The DNA-binding Polycomb-group protein Pleiohomeotic maintains both active and repressed transcriptional states through a single site

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Although epigenetic maintenance of either the active or repressed transcriptional state often involves overlapping regulatory elements, the underlying basis of this is not known. Epigenetic and pairing-sensitive silencing are related properties of Polycomb-group proteins, whereas their activities are generally opposed by the trithorax group. Both groups modify chromatin structure, but how their opposing activities are targeted to allow differential maintenance remains a mystery. Here, we identify a strong pairing-sensitive silencing (PSS) element at the 3' border of the Drosophila even skipped (eve) locus. This element can maintain repression during embryonic as well as adult eye development. Transgenic dissection revealed that silencing activity depends on a binding site for the Polycomb-group protein Pleiohomeotic (Pho) and on pho gene function. Binding sites for the trithorax-group protein GAGA factor also contribute, whereas sites for the known Polycomb response element binding factors Zeste and Dsp1 are dispensable. Normally, eve expression in the nervous system is maintained throughout larval stages. An enhancer that functions fully in embryos does not maintain expression, but the adjacent PSS element confers maintenance. This positive activity also depends on pho gene activity and on Pho binding. Thus, a DNA-binding complex requiring Pho is differentially regulated to facilitate epigenetic transcriptional memory of both the active and the repressed state.

KEY WORDS: Polycomb group, Trithorax group, Epigenetics, Pleiohomeotic, Even-skipped, Drosophila

INTRODUCTION

Polycomb group (PcG) proteins associate with specific DNA regions, forming complexes that modify chromatin and maintain a transcriptionally silent state (Grimaud et al., 2006; Muller and Kassis, 2006; Ringrose, 2007; Schuettengruber et al., 2007; Schwartz and Pirrotta, 2007). Among the genetically identified Drosophila PcG proteins, only Pleiohomeotic (Pho) and its homolog Pho-like (Phol) have sequence-specific DNA-binding activity (Brown et al., 2003; Brown et al., 1998; Fritsch et al., 1999). They, together with other DNA-binding proteins (Américo et al., 2002; Brown et al., 2005; Muller and Kassis, 2006; Ringrose and Paro, 2007; Schuettengruber et al., 2007), have been implicated in targeting each of the known PcG complexes (Cao et al., 2002; Czermin et al., 2002; Kuzmichev et al., 2002; Shao et al., 1999; Wang et al., 2004a) to their target genes. In mammals, PcG proteins are involved in maintenance of the stem cell niche (Buszczak and Spradling, 2006; Sparrmann and van Lohuizen, 2006) and in oncogenesis (Sparrmann and van Lohuizen, 2006).

Trithorax group (trxG) proteins oppose the action of the PcG (Kennison, 2004), form complexes that target DNA (Badenhorst et al., 2002; Bantignies et al., 2000; Fyodorov et al., 2004; Papoulas et al., 1998; Petruk et al., 2001) and maintain an active state, by modifying histones and remodeling chromatin. PcG and trxG proteins are considered to be distinct from other regulators in that they can mediate heritable maintenance of the transcriptional state from one cellular generation to another (Grimaud et al., 2006; Muller and Kassis, 2006; Ringrose and Paro, 2007; Schuettengruber et al., 2007; Schwartz and Pirrotta, 2007). Target sequences that mediate the functions of these proteins are termed PcG- and trxG-responsive elements (PREs and TREs, respectively) or, collectively, maintenance elements (MEs) (Brock and van Lohuizen, 2001), because they often overlap. Dissection of these target elements has proven to be difficult, because of their complexity, and because the associated activities manifest themselves fully only in a developmental context. Consequently, how PcG and trxG complexes are targeted to DNA, and how this targeting varies with the transcriptional state, is just beginning to be elucidated.

Transgenes carrying PREs/TREs in Drosophila have been seen to share a property known as pairing-sensitive silencing (PSS) (Gindhart and Kaufman, 1995; Kassis, 2002). Transgenic flies carrying the mini-white gene typically have eye colors ranging from yellow to orange in a white mutant background. Normally, flies that are homozygous for such a transgene have a darker eye color than heterozygotes, as the genetic dose of mini-white is doubled. However, with transgenes carrying PRE/TREs, the eye color is often lighter in homozygotes than in heterozygotes. PSS is also often accompanied by a reduction in mini-white activity from heterozygous transgenes, causing a relatively faint eye color, or a variegated pattern of eye coloration. This phenomenon was first reported for a pairing-sensitive element (PSE) near the engrailed (en) transcription start site (Kassis, 1994; Kassis et al., 1991). It was also shown that the en PSE can function as a PRE in embryos, in that it can restrict expression of a transgenic reporter gene driven by the Ultrabithorax (Ubx) regulatory region bithoraxoid (bxd) to the posterior part of the embryo, where Ubx is normally expressed, in a PcG-dependent manner (Americo et al., 2002). More generally, although PREs usually exhibit PSS activity, PSEs may not be sufficient to function as a PRE (Kassis, 1994; Kassis, 2002).

Genome-wide predictions of possible Drosophila PREs using sequences common to known PREs, including binding sites for the PcG and trxG proteins Pho/Phol, GAGA factor (GAF) and Zeste,
identified 167 candidates, including the even skipped (eve) promoter region (Ringrose et al., 2003). Other studies using two different techniques to determine in vivo protein binding (ChiP on chip and DamID) identified other candidate PREs with some, although not extensive, overlap (Negre et al., 2006; Schwartz et al., 2006; Tolhuis et al., 2006). These studies suggested that the eve locus is bound by the Polycomb (Pc) protein (Schwartz et al., 2006; Tolhuis et al., 2006). Earlier, mapping of binding sites for Pc and Polyhomeotic (Ph) on polytene chromosomes identified the cytological location of eve (Sinclair et al., 1998). Consistent with this, eve is ectopically expressed in the embryonic nervous system in mutants of the PcG gene ph (Smouse et al., 1988).

Here, we show that the Drosophila eve gene is regulated by a Pho-dependent maintenance element located 9 kb downstream of the promoter. This element maintains repression in cells where eve is turned off during early development, but maintains the active state in other cells. Both negative and positive maintenance depend on Pho binding, and on pho gene activity. The element shares properties with other PREs, including binding sites for several Dsp1 may be dispensable, and that Grainyhead/Eif1 (Bray and Kafatos, 1991), as well as unknown factors, may also contribute. Thus a ‘core’ DNA-binding component, differentially modified or regulated by the existing transcriptional state, mediates epigenetic maintenance of that state.

MATERIALS AND METHODS

Plasmids construction

All sequence coordinates in the eve locus are relative to the transcription start site (+1). The parental P-element plasmid containing Glass-binding sites has been described previously (Fujioja et al., 1999). To construct the PSS assay transgenes of Fig. 1, eve DNA from +8.9 to +9.2 kb (PRE300) was cloned upstream of the Glass-binding sites followed by mini-white DNA. Pho sites also cloned (PRE1, PRE2; details available on request). Then, GFP-RR described above was transferred to this vector. For the PRE assays of Fig. 2, a P-element based bxd-Ubx-Z vector (with a bxd enhancer fragment inserted upstream of the 3′.1 Ubx-Gal fusion in Ubgα) (Muller and Bienz, 1991) was modified by inserting PRE300 (with or without the Pho site mutated) into the Xαd site, orientated such that the PRE300 3′ end was closer to the Ubx promoter. For RMCE, the PRE300 (with or without the Pho site mutated)-bxd-Ubx-Z region was transferred to attB2. PRE300 was also replaced by a 500 bp phage DNA fragment as non-PRE negative control in this context. (500-bxd-Ubx-Z). Binding site mutations used in this study are shown in Fig. 3.

Transgenic and genetic analysis

P-element-based transgenic lines were established as previously described (Fujioja et al., 2000; Rubin and Spradling, 1982). RMCE was performed as previously described (Bateman et al., 2006). The attP target lines used were chosen at chromosomal locations that were not suggested to have PREs nearby (Negre et al., 2006; Schwartz et al., 2006; Sinclair et al., 1998; Tolhuis et al., 2006). The attP target lines 25C, 52D (Bateman et al., 2006) and 78C4 (obtained in our laboratory) were used for inserting GFP-RR. For RMCE of bxd-Ubx-Z constructs, 25C, 52D, 78C4 and 95E5 (obtained in our laboratory) lines were tested. 52D and 95E5 were used for further analysis. For staining with anti-β-gal (ICN, 1:1000 dilution), embryos were collected for 6 hours at room temperature (RT), then incubated at 17°C for 15 hours. The antibody was visualized using biotin-conjugated anti-rabbit IgG followed by peroxidase-conjugated streptavidine, with DAB as a substrate.

For Fig. 4, each central nervous system (CNS) was dissected out in phosphate-buffered saline, placed on a poly-L-lysine-coated cover slip, and covered with a non-coated cover slip using another cover slip as a spacer to prevent flattening.

For pho mutant analysis of PSS, six PRE300-carrying lines (including two GFP-RR lines) that showed PSS were crossed to generate PRE300/pho/ci2. Larvae from these stocks were grown at room temperature, and pharate adults were dissected to analyze their eye color. For pho and phol mutant analysis of positive maintenance in the CNS, a mini-white P-element-based GFP-RR line was used to produce GFP-RR:pho/FM7;TM6β, Th. GFP-RR:pho/ci2 or GFP-RR:pho/FM7;TM6β, Th. pho/ci2, which were then self-crossed. Homozygous phol larvae were tentatively identified as non-Tubby, and confirmed post hoc by PCR. In all cases, homozygous pho and pho/ci2 larvae and pupae were identified post hoc by PCR analysis of their DNA (Brown et al., 2003). GFP-RR at 52D was crossed into mutant backgrounds to produce GFP-RR(52D);E(eve)61/TM6β, Th. GFP-RR(52D);E(eve)61/TM6β, Th. and GFP-RR(52D);Trh1/IC/TM6β, Th. Homozygous mutant larvae from these lines were identified by their non-Th phenotype. For E(eve), eggs were collected at 18°C for 24 hours, kept at 18°C until near hatching, then moved to 29°C until the third larval instar. For trh1, eggs were collected similarly, then moved to 25°C until the third larval instar. For Trh1/IC, eggs were collected similarly, and kept at 18°C until the third larval instar.

To test effects of PgC mutations on eve PRE activity, lines homozygous for bxd-Ubx-Z-derived transgenes (at target site 52D) were each crossed with ph503/FM7, B or Pc/ci2/TM3, Sb. Then, ph503/+, bxd-Ubx-Z/+, (non-B) females were crossed with homozygous bxd-Ubx-Z males, while bxd-Ubx-Z/+, Pc/ci2/+ (non-Sb) males and females were intercrossed. Resulting embryos were collected as described above. Homozygous mutant embryos were identified by ectopic lacZ expression in anterior regions of embryos, which were not present in a wild-type background. For ph503, the ectopic lacZ phenotype of hemizygous mutant embryos was confirmed by double-staining for ectopic expression in the CNS (Smouse et al., 1988).

Chromatin immunoprecipitation

Chromatin immunoprecipitation (ChiP) analysis was performed as follows. Dechorionated embryos were crosslinked with 2% formaldehyde for 15 minutes at room temperature, washed and stored at –80°C. About 200 μl of embryos were homogenized in 1 ml Buffer A (350 mM sucrose, 15 mM HEPES pH 7.6, 10 mM KCl, 5 mM MgCl2, 0.1 mM EDTA, 0.5 mM EGTA). Homogenates were centrifuged at 600 g for 5 minutes to pellet nuclei, which were then washed gently with 1 ml Buffer A and repelleted. Pellets were resuspended in 1 ml Buffer A containing 0.2% Triton-X100, incubated for 5 minutes on ice, then layered on top of 3 ml 800 mM sucrose (in Buffer A) in 15 ml conical-bottom tubes, and centrifuged at 250 g for 10 minutes. The pellets were subjected to ChiP analysis essentially as described previously (Wang et al., 2004b), using Pho-specific antisera (Brown et al., 1998). PCR primer sequences will be provided on request.

RESULTS

The eve 3′ boundary region contains a strong PSE

In a previous study, we reported that a region between +8.6 and +9.2 kb (relative to the eve transcription start site), at the 3′ end of the eve locus, caused PSS of mini-white expression in transgenes (Fujioja et al., 1999). This region also caused repression of mini-white expression in heterozygotes, making it difficult to use a standard mini-white-containing P-element vector to generate transgenic lines, because complementation of the white* phenotype was extremely weak at most chromosomal locations (data not shown). In such a case, it is likely that insertions at many sites are missed, resulting in a biased sampling of potential insertion sites. To overcome this problem, three tandem Glass activator-binding sites, which are active specifically in the eye disc, were introduced just upstream of the mini-white promoter to increase expression (Fujioja et al., 1999). This Glass site vector was also used in the analysis of the en PRE (Americo et al., 2002), where it was shown that the presence of Glass...
sites does not affect the percentage of PRE-carrying transgenic insertions that exhibit PSS. As expected, with the Glass-binding sites, the range of eye colors of heterozygous transgenic flies shifted toward the dark end of the spectrum (Fig. 1, compare ‘with Glass’ with ‘without Glass’; note that none of these lines carry a PSE). Among 53 independent lines carrying the Glass vector without the PSE, 43 were homozygous viable and none showed PSS (Fig. 1, ‘with Glass’).

We dissected the original 600 bp PSE (+8.6 to +9.2 kb, data not shown) down to an active region of 300 bp (+8.9 to +9.2 kb). The resulting element caused repression of Glass-augmented mini-white expression in heterozygous transgenic flies, as evidenced by the resulting shift toward lighter eye colors (‘PRE300’ in Fig. 1; compare with ‘with Glass’). Among homozygous viable lines, 73% of them showed PSS activity (Fig. 1, Fig. 2A,B). We refer to this element as a PRE because of these results together with further results described below.

The eve promoter region (from about −700 to −100 bp), but not the eve 3’ region, was previously identified in a genome-wide prediction of PRE/TREs based on a clustering of Pho-, GAF- and Zeste-binding sites (Ringrose et al., 2003). We discovered that the eve promoter region from −275 to +166 bp also has PSS activity. Fifty-three percent of transgenic lines carrying this region showed PSS (PSEpro, Fig. 1). Although the combination of PRE300 with the eve promoter caused more repression of heterozygous mini-white expression than did either one alone, PSS activity itself was not increased relative to that of PRE300 (PRE300 + PSEpro, Fig. 1).

eve PSS activity depends on a Pho binding site, and requires pho

As the eve 3’ PRE showed stronger activity than the promoter, we focused on the 3’ PRE in further experiments. Previous dissections of PSS regions from the en gene (Americo et al., 2002), the MCP silencer (Busturia et al., 2001) and the lab-7 PRE (Hagstrom et al., 1997; Mishra et al., 2001) (both from the bithorax complex) showed that activity depended on both Pho- and GAF-binding sites. PRE300 contains one perfect match to the Pho-binding site consensus and three close matches to the GAF consensus. Mutating the single Pho site (Fig. 3) strongly reduced PSS activity from 73% to 11% (PRE300Δpho, Fig. 1). This was accompanied by a shift in the spectrum of heterozygous eye colors back to that observed without the PSE, suggesting that the cis-repressive activity of PRE300 is entirely dependent on the Pho site. Mutating two or all three of the GAF sites (Fig. 3) caused a progressive decrease of PSS activity, but only to 53% (Fig. 1: PRE300Δgaga1, Δgaga12 and Δgaga123). Mutating GAF sites also did not have as much of an effect on heterozygous eye color as did mutating the Pho site. These data suggest that the PSS activity of PRE300 depends only weakly on GAF binding sites, whereas, like other PSEs examined in detail, it is strongly dependent on the Pho-binding site.

In order to test whether this Pho-binding-site dependence reflects an actual dependence on Pho binding, or whether it might be due to some overlapping DNA-binding activity, we placed several PRE300-carrying lines in a pho1 mutant background. As pho1 mutants die as pharate adults, it was necessary to dissect pupae in order to examine their eye color. Compared with a wild-type background, the homozygous eye color was darker in pho1 mutants in all six lines examined. This effect was very strong in one line (Fig. 2E,F), whereas the other lines showed less complete, albeit still clear, derepression (Fig. 2C,D; data not shown). Incomplete derepression is expected in the pho1 mutants, because the pho-like gene (phol) provides a partially redundant function with that of pho. It is not possible to carry out this analysis in phol14; pho1 double mutants, because they fail to pupariate (Brown et al., 2003). The irreversibility of these genetic data with the Pho-binding-site dependence of PSS strongly suggests that Pho is directly involved in silencing through PRE300.

The involvement of known factors in eve PSS activity

Among known PREs/TREs, binding sites for Pho/Phol, GAF/Pipsqueak, Sp1/KLF, Zeste and Dsp1 were found to be clustered (Brown et al., 2005; Muller and Kassis, 2006; Ringrose, 2007; Schuettengruber et al., 2007). PRE300 contains all of these
Is the eve PSE a PRE?

Although PSS activity is often seen with transgenes carrying a PRE, not all PSEs can act as a PRE (Kassis, 2002). We directly tested for PRE activity of eve PRE300 by combining it in a transgene with a bxd-Ubx-Z reporter gene. This reporter is expressed throughout the ectoderm and nervous system in late-stage embryos (Muller and Bienz, 1991). However, when a PRE is inserted into this reporter, it can prevent activation of lacZ expression in parasegments 1-5, similar to the endogenous Ubx PRE from the bxd region (Americo et al., 2002; Brown et al., 2005; Busturia and Bienz, 1993; Hagstrom et al., 1997; Horard et al., 2000; Muller and Bienz, 1991). In two out of four P-element-based transgenic lines carrying PRE300 in this reporter, we observed an anteriorly restricted lacZ pattern (similar to Fig. 2H, data not shown). Similarly, studies of other PReS in this reporter found that not all transgenic lines showed repression (Americo et al., 2002; Brown et al., 2005; Busturia and Bienz, 1993; Hagstrom et al., 1997; Horard et al., 2000; Muller and Bienz, 1991), presumably owing to the effects of different chromosomal contexts. In order to further analyze the PRE activity of PRE300, we incorporated the bxd-Ubx-Z reporter into a vector for RMCE (Bateman et al., 2006; Groth et al., 2004), which allows the analysis of multiple

binding sites, including two Dsp1 sites, three GAF sites, two Sp1/KLF sites, one Zeste site and one Pho site (Fig. 3). It has also been shown that the grainyhead (grh) gene product (Bray and Kafatos, 1991), which was originally identified as a transcriptional activator termed Elf-1 (Bray et al., 1989), physically interacts with RING, a PcG gene product (Tuckfield et al., 2002). Importantly, activator termed Elf-1 (Bray et al., 1989), physically interacts with Kafatos, 1991), which was originally identified as a transcriptional grainyhead

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overlapping parts (PRE300-5/H11032)

are required for its PSS activity, PRE300 was split into two consensus site (Fig. 3).

In order to test whether these binding sites are required for its PSS activity, PRE300 was split into two overlapping parts (PRE300-5’ and PRE300-3’). As the Pho site is necessary for the activity, this site was included in both parts (Fig. 3). Surprisingly, PRE300-5’, which includes all of these sites except for one Sp1/KLF, one GAF and the Grh site, showed PSS activity in only 5% of transgenic lines (Fig. 1). By contrast, PRE300-3’, which contains only the Pho site, one Sp1/KLF site, the Grh site and one of the GAF sites, showed almost full PSS activity (69% versus 73% for PRE300, Fig. 1). These data suggest that only a subset of known binding sites are required for the PSS activity of PRE300, and further suggest that other, unidentified factors may well be involved.
transgenic constructs at the same chromosomal location. We initially tested PRE300-bxd-Ubx-Z inserted at four different chromosomal target sites, two of which were used in a previous study (Bateman et al., 2006) and two others that we developed. All four targeted lines showed an anteriorly restricted pattern (Fig. 2H,N, compare with Fig. 2G,M, which carry non-PRE DNA as a negative control, and data not shown). We tested the effect of mutating the Pho site in PRE300 in three of these chromosomal contexts, and all three showed significant anterior derepression (Fig. 2I,O; data not shown). We further tested one of these contexts, and all three showed significant anterior derepression of repression in anteriorly expanded expression, there appears to be a partial loss with 2J). In addition to a strong effect in significantly reduced in each of these mutants (compare Fig. 2K,L PcG genes, using the alleles (Fig. 2I,O; data not shown). We tested the effect of mutating the Pho site in PRE300 in three of these chromosomal target sites, two of which were used in a previous study (Bateman et al., 2006) using the RMCE system, one with an unaltered PRE300 (E), the other with the single Pho site mutated (F). Mutation of the Pho site at 2006) using the RMCE system, one with an unaltered PRE300 (E), the other with the single Pho site mutated (F). Mutation of the Pho site at 2006) using the RMCE system, one with an unaltered PRE300 (E), the other with the single Pho site mutated (F). Mutation of the Pho site at

Fig. 4. Pho is directly involved in maintaining eve CNS expression. (A) GFP expression driven by the eve RR regulatory region in the wandering third instar larval CNS, in a wild-type background. When a region including PRE300 was removed from the RR transgene construct (to generate RN, see text), GFP expression was not maintained to the third larval instar (not shown). (B) Mutation of a single Pho-binding site decreased the intensity and penetrance of GFP expression (sequences shown in Fig. 3). This line is representative of five out of the eight lines with normal embryonic expression; the other three showed essentially complete loss of expression at this stage, similar to F. (C,D) The same GFP-RR transgenic line shown in A in either a doubly homozygous pho1pho1, pho1 (C) or a homozygous pho1 (D) mutant background. (A-D) Arrows/arrowheads indicate eve-positive aCC/RP2 neurons in two adjacent hemisegments. (B-D) Note that GFP expression is decreased in both aCC and RP2 neurons, and the effect tends to be more pronounced in RP2 neurons. (E,F) Two GFP-RR lines inserted at the same chromosomal location (site 25C) (Bateman et al., 2006) using the RMCE system, one with an unaltered PRE300 (E), the other with the single Pho site mutated (F). Mutation of the Pho site at this chromosomal location abolishes specific expression, as well as increasing background expression throughout the CNS.

Fig. 3. Binding site diagram and sequence of eve PRE300. The line diagram at the top and the sequence below show the locations of consensus binding sites for the known PRE-binding proteins Dsp1 (red), Zeste (blue), Sp1 (green) (Brown et al., 2005), Grh (purple) (Blastyak et al., 2006), and the functional Pho- (black, bold) and GAF-binding sites (black, solid underlines) based on our mutational analysis (see text). PRE300Δgaga1 (see Fig. 1) has the 5′-most GAF site mutated, whereas PRE300Δgaga12 has the 5′-most and the 3′-most sites mutated. The extents of the sub-elements PRE300-5′ and PRE300-3′ are shown as solid lines in the diagram. The sequences used to eliminate the GAF and Pho sites are shown under the main sequence. BsrGI and EcoRI restriction enzyme sites are marked with broken underlines.

Pho contributes to positive maintenance of CNS expression

Eve is expressed in several sets of neurons within each hemisegment of the embryonic central nervous system (CNS), including RP2, a/pCC, CQ/U and the EL clusters. Each of these aspects of expression is decreased in both aCC and RP2 neurons, and the effect tends to be more pronounced in RP2 neurons. (A-D) Arrows/arrowheads indicate eve-positive aCC/RP2 neurons in two adjacent hemisegments. (B-D) Note that GFP expression is decreased in both aCC and RP2 neurons, and the effect tends to be more pronounced in RP2 neurons. (E,F) Two GFP-RR lines inserted at the same chromosomal location (site 25C) (Bateman et al., 2006) using the RMCE system, one with an unaltered PRE300 (E), the other with the single Pho site mutated (F). Mutation of the Pho site at this chromosomal location abolishes specific expression, as well as increasing background expression throughout the CNS.
independently inserted transgenes tested, eight gave normal expression in the embryonic CNS. Of these eight, three completely failed to maintain expression to the third larval instar (data not shown, similar to Fig. 4F), and the other five showed relatively weak and variable expression of GFP in third instar larvae (Fig. 4B and data not shown). As the Pho dependence of positive maintenance seemed to be affected somewhat by the chromosomal context, we confirmed these results by examining expression in a pair of lines, one with the Pho site mutated, inserted at the same chromosomal location using RMCE. At this target site, although GFP expression in third instar larvae was somewhat weaker than in the random insertion line shown in Fig. 4A, expression in third instar larvae was nonetheless abolished when the Pho site was mutated (Fig. 4E,F). Thus, the maintenance of CNS expression by PRE300 requires the Pho-binding site.

GAF has been shown to affect the activity of other PREs (Busturia et al., 2001; Hagstrom et al., 1997; Hodgson et al., 2001; Horard et al., 2000; Mishra et al., 2001), and to facilitate binding of Pho to a chromatinized PRE (Mahmoudi et al., 2003). Moreover, mutations in GAF sites affect the PSS activity of PRE300 (Fig. 1). Therefore, we tested the effects of GAF site mutations using both conventional P-element transformation and RMCE. When all three GAF sites were mutated, GFP expression depended strongly on the insertion site. Although two out of 11 random insertion lines showed similar levels of expression in third instar larvae as transgenes carrying wild-type PRE300, four out of 11 lines showed weak expression, and five out of 11 lines showed ectopic expression throughout the CNS, such that we could not discern the intensity in RP2 and dppCC neurons. When RMCE was used to compare directly the activity of wild-type and triply GAF-mutated PRE300, there was no apparent change in GFP expression (data not shown). Thus, mutating sites for GAF can have either a positive or a negative effect on CNS maintenance by PRE300. The ectopic expression observed with the GAF-mutated element also suggests that wild-type PRE300 may have a negative maintenance activity in cells of the CNS where eve is not normally expressed, in addition to its role in positive maintenance.

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As a preliminary test of the involvement of other PcG genes in positive maintenance by PRE300, we tested the allele E76[6], as homozygous larvae survive to the third larval instar. However, we did not see any effects on positive maintenance (data not shown). We also tested some trxG alleles that survive to the third larval instar. Larvae homozygous for trx1 and Trl13C did not show any effects on CNS expression of our GFP reporter (data not shown). Larvae heterozygous for trx111, Trl867 and Trl865 were also tested, and, again, no clear effects were observed (data not shown). However, because these alleles have significant maternal and zygotic contributions that allow them to survive long enough to be assayed, further analysis will be required to determine definitively whether these genes are involved along with pho and phol in positive maintenance by PRE300.

**Pho binds to the eve PRE in vivo**

The convergence of genetic and biochemical evidence presented above strongly suggests that Pho acts directly through the binding site in PRE300. To confirm that Pho interacts with this region, and with this site, in vivo, we performed ChIP assays. First, we surveyed the eve locus for Pho binding using a series of primer sets for detection of immunoprecipitated fragments by PCR. As shown in Fig. 5 (B and E, primer set 13), Pho was detected specifically in the region of PRE300, both in early and later-stage embryos. Pho was also detected in the promoter region where binding sites were previously predicted, primarily in early embryos (Fig. 5B, primer set 6), as well as in the region of enhancers driving mesodermal and anal plate expression (Fig. 5B,E, primer set 8). This confirms that Pho interacts with the endogenous eve locus. Furthermore, it does so through the CNS, such that we could not discern the intensity in RP2 and dppCC neurons. When RMCE was used to compare directly the activity of wild-type and triply GAF-mutated PRE300, there was no apparent change in GFP expression (data not shown). Thus, mutating sites for GAF can have either a positive or a negative effect on CNS maintenance by PRE300. The ectopic expression observed with the GAF-mutated element also suggests that wild-type PRE300 may have a negative maintenance activity in cells of the CNS where eve is not normally expressed, in addition to its role in positive maintenance.

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interacts with the transgenic copy of PRE300 (Fig. 6A).

or with the Pho site mutated. Again, ChIP analysis indicated that Pho tested transgenes carrying PRE300, either with the normal sequence, in maintenance of both the repressed and activated state. To test the specifically with the region that our transgenic analysis implicated element from the 3

In this study, we dissected a strong pairing sensitive silencing locus. We found that boundary of the eve

Surprisingly, we found that the eve PRE is also required for positive maintenance of expression in the larval CNS, and that this activity requires both the Pho-binding site and pho gene function. Together, these data strongly suggest that Pho is directly involved in positive maintenance of gene activity. This is surprising because Pho has heretofore been associated only with direct repression of target genes, by recruiting the PRC2 complex and other PcG proteins (Wang et al., 2004b). However, recent studies have blurred the distinction between PcG genes and trxG genes, as some members of each class appear to have dual functions (Grimaud et al., 2006). Furthermore, PREs usually reside in close proximity to TREs (Ringrose and Paro, 2007), and an element from the promoter region of engrailed that mediates PSS and can act as a PRE was recently shown to have an activating role in its natural context (Devido et al., 2008). Recent studies of the Ubx locus have indicated that PcG proteins are present at PREs in both the off and the on state, and that binding of Ash1 prevents silencing by the PRC complex in cells where Ubx is expressed, suggesting that silencing is actively prevented (Papp and Muller, 2006). A similar situation may pertain to Pho function in the eve locus.

Because trxG proteins are known to be involved in positive regulation by other maintenance elements, we were interested in whether they are involved in pho-dependent positive maintenance by the eve PRE. We were also interested in whether other PcG proteins are involved. Because our positive maintenance assay requires survival to the third larval instar, we have so far been able to test only weak alleles of trx, Trl and E(s2), neither of which showed discernable effects in our assays. At this point, we can not definitively say whether other trxG or PcG proteins are involved in the positive maintenance function of the eve PRE. However, our observation that a consensus Grh binding site is present in the more active half of PRE300 suggests the involvement of Grh. Indeed, Grh has been shown to interact genetically with Pho, and to facilitate cooperative interaction with Pho in vitro (Blastyak et al., 2006).

Consistent with the broad overexpression of eve seen in the CNS of ph mutants (Smouse et al., 1988), the eve PRE may silence expression in many cells by forming a silencing complex. In wild-type embryos, in the subset of CNS cells where eve is expressed, the same Pho-dependent DNA binding platform may recruit a distinct complex that maintains the active state. Consistent with this model, we have found that expression driven by the eve RP2 va/pCC enhancer fades prematurely in late stage embryos in ph mutants, at the same time that endogenous eve is broadly overexpressed (M.F. and J.B.J., unpublished). It will be interesting to determine the composition of Pho-dependent complexes in cells where eve is on, and in those where eve is off.

How can a region 9 kb away from the basal promoter affect the state of gene expression? There are accumulating data suggesting that locus-wide regulation occurs through direct interactions of the promoter with enhancers and locus control regions. For example, a recent study showed that silencing by the bxd PRE directly affects the activity of the transcriptional machinery at the promoter (Dellino et al., 2004). In the eve locus, there are PSEs both at the 3’ end of the locus and at the promoter. Both contain clusters of binding sites typical of a PRE/TRE. It has been suggested that PRE-containing transgenes have a tendency to insert near endogenous PREs (Chiang et al., 1995; Fauvarque et al., 1995), which might be expected if they mediate long-range interactions. Putting these ideas together, the eve 3’ PRE may physically interact with the promoter region in a Pho-dependent manner. This may serve to keep eve on in some cells and to keep it off in others, depending on whether activating or repressive complexes mediate the association.

**Fig. 6. The Pho consensus site is required for Pho binding in vivo.** ChIP analysis of Pho binding (as in Fig. 5) to transgenes carrying PRE300 (GFP-RR, Fig. 2), either with a normal (A-C) or a mutated (D-F) Pho site, in 0-15 hours AED embryos (eggs were collected for 15 hours at temperature; embryos spanned stages 1 to late 16). The signal from the transgene (‘wt t’gene’ or ‘mut t’gen’, using a transgene-specific primer set) is compared in each case with that from the endogenous eve 3’ PRE (‘endo eve’, primer set 13 of Fig. 5), as well as to a gene (actin) that Pho is not expected to bind. Note that the Pho signal is reduced when the Pho site is mutated (transgene signal in D versus that in A), relative both to the endogenous eve signal and to the (presumably background) signal from the actin gene.
We thank Xian Wu for excellent technical assistance, Judy A. Kassis for plasmids and Pho antiserum; Michele P. Calos, C.-Ting Wu and Jack R. Bateman for reagents for the BAC system; and Hugh W. Brock, Paul Schedl, Judy A. Kassis and the Bloomberg Stock Center for mutant strains. We also thank Judy A. Kassis, Alex Mazo and Hugh W. Brock for comments on the manuscript. This work was supported by NSF-060416760, NSF-MCB0818118 and NIH-R01GM050231 awards to J.B. and M.F.

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**Development** 135 (24) 1313-1322


