The *bandit*, a New DNA Transposon from a Hookworm—Possible Horizontal Genetic Transfer between Host and Parasite

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Abstract

**Background:** An enhanced understanding of the hookworm genome and its resident mobile genetic elements should facilitate understanding of the genome evolution, genome organization, possibly host-parasite co-evolution and horizontal gene transfer, and from a practical perspective, development of transposon-based transgenesis for hookworms and other parasitic nematodes.

**Methodology/Principal Findings:** A novel *mariner*-like element (MLE) was characterized from the genome of the dog hookworm, *Ancylostoma caninum*, and termed *bandit*. The consensus sequence of the *bandit* transposon was 1,285 base pairs (bp) in length. The transposon was flanked by perfect terminal inverted repeats of 32 nucleotides in length with a common target site duplication TA, and it encoded an open reading frame (ORF) of 342 deduced amino acid residues. Phylogenetic comparisons confirmed that the ORF encoded a *mariner*-like transposase, which included conserved catalytic domains, and that the *bandit* transposon belonged to the *cecropia* subfamily of MLEs. The phylogenetic analysis also indicated that the Hsmar1 transposon from humans was the closest known relative of *bandit*, and that *bandit* and Hsmar1 constituted a clade discrete from the Tc1 subfamily of MLEs from the nematode *Caenorhabditis elegans*. Moreover, homology models based on the crystal structure of Mos1 from *Drosophila mauritiana* revealed closer identity in active site residues of the catalytic domain including Ser281, Lys289 and Asp293 between *bandit* and Hsmar1 than between Mos1 and either *bandit* or Hsmar1. The entire *bandit* ORF was amplified from genomic DNA and a fragment of the *bandit* ORF was amplified from RNA, indicating that this transposon is actively transcribed in hookworms.

**Conclusions/Significance:** A *mariner*-like transposon termed *bandit* has colonized the genome of the hookworm *A. caninum*. Although MLEs exhibit a broad host range, and are identified in other nematodes, the closest phylogenetic relative of *bandit* is the *Hsmar1* element of humans. This surprising finding suggests that *bandit* was transferred horizontally between hookworm parasites and their mammalian hosts.

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Introduction

Almost one billion people throughout tropical and sub-tropical latitudes are infected with hookworms. In the countries affected, hookworm infection is often the major contributor to iron-deficiency anemia, a direct consequence of the parasite’s blood-feeding activities [1]. Comparatively little is known about the genome or population genetics of hookworms. The karyotype of only one hookworm species, the dog hookworm, *Ancylostoma caninum*, is known where the haploid chromosome number *n* = 6 [2]. Hookworms are dioecious and sex determination is by an XX-XO mechanism as in their free-living relative, the model nematode *Caenorhabditis elegans* [3]. Although the genome size of hookworms has not been reported, it may be of similar dimensions and complexity to that of *C. elegans*—around 100 megabase pairs (Mb) and containing about 20,000 protein-encoding genes (see [3]). By contrast, flow cytometric based techniques have shown that the haploid genome size of two trichostrongyle nematodes, *Haemonchus contortus* and *Teladorsagia circumcincta*, is ~50 Mb in length [4]. Trichostrongyle nematodes are more closely related to hookworms than is the free-living nematode, *C. elegans* [5].

Over 20,000 expressed sequence tags (ESTs) from *A. caninum* and the related parasite, *A. ceylanicum*, have been characterized to some degree [6–8], including transcripts from the gut of adult...
Author Summary

Because of its importance to public health, the hookworm parasite has become the focus of increased research over the past decade—research that will ultimately decipher its genetic code. We now report a gene from hookworm chromosomes known as a transposon. Transposons are genes that can move around in the genome and even between genomes of different species. We named the hookworm transposon bandit because hookworms are "thieves" that steal the blood of their hosts, leading to protein deficiency anemia. The bandit transposon is a close relative of a well studied assemblage of transposons, the mariner-like elements, known from the chromosomes of many other organisms. The founding member of this group—the mariner transposon—was isolated originally from a fruit fly; mariner has been harnessed in the laboratory as a valuable gene therapy tool. Likewise, it may be feasible to employ the bandit transposon for genetic manipulation of hookworms and functional genomics to investigate the importance of hookworm genes as new intervention targets. Finally, bandit may have transferred horizontally from priimates to hookworm or vice versa in the relatively recent evolutionary history of the hookworm–human host–parasite relationship.

worms[9]. Interestingly, most of the genes share homologues in C. elegans, highlighting the suitability of this free-living nematode as a model for hookworm developmental biology [8]. Moreover, the Genome Survey Sequences (GSS) Database at GenBank contains nearly 100,000 genome survey sequences from A. caninum (http://www.ncbi.nlm.nih.gov/dbGSS/dbGSS_summary.html), which when assembled provide a 57.6 Mb unique sequence, establishing a tractable framework for an eventual genome sequence. It can be anticipated that an enhanced understanding of the hookworm genome will aid in the control of hookworm disease and hookworm-associated anemia, including the development of new anti-parasite interventions [10].

A substantial proportion of the genome of most metazoans is composed of repetitive sequences, including various types of mobile genetic elements (MGEs). MGEs are drivers of genome evolution [11]. In addition to this role, from a practical perspective MGEs offer potential as transgenesis and gene silencing vectors [12–14], technologies that have yet to be reliably established for MGEs offer potential as transgenesis and gene silencing vectors [12–14], technologies that have yet to be reliably established for MGEs, but with the endonuclease Hind III and Xba I (Fermentas, Sweden) and size separated through 0.8% agarose gel. Fragments ranging in size from 2–7 kilobase pairs (kb) were excised, eluted from the gel, and ligated into plasmid pBluescript SK (+/+−) (Stratagene). Bacterial E. coli strain XL-1 blue cells were transformed with the ligated products and recombinant colonies selected by blue-white screen on LB agar supplemented with ampicillin. White colonies were transferred to wells of 96-well microtitre plates and cryopreserved in 20% glycerol at −80°C.

Mobile genetic element (MGE)-like gene fragments were identified from dbEST using text and blast searches. MGE fragments were amplified by polymerase chain reaction (PCR) from gDNA and used to probe gDNA libraries (see below). At the outset, a gene probe was obtained by PCR using primers AcCR1F (5’-CAATTTGCTCGATAGCGAATG) and AcCR1R (5’-CGCGATATCCCATAGAATGTCA) specific for an A. caninum transcript annotated in GenBank to have identity to reverse transcriptase (GenBank AW700359), with PCR cycling conditions of 35 cycles of 94°C for 1 min, 55°C for 1 min and 72°C for 1.5 mins, and a final elongation step at 72°C for 10 mins. An amplicon encoding a retrotransposon-like gene was sequenced to confirm its identity, and the probe was named AcCR1 (not shown). Subsequently, a transposon-like gene probe (genomic DNA clone H118; GenBank DQ377715) was obtained by library screening with AcCR1. Nucleotides 118–416 of the insert of H118 were PCR amplified, and after labeling with digoxigenin (DIG), the PCR product was employed to screen ~500 clones from the size selected, Hind III and Xba I libraries of A. caninum gDNA. The inserts of positive clones were sequenced and the sequences used to search the non-redundant database of GenBank using the Blastn, Blastx and tBlastx algorithms [19]. Genomic DNA and cDNA of A. caninum were amplified with the aim of obtaining longer fragments of the A. caninum transposon, using specific primers, AcMarinerF; 5’-GCTGACTCTTGGCTTTGGTC and AcMarinerR; 5’-TAATCGAATTTGCCGAGGC, spanning nucleotide residues 154 to 1,035 of the consensus sequence of the full-length bandit transposon (Figure 1). PCR conditions were 94°C for 1 min, 55°C for 1 min and 72°C for 3 min, 35 cycles after which PCR products were ligated into plasmid pTOPO (Stratagene) and sequenced. A consensus sequence of a new transposon was assembled from the positive clones and also from A. caninum GSS sequences in GenBank with assistance from the contig assembly program of BioEdit version 7.0.5.2 [20] (Figure 1). To identify bandit-like sequences in related hookworm species, the bandit transposase (342 amino acids) was queried against 4,953 polypeptides from A. ceylanicum [8] and 2,328 polypeptides from N. americanus [21].

Methods

Genomic DNA of the hookworm Anclylostoma caninum

Adult A. caninum hookworms were collected from naturally infected dogs from Ta Rae district, Sakonnakorn province, Thailand, as described previously [17]. After removal from the canine small intestines, the hookworms were identified microscopically as A. caninum, and the living worms were snap frozen and stored at −80°C. Subsequently, genomic DNA (gDNA) of adult mixed sexes of A. caninum was isolated from the parasites using a Qiagen genomic tip-100/G column and genomic buffer set kit (Qiagen, Germany) according to the manufacturer's instructions. Briefly, worms (50–100 mg) were lysed in DNase-free lysis buffer supplemented with RNAase (Qiagen) using a DNase-free glass homogenizer. Proteinase K was added to the extracts and incubated at 50°C for 2 hours. The homogenate was clarified by centrifugation, the supernatant applied to a Qiagen genomic-tip column (Qiagen), the eluted A. caninum gDNA recovered by ethanol precipitation, dissolved in TE buffer, and its concentration and purity determined using a spectrophotometer.

Construction and screening of hookworm genomic DNA libraries; bioinformatics

Size selected plasmid libraries of gDNA from adult A. caninum were constructed as described [17]. Briefly, gDNA was digested with the endonuclease Hind III and Xba I (Fermentas, Sweden) and size separated through 0.8% agarose gel. Fragments ranging in size from 2–7 kilobase pairs (kb) were excised, eluted from the gel, and ligated into plasmid pBluescript SK (+/+−) (Stratagene). Bacterial E. coli strain XL-1 blue cells were transformed with the ligated products and recombinant colonies selected by blue-white screen on LB agar supplemented with ampicillin. White colonies were transferred to wells of 96-well microtitre plates and cryopreserved in 20% glycerol at −80°C.

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Only the best homologous sequence is reported, including the identity and similarity values for the longest high-scoring segment pair (HSP) in each subject.

Southern hybridization analysis

Thirty µg of *A. caninum* gDNA were cleaved with the restriction enzymes, *Xho* I and *Xba* I. The bandit probe sequence did not include recognition sites for either of these enzymes. Digested gDNA was fractionated by electrophoresis through 0.8% agarose gel, after which the fragments were transferred to nylon membrane (Hybond-N+, Amersham Biosciences) by capillary action. The bandit-specific probe was obtained by PCR using specific primer AcMarinerF; 5'-GCTCACCTTTGCGTGTTC and AcMarinerR; 5'-TAATCGATTTGGCGAAAGGTC, spanning nucleotide residues 154 to 1,033 of the consensus sequence of the full-length bandit transposon (Figure 1). Southern hybridization analysis was performed using DIG labelled probes and detection system (Roche, USA). The membranes were incubated in hybridization medium under high stringency conditions. High stringency washing conditions were performed as recommended by the manufacturer. Stringency washing conditions were performed as recommended by the manufacturer. Signal was detected by exposure to X-ray film (Fuji).

Reverse transcription-PCR

Total RNA of *A. caninum* mixed sex adult worms was extracted using the Nucleospin RNA II kit (Machery-Nagel, Germany) according to the manufacturer’s procedures. RT-PCR was performed using the RobusT II RT-PCR Kit (FINNZYMES, Finland), primers P118F (5'-CTCTGATAGCGTCGGA and P118R (5'-GGGCGCTCTGATACCATTT) specific for the bandit transposase based on the sequence of genomic clone H118 (GenBank accession number DQ377715) spanning nt. 118–417 (Figure 1), and the following PCR cycling conditions: 42°C for 2 mins for the first cycle, 94°C for 1 min, 55°C for 1 min and 72°C for 1.5 mins, for 40 cycles, and finally an elongation step at 72°C for 10 mins. RT-PCR products were sized by electrophoresis through a 1% agarose gel. To confirm the identity of the RT-PCR products, they were transferred to nylon membranes [22], and probed with a DIG-labelled bandit probe (residues 152 to 1031 of bandit, shown in Figure 1). Southern hybridization analysis was performed using DIG labelled probes and the DIG detection system from Roche. Signals were detected by exposure to X-ray film (Fuji).

Phylogenetic analysis

The entire transposase ORFs of bandit and other related elements were employed for construction of the phylogenetic tree. Alignments of amino acid sequences of functional domains were accomplished with ClustalW [23] and edited with Bioedit version 5.0.9 [20]. Sequence alignments for phylogenetic analysis comparing the conserved transposase domains were adjusted as described previously [24,25]. A phylogenetic analysis was performed on this sequence alignment using PROTDIST in PHYLIP packages and a tree was constructed using the neighbor joining method (PHYLIP, version 3.6 software) [26]. A distance matrix analysis was also carried out using maximum parsimony. The resulting phylogenetic trees were displayed using TreeView [27]. Statistical significance of branching points was evaluated with 1,000 repetitions in a bootstrap analysis (SEQBOOT). The predicted protein sequences were obtained directly from the GenBank entries where provided, otherwise ORFs were predicted by translating the nucleotide sequences provided in GenBank.

Homology modeling

The transposase ORFs of bandit and Homar1 were used as a query for the Swiss-Model comparative protein modeling server (http://swissmodel.expasy.org). Homologues of known structure were sought from the Research Collaboratory for Structural Bioinformatics (RCSB) Protein Data Bank (http://www.rcsb.org/pdb/home/home.do). Models were viewed and manipulated in first approach mode using Swiss-PdbViewer (http://swissmodel.expasy.org/spdbv).

Results

A mariner-like transposon present in the genome of *A. caninum*

A positive clone was identified from an *A. caninum* genomic DNA library that was screened with a reverse transcriptase-like
gene probe, clone H118 (GenBank accession number DQ377715). The clone showed sequence identity with mariner-like transposons from many eukaryotes including mariner from Homo sapiens and mariner from Bos taurus. Sequence analysis revealed that clone H118 contained sequence that encoded part of a transposase protein (Figure 1). The consensus full length transposon was constructed using clone H118 and multiple GSSs identified by homology searches from the GenBank database (GenBank accession numbers CW709686, C213904 and C241797) (Figure 1). We termed the new transposon \textit{bandit}, in keeping with the informal convention of naming mobile genetic elements with terms suggestive of a peripatetic lifestyle (e.g. \textit{mariner}, \textit{hobo} and \textit{fugitive})[28–30]. Given the present results, the name \textit{bandit} seemed appropriate since a bandit is often difficult to apprehend, and in this present context, it appears that \textit{bandit} has moved furtively between hookworms and their mammalian hosts (see below). The consensus sequence of \textit{bandit} was 1,285 bp flanked by 32 nt perfect terminal inverted repeats at each extremity with a common target site duplication TA (Figure 1 and Figure S1). \textit{bandit} has one ORF of 342 amino acid residues encoding for a transposase enzyme. The \textit{bandit} transposase contained the conserved DD34D motif that is found in the active site of the catalytic C-terminal domain of mariner-like transposases as opposed to the DDE motif found in the Tc1-like elements [12] (Figure 2). The ORF of the \textit{bandit} showed highest similarities to \textit{Hsmar1} from human (55% identity, 70% similarity), \textit{Boo taurus} (54% identity, 70% similarity) and \textit{Te1} of \textit{C. elegans} (41% identity, 58% similarity), \textit{HcTc1} of \textit{Haemonchus contortus} (22% identity, 42% similarity). On the other hand, no \textit{bandit}-like sequences were identified in the National Center for Biotechnology Information (NCBI) catalogue of dog sequences (not shown), indicating that \textit{bandit} is not of canine origin.

The perfect inverted repeats of 32 bp are the standard length for mariner-like elements [31] compared with 54 bp for Tc1 from \textit{C. elegans} [32] and 55 bp for \textit{HcTc1} from \textit{H. contortus} [33]. In addition to the catalytic triad, \textit{bandit} contains most of the additional canonical features of mariner-like elements (MLEs), the WVPHEL motif (WVPHEL in \textit{bandit} and YSPDLAP (CSPDLSP in \textit{bandit}) [34]. However, \textit{bandit} did not contain the conserved FLHDNARPH motif that overlaps the second D of catalytic triad in most MLE transposases. In \textit{bandit}, this motif is replaced by a FLHHDNARSH motif [35,36] (Figure S1).

Numerous copies of \textit{bandit} interspersed throughout the \textit{A. caninum} genome

Smeared bands of hybridization were evident when a Southern blot of \textit{A. caninum} genomic DNA (gDNA) was probed with the labeled \textit{bandit}-specific sequence. \textit{Xba I} and \textit{Xho I} were used to cleave the gDNA, and hybridization of each restriction digest to a \textit{bandit}-specific probe revealed a smear-like pattern of numerous bands of hybridization ranging in size from >5–<0.5 kb (Figure 3), confirming the presence of numerous copies of the \textit{bandit} transposon in the genome of natural populations of \textit{A. caninum} from north-eastern Thailand. This also suggests that the \textit{bandit} element is widely dispersed in the hookworm genome rather than being localized at just one or a few isolated sites. To more specifically address the copy number, we queried the \textit{A. caninum} GSS in NCBI with the \textit{bandit} sequence using blastn and tblastx algorithms. Using blastn, we identified 23 GSS with 87–98% identity over at least 250 bp. Using tblastx, we identified >200 GSS with >90% identity over at least 50 amino acids (not shown). The \textit{A. caninum} GSS are predicted to cover about 15% of the genome (M. Mitreva, unpublished). Extrapolating from these numbers there may be between 150–1,500 copies of \textit{bandit} dispersed throughout the genome.

\textit{bandit} is a novel mariner-like transposon of the cecropia subfamily

A phylogenetic tree was constructed based on the sequence alignment of the entire transposase ORFs of \textit{bandit} and 37 other transposon sequences available in public databases. A neighboring tree with 1,000 replicates revealed that \textit{bandit} is most closely related to \textit{Hsmar1} from \textit{Homo sapiens} (Figure 4). Mariner-like transposons can be classified into six subfamilies [24,25]. \textit{Bandit} formed a clade with elements from the cecropia subfamily with solid bootstrap support (564), and this diphylectic clade included a branch containing \textit{bandit} and three primate-originated MLEs, and a branch with \textit{Funnari} from the coral \textit{Fungia} sp., Amar1 from the atlas moth, \textit{Attacus atlas} and Dnmar1 from the planarian, \textit{Girardia tigrina}. The appearance of the branches of the cecropia clade was the same when

![Figure 3. Southern hybridization analysis of \textit{Ancylostoma caninum} genomic DNA to a probe specific for the \textit{bandit} transposon. The genomic DNAs were cleaved with endonucleases \textit{Xba I} (lane 1) and \textit{Xho I} (lane 2). Molecular size standards in kilobase pairs (kb) are shown at the left. doi:10.1371/journal.pntd.0000035.g003](image-url)
Figure 4. Phylogram constructed using the neighbor-joining method to compare the relationships among transposases of the *bandit* transposon and of representative mariner-like elements belonging to the Tc1/mariner superfamily of transposons from a range of host genomes. Representatives of six clades of mariner-like elements including the mori, irritans, mauritiana, and cecropia were included in the analysis. The elements used in the tree include Tc1-like (AAD12818) and Tc1 (P03934), T19261, T23086 and AF003149 from *C. elegans*, HcTc1 (AAD34306) from *Haemonchus contortus*, Tcb1 (CAA30681) from *C. briggsae*, BmMar1 (UI47917) and BmMar6 (AAN06610) from Bombyx mori, Crmar1 (AAK66147) from *Ceratitis rosa*, Himar1 (ABB59013) mutagenesis vector pFN1 TP16H3, Cpmar1 (AAC46945) from *Chrysoperla plumula*, Damar1 (DAU11648) from *Drosophila ananassae*, Bytmar1-8 (CAD45868) and Bytmar1-11 (CAD45369) from *Bythogreus thermoridron*, Dtsmar1 (AAC28261) from *D. teissieri*, Dsecmar1 (AAC16609) from *D. sechellia*, Mdmar1 (AAC16609) from *Musca domestica*, Mos1 (pdb2F77T) from *D. mauritiana*, XP_001099426 (Macaca mulatta), SETMAR (Cercopithecus aethiops) from *Macaca mulatta*, T19261 (C. elegans), T23086 (C. elegans) from *Escherichia coli*, SAF063149 (C. elegans) from *Klebsiella pneumoniae*, Mcmar1 (Meloidogyne chitwoodi), Ammar1 (Apis cerana), Acmar1 (Apis cerana), Famar1 (Forficula auricularia), Xmar1 (Apis mellifera), Ccm1 (Ceratitis capitata), Camar1 (Chymomyza amoena), Capar1 (Chromobasidiumellipticum), Transposose (Escherichia coli), Putative transposose (Klebsiella pneumoniae), Transposase (Bacillus halodurans), XP_001099426 (Macaca mulatta), SETMAR (Cercopithecus aethiops), Mos1 (pdb2F77T) from *D. mauritiana*, SAF063149 (C. elegans) from *Klebsiella pneumoniae*, Mcmar1 (Meloidogyne chitwoodi), Ammar1 (Apis cerana), Acmar1 (Apis cerana), Famar1 (Forficula auricularia), Xmar1 (Apis mellifera), Ccm1 (Ceratitis capitata), Camar1 (Chymomyza anthoena), Capar1 (Chromobasidiumellipticum), Transposose (Escherichia coli), Putative transposose (Klebsiella pneumoniae), Transposase (Bacillus halodurans). Bootstrap values, where 500 or greater from a maximum of 1,000 replicates, are presented at the nodes.

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either neighbor joining or maximum parsimony (not shown) methods were employed in tree construction. Indeed, bootstrap support for the clade that included bandit and the primate elements was even stronger in the maximum parsimony analysis (902) than that obtained using the neighbor joining method (729). The phylogenetic distance between human and hookworm is far greater than that reflected in the phylogenetic analysis of these transposons, suggesting to us that bandit is only distantly related to MLEs from nematodes that are closely related to A. caninum, and is much more similar to transposons from the hookworm’s mammalian hosts. For example, the MLE HcTc1 from the trichostrongyle parasite, H. contortus (a close relative of A. caninum) belongs to the mos1 clade of MLEs (Figure 4). The remarkable identity between bandit and the primate MLEs, Hsmar1 and SETMAR, strongly suggests horizontal transmission of this element from host to parasite (or vice versa).

Homology models confirm close identity of hookworm bandit and human Hsmar1 transposons

The catalytic C-terminal domain of the predicted transposase ORF of bandit was modeled on the crystal structure of the C-terminal catalytic domain (residues 126–345) of mos1 transposase from Drosophila mauritiana (pdb accession number 2LT4). The structural alignment spanned residues 158–345 of mos1 and 178–342 of bandit. The general fold of the bandit catalytic domain was highly conserved with that of mos1 (Figure 5A). The first alpha helix and beta sheet of the catalytic domain of bandit (including the first catalytic Asp residue) were too dissimilar to mos1 to be included in the model; however, the rest of the domain revealed similar active site architecture. Because bandit is most similar to human Hsmar1 at the primary sequence level (Figure 4), we also modeled the catalytic domain of Hsmar1 on the crystal structure of mos1. The sequence conservation between mos1 and Hsmar1 also was high (Figure 2). Surprisingly, when the key active site residues of the catalytic domains [37] of bandit and Hsmar1 were compared with those of mos1, we observed that bandit and Hsmar1 had identical active site residues but, by contrast, three of these residues had non-conservative substitutions in mos1 (Figure 5B, C and D).

bandit is transcribed in the parasitic stages of A. caninum

Transcripts encoding the transposase of bandit were amplified by PCR from cDNA from mixed sex adult hookworms. Products of the expected size, 300 bp, were amplified (Figure 6), and the identity of the amplicons was confirmed by sequence analysis and Southern hybridization using a bandit-specific probe (not shown). Together with the presence of relatively intact inverted repeats, this approach indicated that functional domains of the element are transcribed in the adult hookworm, and suggests that copies of bandit are active and mobile within the genome of A. caninum.

bandit integrates into non-coding regions of the A. caninum genome

Sequences flanking the different individual copies of bandit (from the GSS dataset) were aligned (Figure 7). Blast search analysis of the 5’ and 3’ flanking regions of bandit did not show homology to sequences in the public database. The flanking DNA was however generally AT-rich and appeared to be of non-coding origin.

bandit in related hookworm species

Available transcriptomic data of related hookworm species, A. ceylanicum [8] and N. americanus [21] was explored to identify putative bandit-like transposons. The similarity search (BlastX) resulted in identification of a homologous sequence from A. ceylanicum (contig id AE04671, 44% identity, 64% similarity over 185 amino acids) and from Necator americanus (contig id NAC01255, 45% identity, 58% similarity over 91 amino acids) (data not shown). Based on these interspecific partial matches the conservation is lower compared to A. caninum bandit and Hsmar1 (55% identity, 70% similarity), but higher between the A. caninum bandit and other hookworm bandit-like sequences than with the HcTc1 from the ruminant blood-feeder H. contortus (22% identity, 42% similarity) or the Tc1 from C. elegans (41% identity, 58% similarity). Unavailability of the full length ORF of the bandit from these two related hookworm species contributed to their exclusion from the above described analysis.

Discussion

A new member of the Tc1/mariner superfamily of DNA transposons has been characterized from the genome of a parasitic nematode, and termed bandit. Sequence identity, structure, and phylogenetic relationships demonstrated that the bandit transposon belonged to the cecropia sub-family of mariner-like elements (MLEs). The cecropia clade is populated by transposons from diverse animal taxa including the cecropia moth [38], a coral [39], primates including the African green monkey and humans [40] and now from a hookworm. Earlier reports dealing with members of this clade have suggested that horizontal transmission has likely been involved in the present disposition of its members (e.g., [38]). In like fashion, given that the closest relatives of bandit are Hsmar1 and SETMAR from humans and monkeys, bandit may have been transmitted to or from hookworms and their primate hosts.

The bandit transposon displayed the structural hallmarks of the Tc1/mariner superfamily of transposons including an overall length of ~1.3 kb, a single ORF encoding a transposase of 342 amino acid residues in length, a DD(34)D catalytic motif duplication of TA dinucleotide pairs upon insertion and inverted terminal repeats of 32 bp in length [12]. The DD(34)D motif indicated that bandit was a mariner-rather than a Tc1-family member. Phylogenetic analysis confirmed that bandit was indeed mariner-like and, remarkably, indicated that its closest relative was the primate Hsmar1 transposon. Moreover, homology models established using the crystal structure coordinates of mos1 transposase (from D. mauritiana) revealed closer identity between bandit and Hsmar1 than between bandit or Hsmar1 and Mos1 in active site architecture and catalytic domain residues.

The hookworm, A. caninum, is a parasite of dogs but is frequently found in the human small intestine. Although it does not generally reach sexual maturity in humans, it may now be evolving this capacity [41]. Moreover, A. caninum larvae commonly infect human skin resulting in pruritic dermatitis termed cutaneous larva migrans [42]. A. caninum is closely related to the anthropophilic hookworm, Ancylostoma duodenale, and another close relative, A. ceylanicum, parasitizes both humans and dogs. The human hookworms A. duodenale and N. americanus infect more than 700 million people, causing widespread morbidity–primarily iron deficiency anemia– and mortality [1]. The intimacy of host-parasite relationships is known to facilitate horizontal transmission of genetic material [43], and parasitism is known to facilitate horizontal transmission of transposons. For example, P elements have been transferred among Drosophila species by a parasitic mite [44], as have mariner-like elements between parasitic wasps and their lepidopteran hosts [43]. Since the closest known relative of bandit is Hsmar1 from humans, and given the parasitic association between hookworms and primates–the hosts of bandit and Hsmar1, respectively–it is likely that the presence of bandit and Hsmar1 in both parasite and host genomes reflects parasitism-facilitated horizontal transmission.
After entry into a naive lineage, an active autonomous MLE undergoes unrestrained spread through transposition and sexual exchange for a time until regulatory and/or mutational inactivation dampens transposition activity and associated deleterious mutations [46,47]. Given that transcription of bandit was detected by RT-PCR analysis, and given that the intact integration footprint of bandit within the hookworm genome remains readily apparent, it appears that bandit is transpositionally active within the A. caninum genome. If so, the hypothesized horizontal transmission of Hsmar1/bandit elements between host and parasite is likely to have occurred through the integration of bandit within the A. caninum genome, followed by the mobilization of the Hsmar1 element from the host genome into the parasite genome.

**Figure 5.** Homology models of bandit from Ancylostoma caninum and Hsmar1 from Homo sapiens based on the crystal structure of the mos1 element from Drosophila mauritiana. Ribbon diagram showing the predicted structure of the catalytic domains of bandit and mos1 (A). s1 and h1 refer to β sheet number 1 and α helix number 1 of the mos1 catalytic domain–homologous regions were present in bandit but were not included in the model. Superimposition of the catalytic active sites of bandit (B) and Hsmar1 (C) on the crystal structure of mos1 highlighting the residues involved in catalysis. Conserved active site residues are labeled in red font; where bandit or Hsmar1 active site residues differ from mos1, the substitution is denoted in green font. Yellow arrows denote the three catalytic Asp residues. Numbering of side chains is based on the mos1 sequence. Comparison of the residues predicted to be involved in catalysis from bandit, Hsmar1 and mos1 (D). Residues selected were based on the crystal structure of mos1.

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may be a recent event, and since Hsma1 is now inactive [48], the direction of the horizontal transfer may have been from host to parasite.

Eukaryotic genomes generally include substantial amounts of sequences derived from MGEs, primarily retrotransposons and transposons. These mobile sequences are drivers of genome evolution [11]. A number of MGEs have been characterized from nematode genomes including Tas, a LTR retrotransposon, and R4, a non-LTR retrotransposon, both from *Ascaris lumbricoides* [49,50], mariner-like elements (MLEs) from *Trichostongylus colubriformis* [51] and the RTE1, NeSL, and Cer retrotransposons from *C. elegans*. Recently, it was reported that the *A. caninum* genome includes elements with identity to the *Transib* superfamily of transposons. In vertebrates, the *Transib* transposon has mutated to form the RAG1 protein and recombination signal sequences involved in catalyzing B and T cell receptor gene V(D)J recombination [52]. Also, recently we described the *dingo* non-LTR retrotransposons from the genome of *A. caninum* [17] and numerous transcripts encoding reverse transcriptase are evident in the EST database of *A. caninum*, *A. ceylanicum* and *N. americanus* hookworms (http://nematode.net), indicating the presence of endogenous retroviruses or retrotransposons. Based on the genomes of *C. elegans* [33] and several parasitic helminths including schistosomes [54], it is apparent that the hookworm genome has been colonized not only by the *bandit* transposon, but also by numerous other waves of MGEs. From a practical perspective, understanding of MGE complexity, diversity and copy numbers can be expected to facilitate the assembly and annotation of the hookworm genome sequence (a focus of current genome sequencing effort, http://nematode.net). Finally, as with other MGEs, an endogenous hookworm mariner-like transposon such as *bandit* holds potential as a transgenesis vector for manipulation of the hookworm genome, given the ability of other *Tc1*/mariner superfamily members such as *mos1* to transpose within the genomes of *C. elegans*, planarians and other species (e.g., [55–57]).

### Supporting Information

**Figure S1** Consensus nucleotide and deduced amino acid sequence of the entire *bandit* element. Sequence features of the *bandit* are indicated within duplicated TA dinucleotides. The inverted repeats at both ends are highlighted with green. The ORF starts at the Met encoded at nt. 189 and terminates at the stop codon at nt. 117, encoding an enzyme of 342 amino acid residues. Two conserved hallmark motifs of mariner-like elements [38] are highlighted with grey and the catalytic triad DD34D residues are indicated by red colored font. Found at: doi:10.1371/journal.pntd.0000035.s001 (0.03 MB DOC)

**Figure 6.** Reverse transcription PCR targeting the *bandit* transposon. Transcripts encoding the transposase of *bandit* were amplified by PCR from cDNA of the adult mixed sex of *A. caninum*. Products of the expected size, 300 bp are indicated with the arrow; lane 1, negative control where reverse transcriptase was omitted from the reaction; lane 2, empty lane; lane 3, plasmid DNA of clone H118 (positive control); lane 4, cDNA of mixed sex adult hookworms. Molecular size standards (lane M) are shown at the left. doi:10.1371/journal.pntd.0000035.g006

**Figure 7.** Multiple sequence alignment of the nucleotide sequences flanking the insertion sites of copies of the *bandit* transposons within the genome of *Ancylostoma caninum*. Alignments of nucleotide sequences flanking the 5’- (A) and 3’- (B) termini of *bandit*. Conservation of residues is indicated by the shading of boxes. Target sequences, with GenBank accession numbers as indicated on the left, were identified among entries in the GSS database of *A. caninum* sequences at GenBank. The target site TA duplications are indicated with asterisks. doi:10.1371/journal.pntd.0000035.g007
Author Contributions
Conceived and designed the experiments: AL PB TL. Performed the experiments: AL PB TL SW JS NK. Contributed reagents/materials/analysis tools: AL PB SK PS. Carried out the molecular genetic experiments: AL PB TL SW JS NK. Contributed reagents/materials/analysis tools: AL PB SK PS. Performed the molecular genetic analysis: AL PB TL SW JS NK. Contributed reagents/materials/analysis tools: AL PB SK PS. Wrote the paper: MM AL PB TL. Carried out the molecular genetic experiments: TL. Carried out parasitological and molecular analyses including cloning and sequencing genomic fragments: SW JS NK. Participated in parasitological analyses including identification of the parasites as *A. caninum* SK PS. Performed the homology modeling: AL TL. Participated in analysis of hookworm databases for *bandi*like sequences and in the assembly of the contigs: MM.

References

1. Hotez PJ, Brooker S, Bethony JM, Bottazzi ME, Loukas A, et al. (2004) Hookworm infection. N Engl J Med 351: 799–807.

2. LeJambre LF, Georghi J (1979) Influence of fertilization on oogenesis in *Ancylostoma caninum*. J Parasitol 56: 131–137.

3. Blaxter M (2000) Genes and genomes of *Necator americanus* and related hookworms. J Parasitol 86: 375–373.

4. Leroy S, Depuydt C, Morand S (2003) Flow cytometry for parasite nematode genome size measurement. Mol Biochem Parasitol 128: 91–93.

5. Holterman M, van der Wurff A, van den Elsen S, van Megen H, Bongers T, et al. (2006) Phylum-wide analysis of SSU rDNA reveals deep phylogenetic relationships among nematodes and accelerated evolution toward crown Clades. Mol Biol Evol 23: 1792–1800.

6. Daub J, Loukas A, Pritchard DL, Blaxter M (2000) A survey of genes expressed in adults of the human hookworm, *Necator americanus*. Parasitol. 120 (P1): 171–184.

7. Miranda RR, Costa-Junior LM, Campos AK, Santos HA, Rabelo EM (2004) Identification of specific male and female genes in adult *Ancylostoma caninum*. Ann N Y Acad Sci 1020: 199–202.

8. Mitreva M, McFadden JP, Arasu P, Hawdon J, Martin J, et al. (2005) Investigating hookworm genomes by comparative analysis of two *Ancylostoma* species. BMC Genomics 6: 38.

9. Ranjit N, Jones MK, Stensland DJ, Gasser RB, Loukas A (2006) A survey of the intestinal transcriptomes of the hookworms, *Necator americanus* and *Ancylostoma caninum*, using tissues isolated by laser microdissection microscopy. Int J Parasitol 36: 701–710.

10. Loukas A, Bethony J, Boechler S, Hotez P (2006) Hookworm vaccines: past, present, and future. Lancet Infect Dis 6: 173–741.

11. Kazazian HH Jr (2004) Mobile elements: drivers of genome evolution. Science 303: 1626–1632.

12. Plasterk RH, Izsvák Z, Ivics Z (1999) Resident aliens: the Tc1/mariner superfamily of transposable elements. Trends Genet 15: 326–332.

13. Yang N, Zhang L, Kazazian HH Jr (2005) L1 retrotransposon-mediated stable gene silencing. Nucleic Acids Res 33: e57.

14. Brindley PJ, Laha T, McManus DP, Loukas A (2003) Mobile genetic elements colonizing the genomes of metastrongylid parasites. Trends Parasitol 19: 79–87.

15. Venter JC, Adams MD, Myers EW, Li PW, 95–98.

16. Fischer C, Bouneau L, Coutanceau JP, Weissenbach J, Vallot JN, et al. (2004) Global heterochromatic colocalization of transposable elements with microtubules in the compact genome of the pufferfish Tetraodon nigroviridis. Gene 336: 175–183.

17. Laha T, Kewsgai N, Loukas A, Brindley PJ (2006) The dingo non-long terminal repeat retrotransposons from the genome of the hookworm, *Ancylostoma caninum*. Exp Parasitol 113: 142–153.

18. Shao H, Tu Z (2001) Expanding the diversity of the *BSG30-Tc1*-mariner superfamily: discovery of a unique *BSG30*-transposon and reclassification of the *BSG30* and *BSG49* transposons. Genetics 159: 1103–1115.

19. Alsulh SF, Madden TL, Schaller AA, Zhang J, Zhang Z, et al. (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res 25: 3389–3402.

20. Hall T (1999) BioEdit: a user friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symposium Series 41: 95–98.

21. Parkinson J, Mitreva M, Whitton G, Thomson M, Daub J, et al. (2004) A transcriptomic analysis of the phylum Nematoda. Nat Genet 36: 1259–1267.

22. Souther EM (1975) Detection of specific sequences among DNA fragments separated by gel electrophoresis. Journal of Molecular Biology 98: 503–517.

23. Thompson JD, Higgins DG, Gibson TJ (1994) CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. Nucleic Acids Res 22: 4673–4680.

24. Fisher CW, Rasmussen CA, Jones MA, Demattei MV, Renault S, Pradier E, et al. (2006) The *CGI*-rich transposon *Bytmar1* from the deep-sea hydrothermal crab, *Orcaella huegelii*. J Mol Evol 59: 747–760.

25. Prasad MD, Nurminsky DL, Nagaraju J (2002) Characterization and molecular characterization of the *Bytmar1* transposable element in the nematode *Caenorhabditis elegans*. Nucleic Acids Res 30: 1125–1128.

26. Richardson JM, Dawson A, O’Hagan N, Taylor P, Finnegan DJ, et al. (2006) Mechanism of Mos1 transposition: insights from structural analysis. Embo J 25: 1330–1344.

27. Lohse DA, Gudmunson GH, Boman HG (1991) A highly repetitive, mariner-like element in the genome of *Haemaphora coccopha*. J Biol Chem 266: 11510–11521.

28. Nakajima Y, Fujimoto H, Negishi T, Hashido K, Shiino T, et al. (2002) Possible horizontal transfer of mariner-like sequences into some invertebrates including Lepidopteran insects, a grasshopper and a coral. J Insect Biotechnol Sericology 1: 109–125.

29. Cordaux R, Udri S, Batzer MA, Fruchette C (2006) Birth of a chimeric primate gene by capture of the transposase gene from a mobile element. Proc Natl Acad Sci U S A 103: 8101–41006.

30. Crosse J, Loukas A, Opdebeck J, Fairley S, Proovic P (1994) Human enteric infection with canine hookworms. Am J Trop Med Hyg 50: 369–374.

31. Brenner MA, Patel MB (2003) Cutaneous larva migrans: the creeping eruption. Cutis 72: 111–113.

32. Mower JP, Stefanovic S, Young JG, Palmer JD (2004) Plant genetics: gene transfer from parasitic to host plants. Nature 432: 165–166.

33. Houck MA, Clark JB, Peterson KR, Kidwell MG (1991) Possible horizontal transfer of *Drosophila* genes by the microtubule-binding protein *Tc1*. Nature 352: 387–390.

34. Robertson HM (1993) The mariner transposable element is widespread in the nematode *Trichuris suis* and *Ancylostoma caninum*. J Parasitol 79: 1151–1153.

35. Richardson JM, Dawson A, O’Hagan N, Taylor P, Finnegan DJ, et al. (2006) Mechanism of Mos1 transposition: insights from structural analysis. Embo J 25: 1330–1344.

36. Lohse DA, Gudmunson GH, Boman HG (1991) A highly repetitive, mariner-like element in the genome of *Haemaphora coccopha*. J Biol Chem 266: 11510–11521.

37. Nakajima Y, Fujimoto H, Negishi T, Hashido K, Shiino T, et al. (2002) Possible horizontal transfer of mariner-like sequences into some invertebrates including Lepidopteran insects, a grasshopper and a coral. J Insect Biotechnol Sericology 1: 109–125.

38. Cordaux R, Udri S, Batzer MA, Fruchette C (2006) Birth of a chimeric primate gene by capture of the transposase gene from a mobile element. Proc Natl Acad Sci U S A 103: 8101–8106.

39. Crosse J, Loukas A, Opdebeck J, Fairley S, Proovic P (1994) Human enteric infection with canine hookworms. Am J Trop Med Hyg 50: 369–374.

40. Brenner MA, Patel MB (2003) Cutaneous larva migrans: the creeping eruption. Cutis 72: 111–113.

41. Mower JP, Stefanovic S, Young JG, Palmer JD (2004) Plant genetics: gene transfer from parasitic to host plants. Nature 432: 165–166.

42. Houck MA, Clark JB, Peterson KR, Kidwell MG (1991) Possible horizontal transfer of *Drosophila* genes by the microtubule-binding protein *Tc1*. Nature 352: 387–390.
54. Laha T, Kewgrai N, Loukas A, Brindley PJ (2005) Characterization of SR3 reveals abundance of non-LTR retrotransposons of the RTE clade in the genome of the human blood fluke, Schistosoma mansoni. BMC Genomics 6: 154.

55. Ivics Z, Izsvak Z, Hackett PB (1999) Genetic applications of transposons and other repetitive elements in zebrafish. Methods Cell Biol 60: 99–131.

56. Bessereau JL, Wright A, Williams DC, Schuske K, Davis MW, et al. (2001) Mobilization of a Drosophila transposon in the Caenorhabditis elegans germ line. Nature 413: 70–74.

57. Han JS, Boeke JD (2004) A highly active synthetic mammalian retrotransposon. Nature 429: 314–318.