the promoter, and to identify sequences required for the previously described differential expression of Penelope in the ovaries and carcasses of D. virilis dysgenic hybrids and in D. melanogaster transgenic strains transformed with full-sized Penelope (3,16).

**MATERIALS AND METHODS**

**Fly stocks**

The D. melanogaster strain Df(1), y w 67c23(2) was used as recipient in transformation experiments. D. virilis strain 160 (with about 35 copies of Penelope) and D. virilis strain 9 (lacking active Penelope) were used in the study to get dysgenic hybrids as described (3). Flies were reared on standard resin-sugar-yeast-agar medium containing propionic acid and methylparaben as mold inhibitors.

**Construction of transformation vectors**

pWP-CAT vector containing unique XbaI and BamHI sites upstream of the CAT gene was made by Acc65 I and XhoI digestion of p186W8 (17) and subsequent self-ligation. Promoter fragments were amplified by the polymerase chain reaction (PCR), using the following pairs of primers: PenPr1 up–PenPr850 lo; Pen250 up–PenPr850 lo; PenPr570 up–PenPr850 lo; PenPr1 up–PenPr680 lo; PenPr1 up–PenPr611 lo; PenPr1 up–PenPr487 lo; PenPr1 up–PenPr544 lo; PenPr1 up–PenPr416 lo; PenPr1 up–PenPr369 lo; PenPr1 up–PenPr302 lo. The resulting fragments were digested with XbaI, BamHI and ligated into XbaI/BamHI-cut pWP-CAT, yielding plasmids pPenPr A, pPenPr B, pPenPr C, pPenPr D, pPenPr F, pPenPr M, pPenPr N, pPenPr O, pPenPr P and pPenPr R, respectively (Supplementary Table 1). The intronless promoter fragment was synthesized by PCR using primers PenPr1 up–int lo; int up–PenPr850 lo, followed by PCR assembly with primers PenPr1 up–PenPr850 lo. The resulting fragment was digested with XbaI, BamHI and ligated into XbaI/BamHI-cut pWP-CAT to generate plasmid pPenPr G. The construct PB containing 366 bp of the Penelope regulatory region (interval 352–718 in clone p6) was cloned into pCaSpeR-AUG-β-gal as described previously (18).

**P-element-mediated transformation**

The DNA used for transformation of D. melanogaster was purified by QIAprep Spin Miniprep Kit (Qiagen) and used for embryo injection as described previously (19). Transposase activity was provided by the helper plasmid Turbo Δ2-3 (20) and the recipient embryos were from the D. melanogaster Df(1), y w 67c23(2) strain. Adults emerging from the injected embryos were crossed with Df(1), y w 67c23(2) virgin of the opposite sex, and the eye colour of their progeny was examined. Transformed lines homozygous for the transgene were established by full sibling mating. The presence of homozygous intact transgene copies in each line was confirmed by PCR and Southern blotting. In most cases, the number and exact localization of the inserts were checked by in situ hybridization as described (21). Each transformed line was routinely maintained en masse in 5–6 vials initiated with 20–30 flies per vial.

**β-Galactosidase staining**

X-gal staining of ovaries was performed essentially as described (22). Ovaries were dissected in PBS and fixed for 10 min in fixing solution (1% glutaraldehyde in PBS). They were washed in PBS for 3 x 10 min, and then incubated for 1 day in staining solution [(10 mM Na2/Na3PO4 pH 7.2; 150 mM NaCl; 1 mM MgCl2; 3.1 mM potassium ferricyanide; 3.1 mM potassium ferrocyanide; 0.5 mM Xgal (5-bromo-4-chloro-3-indolyl-β-D-galactopyranoside)]
at 37°C. The X-gal was added shortly before incubation from a 10% stock solution in DMSO. After staining, the ovaries were washed in PBS and mounted in 50% glycerol solution prior to histological analysis.

**RNA preparations and analysis**

Total RNA was extracted from carcasses and ovaries of 2–5-days-old females of each independent transgenic strain using TriZol Reagent according to protocol provided by Invitrogen. The integrity of each RNA preparation was checked on ethidium bromide-stained 1% agarose/MOPS-formaldehyde gels. A SMART RACE cDNA amplification kit (Clontech) was used for cDNA synthesis and amplification of 5'-ends of cDNAs, as described (23). The sequence of the oligonucleotides used for amplification of 5'-ends of *Penelope*-containing cDNAs, PenRev1, PenRev2 and PenRev3 and of the SMART PCR, ‘heel-carrier’ and ‘heel-specific primers are given in Supplementary Table 1. Semi-quantitative RT–PCR was used to reveal *Penelope*-CAT transcripts in total RNA from carcasses ovaries of transformants with constructs N or P, and to study tissue-specific slicing. SMART amplification templates served as the samples for specific amplification using primers IstPenDir10 and PenRev2 (Supplementary Data). Samples were normalized using primers, β-actin *D. melanogaster* D1 and β-actin *D. melanogaster* R1, for *D. melanogaster* β-actin.

Each oligonucleotide was purified through polyacrylamide gel before use. PCR reactions were performed in a 25 μl reaction mixture and contained 1× Advantage KlenTaq Polymerase Mix with provided buffer (Clontech), 200 μM dNTPs, 0.15 μM of gene-specific primers, 0.02 μM of ‘heel-carrier’ oligo and 0.15 μM of ‘heel-specific’ oligo. PCR was carried out using MJ Research PTC-200 DNA Thermal Cycler for 25–30 cycles (95°C for 7 s; 63°C for 20 s; 72°C for 2 min) depending on the transcript’s abundance. Reactions without reverse transcriptase have been carried out for all templates to exclude DNA contamination.

**Cloning and sequencing**

All standard DNA procedures were performed in accordance with published laboratory protocols (24). PCR fragments obtained in the course of 5’-RACE were cloned in the pGEM T-easy vector (Promega) and sequenced. DNA sequence was determined using the Amersham Biosciences Megabase 1000 automated sequencer and FS dye terminator chemistry.

**Drosophila CAT assays**

One hundred and twenty females of each independent strain (2–5 days old) were used to isolate ovaries and carcasses. The tissues were homogenized in 0.25 M Tris–HCl, pH 7.8 and passed through five freeze–thaw cycles. The extract was then spun in a microcentrifuge to pellet cell debris and denatured proteins, and the supernatant was used as CAT extract (17). The concentration of protein in the supernatant was determined by the BCA Protein Assay Kit (Pierce). CAT assays were performed according to the instruction manual of CAT ELISA kit (Roche). The levels of CAT expression were expressed as pgCAT/μg of total protein estimated.

In our experiments, the original strain *Df(1), y w^67C2M^2* used for obtaining transgenic strains always exhibited significant and varying background levels of CAT expression. The background was consistently higher in the carcasses than in the ovaries. Therefore, we routinely took the level of CAT expression in the original strain as a unit for each individual ELISA and calculated the CAT levels in the transgenic strains assuming that *Df(1), y w^67C2M^2* CAT expression equals 1 U. Thus, the formula is: the expression level observed in the transgenic strain divided by the background CAT level (observed in control recipient strain). This approach enabled us to compare the CAT levels measured in ovaries and carcasses and the results obtained in independent ELISA experiments.

**Bioinformatics**

Promoter prediction was carried out with the BDGP Neural Network Promoter Prediction server with eukaryotic settings (http://www.fruitfly.org/seq_tools/promoter.html; (25), and McPromoter MM:II with Drosophila settings (http://genes.mit.edu/promoterMMII.html; (26). Alignments were generated by ClustalW (http://www.ebi.ac.uk/clustalw/) and presented in the BoxShade format (http://www.ch.embnet.org/software/BOX_form.html).

**RESULTS**

**The promoter region of Penelope**

**Reporter gene analysis.** We have previously shown that the p6 copy of *D. virilis Penelope* (Figure 1B) is functional in *D. melanogaster* and can actively transpose in transgenic strains (16). Moreover, the full-sized *Penelope* transcript is restricted to the ovaries of *D. melanogaster* strains transformed with an active *Penelope* copy, as is the case with dysgenic females of *D. virilis*. In order to show that the *Penelope* 5’ regulatory sequences are able to drive the expression of a reporter gene in the cells of the two species studied, we performed preliminary experiments which have shown that nucleotides 1–850 of this element (Figures 1B and 3B) are sufficient to drive expression of the chloramphenicol acetyl transferase (CAT) reporter gene upon transfection into *D. virilis* tissue culture cells (data not shown). Furthermore, we observed *lacZ* expression in the egg cyst and in the cytoplasm of the oocyte at different stages of oogenesis (Figure 2A–D) in the ovaries of transgenic *D. melanogaster* flies carrying the construct ‘PB’ (see Materials and Methods section) containing nucleotides 352–718 of *Penelope* linked to a *lacZ* reporter gene (11).

We have previously identified the first nucleotide of *Penelope* transcripts as being predominantly at position 371 (Figure 3B) (8). Since other non-LTR retrotransposons in Drosophila are transcribed from internal promoters (17,27,28) it is likely that the same is true of *Penelope*. We have analysed the first 850 nucleotides of the p6 *Penelope* element (Figure 1B) using two programs previously applied to Drosophila promoters, ‘McPromoter’ (26), which combines a generalized hidden
RNA analysis. We have complemented our measurements of CAT proteins levels by RNA analysis of transcripts from some of the transgenic lines in Figure 3A to distinguish effects on CAT expression due to changes in transcription or RNA stability from those due to changes in translation and to check that transcription originated from the Penelope promoter rather than from adjacent chromosomal sequences. RT–PCR and 5′ RACE, with the primers indicated in the Materials and Methods section and Supplementary Data, was used to analyse RNA from ovaries and carcass of strains carrying constructs N or P, each of which contains sequences from the Penelope promoter region. Canonical Penelope transcripts are normally detected in ovaries in both D. virilis dysgenic hybrids and in D. melanogaster strains transfected with active copies of Penelope (30,31). We could not detect such transcripts in ovaries of strains with constructs N or P, although they were present in carcass RNA. (Figure 5), suggesting that the lack of CAT expression in ovaries was the result of an effect on transcription.

In the case of strain P-25, which is exceptional in showing CAT expression in ovaries (Figure 3A), 5′ RACE revealed a long ovarian transcript that had initiated within the Cct1 (phosphocholine cytidylyltransferase 1) gene (Supplementary Figure 1), which we have confirmed, by in situ hybridization, is the site of insertion of the P construct in this strain (data not shown). This gene is active in ovaries and we conclude that expression of the P construct in this line results from read-through transcription from the Cct1 gene, and have excluded it from further analysis.

We have previously shown that all active copies of Penelope isolated from D. virilis contain a copy of the 34-bp repeat at the beginning of the ORF and there is often a second copy at the 3′ end. Moreover, structurally similar copies with 34-bp repeats flanking the Penelope ORF in direct orientation have been found in two other species of the virilis group (13). In D. virilis, the most frequently observed structure of a Penelope element contains a partial-tandem repeat of two Penelope ORFs flanked with inverted terminal repeats (Figure 1C) and may have evolved from a single Penelope ORF flanked by 34-bp repeats (Figure 1A). Our computer analysis of the promoter regions suggested that this sequence may be part of a strong promoter. We have tested this using transgenic lines carrying construct C which has nucleotides 570–850 linked to the CAT gene, and have excluded it from further analysis.

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### Tissue-specific regulation of Penelope expression

The data in Figure 3A and B indicate that the sequence in between positions 611 and 680 controls tissue-specific expression from the presumptive Penelope promoter. Strains containing constructs A, B, C or D each express...
CAT in the ovary whereas strains carrying constructs F, N, O and P that lack this sequence do not. This suggests that the sequence between 611 and 680 enhances expression in the ovary. Strains carrying constructs F, N, O, P that contain the Penelope promoter and sequences up to position 611, show high CAT expression in the carcass but none in the ovary, whereas strains with constructs containing the promoter and nucleotides 611 to 680 show reduced CAT protein in the carcass. This suggests that the sequence between positions 611 and 680 also down-regulate expression in the carcass.

Previous studies have shown that the minority of Penelope transcripts in both D. virilis dysgenic hybrids and transgenic D. melanogaster contain the intron that lies between nucleotides 416 and 491 while a majority of transcripts lack the intron (7), but as yet there is no indication as to whether the distribution of these RNAs differs between tissues. We have addressed this question by RT–PCR using primers that allow detection of both the spliced and unspliced forms, and RNA extracted from carcass or ovary. Both spliced and unspliced forms were detected in RNA from each tissue of both dysgenic D. virilis females and females of the Penelope containing D. virilis strain 160, and from each tissue of flies containing construct A or G (Figure 6A, B and Supplementary Figure 2).

Transgenic flies containing construct G show virtually no CAT activity in either carcass or ovary extracts.

Figure 3. (A) Histogram illustrating CAT levels in the ovaries and in carcasses of the transgenic strains. The schematic structure of all constructs used is depicted at the bottom. (B) Presumptive structure of the Penelope regulatory region with positions of promoter and other regulatory sequences indicated. Letters denote the constructs used, and CAT expression in ovaries (ov) and carcasses (ca) is illustrated by + or −. Figures at the bottom indicate the boundaries of constructs within the Penelope 5′ region (interval 1–850 bp). The dotted grey line shows promoter prediction scores from the NNPP program (from 0 to 1, indicated on the right). McPromoter scores yielded a qualitatively similar picture with different ratios of peak intensities (data not shown). The shaded region at the beginning of the ORF marks the 34-bp repeat.
Figure 4. Multiple sequence alignment of the putative Penelope promoter from D. virilis (Dv) and D. willistoni (Dw) with internal promoters of Drosophila LINE elements (I-factor, Jockey, F and Doc) listed in refs. 17 and 19). Transcription start site is indicated by an arrow. Inr, initiator, DPE, downstream promoter element; SD, splice donor site conserved in D. virilis and D. willistoni Penelope elements. ’de1 and ’de2’ represent motifs which stimulates transcription in various Drosophila LINEs (27).

DISCUSSION

The active Penelope retrotransposon from D. virilis was the first PLE retrotransposon to be described, and its structural and functional organization can be expected to display characteristics that are typical of other members of this widespread but relatively little-studied class of elements. The present study demonstrates that sequences necessary and sufficient for expression of Penelope in vivo reside within the element itself, in the region previously characterized as the pseudo-LTR. This region results from a partial-tandem arrangement of two elements, one 5'-truncated and one full-length, and consists primarily of the 3' UTR of the upstream copy which, because of the partial tandem duplication, is also part of the 5' UTR of the downstream copy. This is reminiscent of the composite promoter previously described in HeT-A retrotransposons in D. melanogaster for which the sequences in the 3' UTR of the upstream copy drive transcription of the downstream copy in a tandem repeat (15). In the case of Penelope, all the sequences necessary for transcription in the carcass are present in the 3' pseudo-LTR. This gives Penelope elements the ability to change patterns of gene expression by driving transcription of downstream genes, or downstream exons of genes into which they insert.

Our data show that sequences controlling the tissue-specific transcription directed by the Penelope promoter are also downstream of the RNA start site and in the region that includes the 34-bp repeat and part of the ORF. Sequences directing tissue-specific expression have been identified in a similar position in the I factor (32) and F element (33), two other non-LTR retrotransposons of Drosophila. These regulatory elements apparently confer tissue specificity on the Penelope promoter, and may be essential for the expression in ovaries that results in germ-line transposition and gonadal sterility during hybrid dysgenesis in D. virilis. This suggests that these signals may have been conserved for over 60 million years, the time since the divergence of the lines that lead to D. virilis and D. melanogaster.

LTR retrotransposons are transcribed from a promoter within the U3 region of the 5' LTR while all non-LTR retrotransposons studied so far, with the possible exception of R2Bm from Bombyx mori which is thought to be
transcribed from an adjacent rDNA promoter (34), are
transcribed from a promoter that lies within the transcription
unit. The fact that most PLEs appear to require a
partial-tandem repeat, rather like an LTR, for transcription
sets them apart from both LTR and non-LTR
retrotransposons. There is no obvious mechanism for
pseudo-LTR regeneration other than the propensity
to form tandem repeats. In fact, as many as 30% of all
D. virilis genomic Penelope copies, as well as most Penelo-
pe copies amplified in D. melanogaster strains trans-
formed by full-sized Penelope (Figure 1B), possess a
tandem structure, with a full-length downstream copy
and a variably 5′-truncated upstream copy (30). In future
studies, we plan to investigate the basis for frequent
tandem formation in PLEs.

The 34-bp repeat sequence, which is found at both ends
of the ORF in ancient copies of Penelope from other
species of the virilis group (13), generates relatively high
scores in computational analyses of basal promoter
elements but is not required for transcription from the
normal initiation site. The 34-bp repeat may be a simple
basal promoter of ancestral nature, and more complex
structures, including upstream promoter elements as seen
in LTR retrotransposons and retroviruses, may have
arisen later.

The 75-bp intron located 46-bp downstream from the
Penelope transcription start site is within the promoter
region. The splice donor and acceptor sites of the intron are
well conserved in two Penelope elements from D. willistoni,
that display 67% overall nucleotide sequence identity to
Penelope from D. virilis (I.A., unpublished data). The intron appears to have a role in post-transcriptional
regulation of Penelope as deleting it virtually abolishes
CAT expression in transgenic strains with construct G,
without apparently affecting RNA levels in ovary or
carcass. The difference in CAT activity from constructs A
and G could reflect differences in the secondary structure
of the corresponding RNAs in the context of CAT reporter,
as has been described for CAT reporter constructs of the
Doc retrotransposon (27). It is also possible that nuclear
export and/or translation of spliced Penelope RNA is
facilitated by a component of the intron junction complex,
indeed introns have been shown to affect RNA and protein
levels in S. cerevisiae (35). RNA lacking the intron,
such as transcripts from construct G, would not have this
complex and might therefore be exported or translated
inefficiently, or not at all. If this is the case, then Penelope
elements without the intron would be at a selective
disadvantage, providing an explanation for retention of the
intron.

**SUPPLEMENTARY DATA**

Supplementary Data are available at NAR Online.

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