DNA-binding activity and subunit interaction of the \textit{mariner} transposase

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ABSTRACT

\textit{Mos1} is a member of the \textit{mariner}/\textit{Tc1} family of transposable elements originally identified in \textit{Drosophila mauritiana}. It has 28 bp terminal inverted repeats and like other elements of this type it transposes by a cut and paste mechanism, inserts at TA dinucleotides and codes for a transposase. This is the only protein required for transposition \textit{in vitro}. We have investigated the DNA binding properties of \textit{Mos1} transposase and the role of transposase–transposase interactions in transposition. Purified transposase recognises the terminal inverted repeats of \textit{Mos1} due to a DNA-binding domain in the N-terminal 120 amino acids. This requires a putative helix–turn–helix motif between residues 88 and 108. Binding is preferentially to the right hand end, which differs at four positions from the repeat at the left end. Cleavage of \textit{Mos1} by transposase is also preferentially at the right hand end. Wild-type transposase monomers interact with each other in a yeast two-hybrid assay and we have used this to isolate mutations resulting in reduced interaction. These mutations lie along the length of the protein, indicating that transposase–transposase interactions are not due to a single interaction domain. One such mutation which retains both DNA-binding and catalytic activity has greatly reduced ability to excise \textit{Mos1} from plasmid DNA through coordinate cleavage of the two ends and transposition \textit{in vitro} is lowered to a level 20-fold below that of the wild-type. This suggests that transposase–transposase interaction is required to form a synaptic complex necessary for coordinate cleavage at the ends of \textit{Mos1} during transposition. This mutant enzyme allows insertion at dinucleotides other than TA, including sequences with GC base pairs. This is the first example of a \textit{mariner}/\textit{Tc1} transposase with altered target specificity.

INTRODUCTION

\textit{Mariner} is a transposable element with short terminal inverted repeats and was first identified during analysis of an unstable mutation in the \textit{white} gene of \textit{Drosophila mauritiana}. This mutation results in a peach eye colour and is due to insertion of a 1.3 kb transposable element, \textit{mariner}. This can excise in somatic cells to give mosaic eyes and in germ cells to give progeny with wild-type red eyes in the next generation. This particular element does not produce functional transposase and excises at high frequency in strains carrying autonomous \textit{mariner} elements (1,2). The autonomous element \textit{Mos1} was isolated from one such strain (3). \textit{Mariner} and elements closely related to it, \textit{mariner}-like elements (MLEs), have been found to occur naturally in other species of \textit{Drosophila}, although not \textit{Drosophila melanogaster}, and in a wide variety of insects, other arthropods, planaria, nematodes, fungi, fish and mammals, including man (4–8).

The \textit{Mos1} element is 1286 bp long, has 28 bp imperfect terminal inverted repeats and contains a single open reading frame which codes for a 345 amino acid polypeptide (3). This is the transposase responsible for \textit{mariner} transposition (9,10). Comparison of the putative amino acid sequences of the proteins encoded by MLEs from different families shows that they have an average of 34% sequence identity and that they are similar to the transposases encoded by another large family of elements, including the Tc1 and Tc3 elements found in \textit{Caenorhabditis elegans} (11,12). The transposases encoded by \textit{mariner}/\textit{Tc1} elements contain conserved acidic residues equivalent to the D,D(35)E motif found in retroviral integrases and the transposases of several transposable elements in prokaryotes (13,14), where it is required for coordination of a divalent cation needed to catalyse phosphoryl transfer reactions during transposition (14). In the Tc1 family this motif takes the form D,D(34)E whereas it is D,D(34)D in MLEs (15). This catalytic domain is located in the C-terminal two-thirds of the transposases encoded by MLEs. The N-terminal region contains the DNA-binding domain including a helix–turn–helix motif which is required for recognition of the terminal inverted repeats of the corresponding elements (16,17).

Our understanding of the mechanism by which \textit{mariner}/\textit{Tc1} elements transpose is based on the results of experiments using the transposases of Tc1 (18), Tc3 (19), \textit{mariner} (10) and a reconstructed MLE, \textit{Himar1} (20). These elements are believed to transpose by cut-and-paste mechanisms similar to that used by Tn10 (21), Tn5 (22) and Tn7 (23) of \textit{Escherichia coli} and \textit{P} elements of \textit{Drosophila} (24,25). Transposition of these elements is initiated by binding of transposase to each end of...
the element, bringing the ends together to form a synaptic complex. Each DNA strand is then cleaved at, or near, the junction of the element and flanking DNA. Cleavage at the 3'-end of each strand of Tc1, Tc3 and Himar1 occurs precisely at the junction of the element and flanking DNA. Cleavage at the 5'-end occurs within the element, 2 nt in the case of both Tc1 and Tc3 and 3 nt for Himar1 (18–20,26). A transposable element released in this way is thought to integrate at a new site as the result of nucleophilic attack on the target DNA by the 3'-hydroxyl residue of the excised element followed by trans-esterification that covalently links each strand of the transposon to the target. This is always to the 5'-side of thymidine nucleotides at the sequence TA in the target. After integration the single-stranded gaps at the 5'-ends of the transposed element are repaired by host enzymes generating a TA target site duplication and replacing nucleotides lost at the ends of the element during excision.

We have purified the transposase encoded by Mos1 after expression in E.coli. This can excise Mos1 from plasmid DNA and mediate transposition of a marked element in vitro. We have shown that the protein recognises the inverted repeats at the ends of Mos1 in a sequence-specific manner via a DNA-binding domain located within the N-terminal 120 amino acids and that it binds the right hand inverted repeat about five times more strongly than the left. Yeast two-hybrid assays have shown that transposase monomers bind to each other (27) and we have isolated mutations which reduce this interaction. These are distributed along the length of the protein, indicating that no single protein–protein interaction domain is involved. One of these mutations lies between the DNA-binding and catalytic domains of the protein and reduces coordinate cleavage at the ends of mariner during excision, reduces in vitro transposition 20-fold and alters target site selection, indicating the importance of interaction between transposase monomers during transposition.

**MATERIALS AND METHODS**

**DNA constructs**

DNA coding for amino acids 1–150 of the Mos1 transposase was amplified from pBSMos1 using primers N6799 (GGCATATGTGCTTTTTCGTGCA) and A6499 (GCGATATGTTAAATGCAAAACGACTTCC). These primers contain a NdeI restriction site for insertion of the amplified fragment into PET-15b (Novagen, Madison, WI) after first cloning into pGEM-T (Promega). Deletion derivatives of this 150 amino acid sequence were made similarly using appropriate primers. In each case the downstream primer places a stop codon immediately following the transposase coding sequence. Site-directed mutagenesis was used to change codon 106 from GCC to GGC and codon 112 from AAG to GCG. The identity of each clone was confirmed by DNA sequencing.

The Mos1 sequence encoding the mariner transposase was inserted into the expression vector pBCP368 (28). PCR was carried out using pBSMos1 as the template and primers GCCATATGTGCTTTTTCGTGCC and GCGATATGTTAATGCAAAACGACTTCC, which contain sites for the restriction enzymes NdeI and EcoRI, respectively. The 1 kb fragment generated in this way was initially inserted into the pGEM-T vector. The resulting plasmid, pGEM-Mos1, was digested with EcoRI, the cohesive end filled in using Klenow polymerase, digested with NdeI and the fragment containing the transposase gene was inserted into pBCP368 which had previously been digested with NdeI and Smal. This gave the plasmid pBCP Mos1. The sequence of the transposase gene was confirmed at the end of the construction.

All recombinant plasmids were initially grown in strain DH5α (29). Recombinant proteins were expressed in strain BL21 (DE3).

**Protein purification**

Cells expressing the N-terminal derivatives of Mos1 transposase were grown in L broth at 37°C to an OD600 of 0.6 and then induced with 1 mM IPTG for a further 4 h. The cells were harvested and lysed by sonication in 5 mM imidazole, 500 mM NaCl, 20 mM Tris–HCl pH 7.9. The lysate was centrifuged and the supernatant filtered through a 0.45 µm filter before being loaded on a column of nickel resin (Novagen). Bound protein was eluted with TBS (150 mM NaCl, 20 mM Tris–HCl pH 7.9) with 50 mM EDTA and then dialysed against TBS.

The full-length mariner transposase used in these experiments was purified from E.coli strain BL21 DE3 carrying the plasmid pBCP Mos1. These cells were grown in L broth in an orbital shaker (200 r.p.m., 37°C) to an OD600 of 0.4, when they were induced for 2 h by the addition of IPTG to 0.5 mM. Following induction the cells were harvested and stored at –20°C until required. The cells in the pellet from a 1 l culture were resuspended in 5 ml of 20 mM Tris–HCl pH 7.5, 10% glycerol, 2 mM MgCl₂, 1 mM DTT. Lysozyme was added to a concentration of 0.1 mg/ml and the cells incubated for 5 min at room temperature. They were then lysed by the addition of 5 ml of detergent buffer containing 25 mM Tris–HCl pH 7.5, 4 mM EDTA, 0.2 M NaCl, 1% deoxycholate, 1% NP-40, 1 mM DTT and incubated at room temperature for a further 15 min. MgCl₂ was added to a final concentration of 10 mM together with 100 µl of a 2000 U/ml DNase I solution. The extract was pipetted up and down until the viscosity decreased and was left at room temperature for 10 min. The whole cell extract was then centrifuged at 20 000 g for 30 min. The pellet was washed three times in 0.5% NP-40, 1 mM EDTA, followed by one wash in 6 M urea before finally being resuspended in 1 ml of 25 mM Tris–HCl pH 7.5, 6 M guanidine hydrochloride, 5 mM DTT. After centrifugation at 13 000 g for 10 min the supernatant was diluted 100-fold into 25 mM Tris–HCl pH 7.5, 8 M urea, 5 mM DTT, 10% glycerol buffer and loaded onto a 2 ml fast flow CM Sepharose column (Sigma) pre-equilibrated with the same buffer supplemented with 50 mM NaCl. Under these conditions denatured mariner transposase bound to the column. Protein was renatured on the column by passing a 200 µl linear gradient of 8–0 M urea in buffer at a rate of 1 ml/min. Following renaturation bound protein was eluted with a 20 ml linear NaCl gradient of 50 mM–1.0 M in 25 mM Tris–HCl pH 7.5, 1 mM DTT, 10% glycerol. Fractions containing mariner transposase were identified by SDS–PAGE and further concentrated by spinning through a centricon column (30 kDa molecular weight cut-off). The protein was stored at –70°C at a concentration of 0.25–0.5 mg/ml.
Gel retardation assays
Purified protein was incubated at 25 mM with 50 ng of poly(dl–dC) on ice in binding buffer [25 mM HEPES pH 7.5, 100 mM NaCl, 5 mM dithiothreitol (DTT), 5 mM spermidine, 1 mg/ml BSA, 5 mM CaCl$_2$, 20% glycerol] for 10 min before 2 ng of probe DNA was added and incubated for a further 4 h at 4°C. The DNA–protein complexes were then fractionated on an 8% polyacrylamide gel.

In vitro excision of the Mos1 element
Two hundred nanograms of supercoiled pMos plasmid (final concentration 1.89 nM), which contains the Mos1 element within a fragment of DNA from Drosophila simulans, was incubated in 25 mM HEPES pH 7.5, 100 mM NaCl, 10% glycerol, 2 mM DTT, together with 1 µg of BSA and 1 µg of poly(dl–dC)–(dl–dC), 5 mM MgCl$_2$, or 5 mM Mn(CH$_3$COO)$_2$, or Mos1 transposase to give a final concentration of 304 nM in a total volume of 20 µl at 30°C. Reactions were analysed by Southern blotting following separation on a 1% agarose gel (1× TAE). Fragments containing Mos1 sequences were detected by hybridisation with 32P-labelled pMos.

In vitro transposition assays and product analysis
In vitro transposition assays were carried out essentially as described for P element transposition by Kaufman and Rio (24). Three hundred nanograms (38 fmol) of donor plasmid, pBR334MosTet, was incubated with 200 ng (25 fmol) of pBSKS+ tetramer in the presence of varying concentrations of renatured Mos1 transposase and either 5 mM MgCl$_2$, 5 mM Mn(CH$_3$COO)$_2$, or 5 mM EDTA. Incubations were carried out at 30°C in 25 mM HEPES pH 7.5, 100 mM NaCl, 10% glycerol, 200 mg/ml acetylated BSA and 2 mM DTT for 60 min in a final volume of 20 µl. Reactions were stopped by the addition of 80 µl of STOP buffer (50 mM Tris–HCl pH 7.5, 0.5 mg/ml proteinase K, 10 mM EDTA, 250 µg/ml yeast RNA) and incubated at 37°C for 1 h. Samples were then extracted once with an equal volume of phenol:chloroform (1:1) and ethanol precipitation to give final resuspension in 10 µl of TE buffer (10 mM Tris–HCl pH 8.0, 1 mM EDTA). One microlitre of each sample was used to transform DH5α and incubating overnight at 37°C. The transformed cells were incubated at 37°C in 25 mM HEPES pH 7.9, 100 mM NaCl, 10% glycerol, 200 mg/ml acetylated BSA and 2 mM EDTA for 1 h with 50% SDS, 5 mM EDTA, 250 µg/ml yeast RNA, 2 µg/ml proteinase K, 10 mM EDTA, 250 µg/ml yeast RNA. The transformed cells were incubated at 37°C for 45–60 min with shaking before plating out 0.5 ml on L broth plates containing ampicillin (100 µg/ml) and tetracycline (12 µg/ml) and incubating overnight at 37°C. At the same time viable counts were performed on transformed cells and the number of ampicillin-resistant colonies calculated. Restriction enzyme analysis of DNA isolated from colonies growing on LB+amp+tet was used to check for the presence of the marked mariner element.

The DNA flanking de novo insertions of the Mos1 Tet element was also sequenced using primers directed outward from the ends of the Mos1 open reading frame. Primer V6892 anneals to nucleotides 123–101 of Mos1 sequence (CTATGGTTGGTCCAGACGTCAAGG) and primer V5054 (GGGGAAAAATGGTAAGGGTACGACGGGC) anneals to nucleotides 1169–1194 of Mos1. Sequencing reactions were carried out in the presence of [35S]dATP using the Sequenase v.2.0 DNA sequencing kit according to the manufacturer’s instructions (Amersham, Little Chalfont, UK).

Yeast two-hybrid assay
Yeast two-hybrid assays (30) were carried out using the host strain L40 [MATα, ade2, his3Δ200, trp1-901, leu2-3,112,ade2, lys2-801am, URA3::(lexAop)$_2$-lacZLYS2::(lexAop)$_2$-HIS3; 31] transformed as described (32).

Western blotting
Yeast transformants were grown in 5 ml of selective medium overnight at 30°C. Cells were then diluted into 50 ml of YPDA and incubated to an OD$_{600}$ of ~0.5. Aliquots of 3 ml of cells were pelleted and resuspended in 80 µl of ‘crack buffer’ (2% SDS, 80 mM Tris–HCl pH 6.8, 10% glycerol, 10 mM EDTA, 0.4 mg/ml bromophenol blue, 0.1 M DTT, 2 mM PMSF). About 40 µl of glass beads were added and the cells were vortexed for 1 min. After centrifugation for 3 min at 13 000 r.p.m., the supernatants were boiled for 3 min and fractionated on a 10% SDS–polyacrylamide gel.

Proteins separated by SDS–PAGE were transferred onto PVDF (Boehringer Mannheim) membranes, which were pre-soaked in methanol. Transfer was conducted at 40 V for 1.5 h in transfer buffer (9 g Tris, 43.2 g glycine to 3 l) using a Bio-Rad Trans-Blot cell. The membranes were incubated in 1% blocking solution (Boehringer Mannheim) overnight and then incubated with primary antibody (usually 1:1000–2000 dilution in 0.5% block) for 2 h. After washing with TBST for 1 h with four wash changes, the membranes were incubated with peroxidase-conjugated rabbit anti-mouse IgG (Santa Cruz) for 1 h. Following washing in several changes of TBST for 1 h, the bound antibodies were detected by chemiluminescence using a Boehringer Mannheim Chemiluminescence Western blotting kit. The membrane was incubated with detection solution for 1 min at room temperature and then exposed to film for 2–30 s.

RESULTS
DNA-binding domain of mariner transposase
The transposases of Tc1, Tc3 and pogo contain DNA-binding domains comprising helix–turn–helix motifs near their N-termini (16,17,33,34) and a helix–turn–helix motif is predicted to lie between residues 88 and 108 of the Mos1 transposase (35). In order to determine whether this forms the DNA-binding properties in gel retardation experiments. The probe for these experiments was a 176 bp fragment containing the left hand inverted repeat of a Mos1 element (17; see Fig. 3) it must be recognising the terminal inverted repeats, since these are the only sequences in common between their DNA-binding properties in gel retardation experiments. The probe for these experiments was a 176 bp fragment containing 108 bp of DNA from the right end of Mos1, including the 28 bp inverted repeat, and 66 bp of flanking DNA. Since transposase also binds to DNA from the left end of Mos1 (see Fig. 3) it must be recognising the terminal inverted repeats, since these are the only sequences in common between the two ends. We have confirmed this by DNase I protection (data not shown).

The N-terminal 150 amino acids of the transposase (N150) bound the right end of Mos1 in a sequence-specific manner since binding was competed by an excess of unlabelled probe fragment but not by equivalent amounts of a 131 bp fragment containing the left hand inverted repeat of a pogo element (17; Fig. 1A, lanes 2 and 3). We have mapped in more detail the
region of transposase required for binding using soluble extracts of *E. coli* cells expressing derivatives of N150 (Fig. 1B). Binding was still detected if 30 amino acids were deleted from the C-terminus of N150 but not if a similar deletion was made from the N-terminus (Fig. 1C). This indicates that a sequence-specific binding domain lies within the N-terminal 120 residues of Mos1 transposase. This appears to require the helix–turn–helix motif predicted to lie within this part of the protein, as changing the arginine at the seventh position of the second helix to alanine (R106A) abolishes DNA binding, whereas a similar mutation of the lysine six residues downstream and beyond the predicted helix (K112A) has no detectable effect (Fig. 2). This is consistent with the results of Augé-Gouillou *et al.* (36), who have determined that the DNA-binding domain of Mos1 transposase is within the first 140 residues.

### Transposases bind differentially to the two ends of Mos1

There are four mismatches between the inverted repeats of Mos1, including a difference at the first position, raising the possibility that the two ends of the element may be recognised by transposase with different efficiencies. We have investigated this by comparing the ability of cold left or right end competitor fragments to titrate transposase–DNA complexes formed with either left or right end probes. The right end competes ∼5-fold more efficiently for binding of the left end probe than does the left end competitor (Fig. 3, compare lane 4, which contains 20 ng of right end competitor, with lane 10, containing 100 ng of left end competitor). We have obtained similar results using the right hand probe, for which 35 ng of the right hand end competitor was equivalent to 180 ng of left end competitor (data not shown). These results indicate that transposase binds preferentially to the right hand end of Mos1. Similar results have been reported by Augé-Gouillou *et al.* (37), who have shown that an element with two right hand ends transposes more efficiently than the wild-type.

![Figure 1](image1.png)

**Figure 1.** Binding of Mos1 transposase to the ends of Mos1 DNA. (A) A 32P-labelled 176 bp fragment of DNA containing 108 bp from the right end of Mos1, including the inverted repeat, was mixed with 10 ng of purified N150 in the presence or absence of a 100-fold molar excess of competitor DNA as follows: lane 1, probe alone; lane 2, pogo DNA as competitor; lane 3, unlabelled probe DNA as competitor; lane 4, no competitor. (B) SDS–PAGE analysis of N-terminal deletion fragments of Mos1 transposase expressed in *E. coli*. Soluble proteins from sonicated cells were loaded on the gel. Lane 1, extract of cells containing the plasmid vector; lanes 2–5, extracts of cells containing plasmids containing DNA coding for amino acids 1–130, 1–120, 1–100 and 30–130, respectively. (C) DNA-binding ability of proteins shown in (B). The 32P-labelled fragment used in (A) was incubated with each of the extracts shown in (B) and fractionated on an 8% polyacrylamide gel. Lane 2, control extract; lane 3, amino acids 1–130; lane 4, amino acids 1–120; lane 5, amino acids 1–100; lane 6, amino acids 30–130.

![Figure 2](image2.png)

**Figure 2.** The DNA-binding domain of Mos1 transposase contains a helix–turn–helix. (A) The region of Mos1 transposase containing a putative helix–turn–helix. The amino acid residues concerned are indicated in bold, indicating those believed to be in the helices (H) and the turn (t). Asterisks indicated the residues mutated *in vitro*. (B) Gel retardation showing that mutation of Arg106 within the second helix abolishes DNA binding whereas mutation of Lys112 outside the helix does not. The same probe and conditions were used as in Figure 1A.
Transposase has to recognise both ends of *mariner* to excise the element from one site and insert it at another and it is likely that the ends are brought together as a result of interactions between transposase bound to the left and right end inverted repeats. This has been demonstrated in vitro for Tn5 and Tn10, each of which forms a synaptic complex comprising two transposase molecules and the two ends of the corresponding element (38,39). A similar synaptic complex may be formed by *mariner* transposase; indeed, transposase monomers have been shown to interact in a yeast two-hybrid assay (27).

In order to identify the region of transposase required for this interaction and to determine whether or not this is required for transposition we have isolated mutations which show reduced interaction. Cells of the *Saccharomyces cerevisiae* strain L40 containing lacZ and HIS3 reporter genes downstream of four and eight copies of the LexA binding site, respectively, were transfected with a derivative (pACTIIst-Mos1) of the plasmid pBTM116-Mos1, including the DNA-binding and catalytic domains of the protein. Of the 23 mutant plasmids sequenced and of these, 12 contained single base changes resulting in amino acid substitutions. The single amino acid changes affecting the interaction of transposase monomers while the amount of 3-amino-1,2,3-triazole (3-AT) required to prevent growth by inhibition of His3 protein gave a quantitative measure of the interaction.

When both pACTIIst and pBTM116 contained the full-length transposase sequence there was a strong interaction, giving colonies which stained well with X-gal and grew on medium with 20 mM 3-AT. No staining was seen with L40 cells carrying either plasmid alone and these cells were unable to grow in the presence of 0.5 mM 3-AT. In order to detect any single region of the protein which might be required for protein–protein interaction we first tested various deletion derivatives of the protein for their ability to interact with full-length transposase. The deleted sequences coding for amino acids 1–177, 1–300, 30–345, 90–345 and 170–345 were placed downstream of the LexA DNA-binding domain in pBTM116 and introduced into L40 cells together with pACTIIst-Mos1. In no case was the expression of lacZ or HIS3 above background. This was not due to lack of expression of the deleted transposase fusions as this was checked using antibodies to the LexA DNA-binding domain (data not shown). These results suggest that residues required for the interaction of transposase monomers are distributed along the length of the protein.

We have analysed the interaction between transposase subunits further by screening for point mutations which reduce subunit interaction. The transposase coding sequence with 50 bp of flanking DNA was amplified by PCR from pBTM116-Mos1 using *Taq* polymerase, either under standard conditions or conditions favouring the introduction of mutations (reduced concentration of one dNTP or with Mn<sup>2+</sup> rather than Mg<sup>2+</sup>; 42). The amplified DNA was then introduced, together with pBTM116 DNA digested with *EcoRI* and *PstI*, into L40 cells carrying pACTIIst-Mos1. The transfected cells were plated on medium lacking Leu, Trp and His (**L-WH**) to select for transformants in which pBTM116 had incorporated a molecule of amplified DNA by gap repair recombination. Transformants were streaked on –**L-WH** medium containing 0.5, 5 and 10 mM 3-AT to test their ability to form colonies, a reflection of the strength of the interaction between transposase monomers. About 10% of transformants grew poorly or not at all on 5 mM 3-AT, indicating a reduced interaction between monomers. The pBTM116-Mos1 plasmids from these transformants were cloned in *E.coli* and then introduced into L40 cells containing pACTIIst-Mos1 to check that they still showed reduced growth on 3-AT. Most gave a wild-type interaction.

The transposase coding sequence of each plasmid giving reproducibly reduced growth on 3-AT (Fig. 4A–C) was determined. Twenty-three mutant plasmids were sequenced and of these, 12 contained single base changes resulting in amino acid substitutions. The remainder had multiple base substitutions resulting in two or more amino acid changes. The single amino acids 1–177, 1–300, 30–345, 90–345 and 170–345 were placed downstream of the LexA DNA-binding domain in pBTM116 and introduced into L40 cells together with pACTIIst-Mos1. In no case was the expression of lacZ or HIS3 above background. This was not due to lack of expression of the deleted transposase fusions as this was checked using antibodies to the LexA DNA-binding domain (data not shown). These results suggest that residues required for the interaction of transposase monomers are distributed along the length of the protein.

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**Is interaction between transposase monomers required for transposition?**

If interaction between transposase monomers is required to form a synaptic complex, a mutation which disrupts this interaction would reduce transposition. Since transposition requires both the DNA-binding and catalytic activities of transposase we chose for analysis a mutation lying between the DNA-binding and catalytic domains of the protein. Of the
12 single amino acid substitutions affecting protein–protein interaction, six lie within the N-terminal 120 amino acids which we have shown are required for DNA binding, and of these five are within the putative helix–turn–helix motif. These are likely to have reduced DNA binding and we have confirmed this for one of them, S104P (data not shown). The catalytic domain presumably includes residues 156–284, the positions of the first and last residues of the DD(34)D triad. Four mutations lie within this region. Mutation L124S does not lie in either region (Fig. 4D).

We have purified L124S as described for wild-type transposase and confirmed that it recognises mariner ends in a gel retardation assay as described previously and tested its catalytic activity, together with that of wild-type transposase, in an in vitro excision assay using the plasmid pMos as substrate (Fig. 5A). Wild-type transposase generated a 1.3 kb fragment, the size of the Mos1 element, from supercoiled plasmid DNA, as well as a 6.7 kb fragment the size of the plasmid vector, and an 8 kb band the size of linear pMos. We have confirmed that, as expected, the 6.7 kb fragment hybridises to a pMos but not a Mos1 probe and that the 8 kb band hybridises to both (Fig. 5A). Since the 1.3 and 6.7 kb bands were seen with even the lowest amounts of enzyme used, we conclude that cleavage at the two ends of Mos1 is coordinated.

The mutant transposase, on the other hand, produced 6.7 and 1.3 kb bands only at the highest protein concentrations. This was not because of low catalytic activity, since the 8 kb full-length plasmid band, but not the 6.7 kb vector, accumulated in a similar manner with both the wild-type and mutant enzymes. This suggests that the mutant enzyme cuts the two ends of Mos1 independently of each other (Fig. 5A).

We have confirmed that the 8 kb molecules are due to cleavage at a single end by purifying them and digesting with Sall, which cuts once within mariner. This would produce a 937 bp fragment if the 8 kb band had been cut at the right end of mariner or 349 bp if cut at the left end. Both fragments were generated from the 8 kb band produced by wild-type transposase but the 937 bp fragment was about 10 times more abundant than the 349 bp fragment (Fig. 5C), presumably reflecting the preferential binding to the right hand inverted repeat. A similar pattern was seen when the 8 kb fragment generated by the L124S transposase was digested with Sall, demonstrating that catalytic activity and preferential binding to the right hand inverted repeat are retained by the mutant enzyme. This indicates that its reduced ability to excise Mos1 DNA is the result of reduced protein–protein interaction.

In order to determine the effect of reduced transposase–transposase interaction on transposition we have compared the efficiency of wild-type and mutant proteins to mediate transposition in vitro using a plasmid-based assay. The donor plasmid
contained a derivative of Mos1 into which we had inserted a tetracycline resistance cassette while the target plasmid was a tetramer of pBSKS+ (24). After incubating these plasmids with transposase for 1 h at 30°C the mixture was electroporated into E.coli strain DH5α (29) and the cells plated on nutrient agar containing either ampicillin alone or both ampicillin and tetracycline. Cells transfected with plasmids into which the marked Mos1 element had transposed would be AmpR,TetR so the ratio of AmpR to AmpR,TetR colonies gives a measure of the transposition frequency. The donor plasmid is unable to replicate in DH5α cells, reducing the chance that AmpR,TetR colonies could arise by other means.

Transposition was 10-fold higher in the presence of Mn2+ than with Mg2+ and was dependent on the concentration of transposase. No AmpR,TetR colonies were obtained in the absence of transposase or in the presence of 5 mM EDTA. The maximum frequency of transposition (0.8 × 10−3 per recipient plasmid) was obtained with transposase at a concentration of 12–24 nM, a ratio of protein to target DNA of 5:1. As we do not know what proportion of transposase molecules are active in our preparations we cannot say what ratio of active protein to DNA gave maximum activity. Transposition decreased rapidly at concentrations of transposase either above or below this, a 2-fold change in concentration reducing transposition ∼2-fold. This differs from results reported previously in which transposition increased with increasing amounts of Mos1 transposase (10) but is similar to the behaviour of Himar1 transposase (43).

Plasmid DNA isolated from 35 AmpR,TetR colonies derived from transposition in the presence of Mg2+ and 11 from transposition in Mn2+ were analysed by restriction digestion and agarose gel electrophoresis. In each case the plasmid had increased in size by 2.7 kb, as expected if they were the result of transposition of the marked mariner element. We have sequenced the DNA flanking the transposed elements in these plasmids to ensure that they are the result of bona fide transposition events (Fig. 6). All 35 insertions generated in the presence of Mg2+ were flanked by TA target site duplications, plasmids to ensure that they are the result of bona fide transposition events (Event 6). All 35 insertions generated in the presence of Mg2+ were flanked by TA target site duplications,
as is the case for mariner elements transposing in vivo (44). The distribution of insertions amongst the 306 TA dinucleotides in the target plasmid was non-random (P < 0.01) and the site used most frequently is also a hot spot for insertion of Himar1 (43). Six of the 11 insertions which took place in the presence of Mn2+ also had inserted at TA dinucleotides. The remainder had inserted at other A/T-containing dinucleotides, indicating that increased transposition in Mn2+ is at the expense of relaxed target site selection (Fig. 6).

In vitro transposition stimulated by the L124S mutant transposase was -20-fold lower than with wild-type in the presence of Mn2+ and was reduced further in Mg2+, indicating that the ability of transposase monomers to bind to each other is essential for normal transposition as well as for excision. We have analysed the target site duplications of insertions stimulated by L124S transposase under both conditions. While some of the insertions were into the dinucleotide TA the majority were at L124S transposase under both conditions. While some of the insertions were into the dinucleotide TA the majority were at

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**DISCUSSION**

Transposition of elements which move by excision and insertion requires recognition of the ends of the element by transposase, formation of a synaptic complex, cleavage at the ends of the transposon, capture of target DNA and integration to generate a characteristic target site duplication. All transposases studied so far recognise the ends of the corresponding element through an N-terminal DNA-binding domain, which is generally a helix–turn–helix motif. This has been most clearly demonstrated for Tc3, for which a polypeptide comprising the N-terminal 64 amino acids has been crystallised with its target DNA (16). We have shown that the same is true of Mos1 transposase, which has a DNA-binding domain within the N-terminal 120 amino acids, and that a helix–turn–helix predicted to run from residues 87 to 108 (35) is required for binding, as changing a basic residue (R106A) within the putative second helix abolishes binding whereas similar changes to the right (25). In this case it must be the sequence which lies between the transposase-binding sites and the terminal inverted repeats, or simply the distance of the transposase from the ends of the elements, which are critical for transposition (24).

Transposase molecules bound to the ends of a transposon associate to form a synaptic complex which may serve to ensure that cleavage of the ends is coordinated, reducing the possibility that cleavage of a single end, or of a fortuitous transposase-binding site, will produce a chromosome break. Tn10 (39) and Tn5 (38) form synaptic complexes which contain transposase dimers whereas bacteriophage Mu forms a synaptic complex with four monomers of MuA transposase, although only two of these take part in cleavage of the donor DNA (46).

There is no direct evidence for synaptic complex formation by transposases of the mariner/Tc1 family but the DNA-binding domain of Tc3 transposase forms a dimer when crystallised with DNA (16) and isolation of point mutations of Mos1 which reduce in vivo excision of mariner when heterozygous with wild-type Mos1 suggest that Mos1 transposase acts as an oligomer (27). Moreover, we have found that during in vitro excision the ends of Mos1 are cleaved coordinately, which presumably requires interaction between transposase molecules at either end.

We have confirmed earlier observations that Mos1 transposase interacts with itself in a yeast two-hybrid experiment (27) and have used this to isolate mutations which show reduced interaction. The results show that there is no single protein–protein interaction domain and these mutations were distributed along the length of the protein. Presumably interaction between transposase monomers involves regions of the protein brought together in the tertiary conformation. Several of the mutations lie within the helix–turn–helix required for recognition of the terminal inverted repeats. Sequence-specific DNA binding is not required for protein–protein interaction in the two-hybrid assay as the terminal inverted repeats are not present.

One mutation, L124S, which retains both DNA-binding and catalytic activities nevertheless has a 20-fold reduced ability to mediate transposition in vitro. It has also lost the ability to cleave the ends of Mos1 coordinately, suggesting that formation of a synaptic is required for mariner transposition. Although cleavage at the left and right ends is coordinated, it is not necessarily simultaneous, and preferential cleavage of the right end suggests that this is cleaved first. Since Mos1 transposase both binds and cleaves the right end preferentially it is likely that in the synaptic complex transposase monomers cleave the ends of the element in cis rather than in trans, as is the case for Tn5 (47) and Mu (48).

Surprisingly the L124S mutation also affects target site selection. mariner/Tc1 elements insert exclusively at TA dinucleotides in vivo and this specificity is retained in vitro if
transposition is carried out in the presence of Mg^{2+}. In the presence of Mn^{2+} insertion is still preferentially at TA, although insertions at other T/A-rich sequences are found. Although the L124S mutant still generates 2 bp target site duplications during in vitro transposition these include many sequences with a G or C at either position.

Mutations affecting target site selection have been identified for Tn10 transposase. These alter two residues within the catalytic domain but do not significantly reduce transposition frequencies (49), suggesting that interaction between transposase monomers and formation of a synaptic complex are not affected. Changing the glutamate residue of the DDE motif also reduces target site selection (50). No mutation affecting target site selection has been reported previously for a member of the mariner/Tc1 family of transposases. Our results suggest that L124 is either directly involved in target site selection or that this has changed as a consequence of the reduced ability of mutant transposase monomers to form a normal synaptic complex, with this being a prerequisite for normal integration.

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