A novel promoter-tethering element regulates enhancer-driven gene expression at the bithorax complex in the *Drosophila* embryo

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A key question in our understanding of the cis-regulation of gene expression during embryonic development has been the molecular mechanism that directs enhancers to specific promoters within a gene complex. Promoter competition and insulators are thought to play a role in regulating these interactions. In the bithorax complex of *Drosophila*, the IAB5 enhancer is located 55 kb 3′ of the *Abdominal-B* (*Abd-B*) promoter and 48 kb 5′ of the *abdominal-A* (*abd-A*) promoter. Although roughly equidistant from the two promoters, IAB5 specifically interacts only with the *Abdominal-B* promoter, even though the enhancer and promoter are separated by at least two insulators. Here we demonstrate that a 255 bp element, located 40 bp 5′ of the *Abd-B* transcriptional start site, has a novel cis-regulatory activity as it is able to tether IAB5 to the *Abd-B* promoter in transgenic embryos. The tethering element is sufficient to direct IAB5 to an ectopic promoter in competition assays. Deletion of the promoter-tethering element results in the redirection of enhancer-driven gene expression on transgenes. Taken together, these results provide evidence that specific long-range enhancer-promoter interactions in the bithorax complex are regulated by a tethering element 5′ of the *Abd-B* promoter. We discuss a bioinformatic analysis of the tethering element across different *Drosophila* species and a possible molecular mechanism by which this element functions. We also examine existing evidence that this novel class of cis-regulatory elements might regulate enhancer-promoter specificity at other gene complexes.

KEY WORDS: cis-regulation, Enhancer, *Drosophila*, Bithorax, *Abdominal-B*, Promoter

INTRODUCTION
A long-standing issue in our comprehension of gene expression has been the mechanism by which enhancers are recruited to specific promoters over long distances. Insulators, tissue-specific silencer elements and promoter competition are three possible mechanisms by which enhancers are directed to specific promoters (for summary see Fig. 1A). Insulator DNAs have been identified at a number of genetic loci and act to disrupt the interaction of a shared enhancer with a promoter (Fig. 1A, promoter A) when positioned between them (Geyer, 1997; West et al., 2002). Tissue-specific silencer elements act to repress transcription in a sub-set of cells where the promoter might otherwise be activated by an enhancer (Fig. 1A, promoter B) (Drewell et al., 2000). Neither of these mechanisms prevents the enhancer from interacting with other promoters. Promoter competition is responsible for the preferred interaction of an enhancer with a specific promoter when linked to two or more promoters. In this way the distal 'strong' promoter (Fig. 1A, promoter D) competitively recruits the enhancer in preference to the proximal 'weak' promoter (Fig. 1A, promoter C). This is thought to occur via selective recognition of distinct core promoter elements by the shared enhancer (Butler and Kadonaga, 2002). However, at the bithorax complex (BX-C) in *Drosophila* none of these mechanisms can explain enhancer-promoter specificity. We present evidence of a fourth mechanism, promoter tethering, capable of regulating enhancer-promoter specificity.

The BX-C contains over 300 kb of genomic DNA but codes for only three homeotic transcription factors which pattern the thorax and abdomen: *Ultrabithorax* (*Ubx*), *abdominal-A* (*abd-A*) and *Abdominal-B* (*Abd-B*) (Lewis, 1978; Martin et al., 1995; Sanchez-Herrero et al., 1985). In the case of *abd-A* and *Abd-B*, the cis-regulatory DNA required for accurate spatial and temporal expression during embryonic development lies in an organized array of genetically defined domains: *infraabdominal* (*iab*) regions, *iab2* to *iab8* (Fig. 1B) (Akbari et al., 2006; Celniker et al., 1990; Maeda and Karch, 2006; Sanchez-Herrero, 1991). Each *iab* region is thought to contain an enhancer capable of directing expression in the corresponding abdominal parasegment (Hogga et al., 2001; Karch et al., 1985; Mihaly et al., 2006). For example, the IAB5 enhancer is located 55 kb 3′ of the *Abd-B* promoter and 48 kb 5′ of the *abd-A* promoter (Fig. 1B) but preferentially directs expression only of *Abd-B* in presumptive abdominal segment 5 (parasegment 10) (Busturia and Bienz, 1993; Ohtsuki et al., 1998). By contrast, the IAB2 enhancer is located 18 kb 3′ of the *abd-A* transcription start site (Fig. 1B) and interacts only with the *abd-A* promoter, directing expression in presumptive abdominal segment 2 (parasegment 7) (Shimell et al., 2000). Disruption of IAB5-*Abd-B* or IAB2-*abd-A* interactions disrupts normal embryonic development and results in homeotic segment transformations (Busturia and Bienz, 1993; Karch et al., 1985; Shimell et al., 2000).

A critical question is how the IAB5 enhancer is selectively recruited only to the *Abd-B* promoter. IAB5 has been shown to have a preference for TATA-containing promoters on synthetic transgenes with exogenous promoters (Ohtsuki et al., 1998). However, at the endogenous locus neither of the *Abd-B* or *abd-A* promoters contains a TATA box. We also examined whether the *Abd-B* or *abd-A* promoters contained the other known core promoter elements: initiator (Inr) or downstream promoter element (DPE) (for a review, see Butler and Kadonaga, 2002). Neither promoter has 100%

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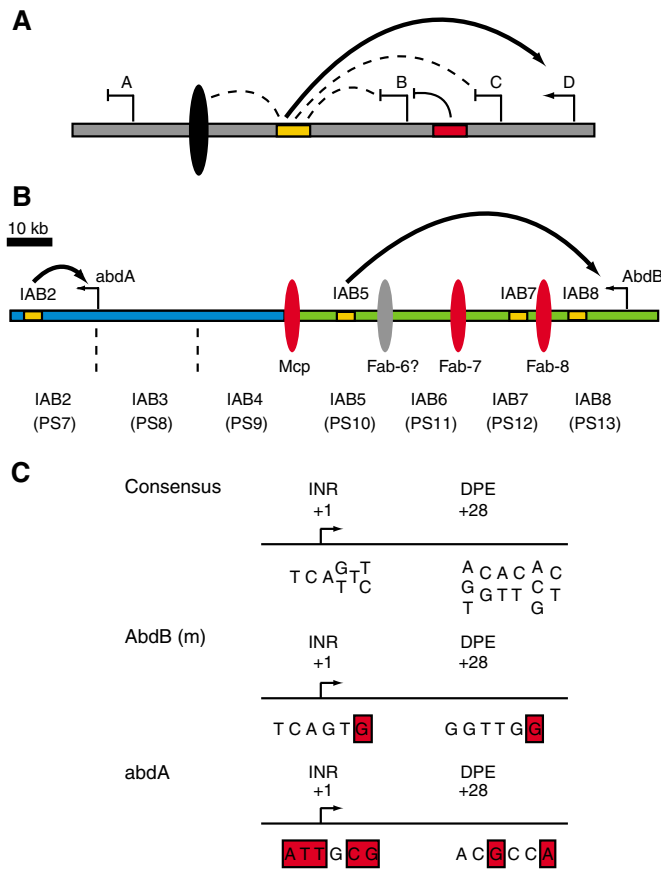
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Fig. 1. Molecular organization of cis-regulatory sequences at the *Drosophila* bithorax complex. (**A**) Regulation of promoter-enhancer interactions. The diagram depicts a common enhancer (orange rectangle) at a model gene complex. The enhancer is able to interact with any of the promoters A, B, C or D. An insulator DNA (black ellipse) located between the enhancer and gene A prevents the enhancer from interacting with gene A but leaves it free to activate other promoters. A silencer element (red rectangle) represses gene B in cell types where it would otherwise be activated by the enhancer. Promoter competition regulates the interaction of the enhancer with gene C and gene D. The enhancer can activate either gene, but prefers the core promoter region of gene D. (**B**) Summary of the *Abd-B-abd-A* region of the BX-C. The *abd-A* and *Abd-B* transcription start sites are indicated by leftward arrows. The intergenic region is ~100 kb in length. The *iab* regions that control expression of the two homeotic genes are indicated: IAB2-IAB8 (shown with respect to the corresponding embryonic parasegment). IAB2, IAB3 and IAB4 (shown in blue) regulate expression of *abd-A*. IAB5, IAB6, IAB7 and IAB8 (shown in green) direct *Abd-B* expression. The insulator DNAs that separate the different *iab* regions are marked by red ellipses. Characterized enhancers within the *iab* regions are shown as orange rectangles. The IAB5 enhancer is located 55 kb 3′ of the *Abd-B* promoter and 48 kb 5′ of the *abd-A* promoter, but only interacts with *Abd-B* over the intervening insulator sequences. The IAB2 enhancer is located 18 kb 3′ of the *abd-A* promoter and directs expression specifically from *abd-A*. (**C**) Core promoter sequences at *abd-A* and *Abd-B*. The consensus sites for initiator (INR) and downstream promoter elements (DPE) in *Drosophila* are shown (Butler and Kadonaga, 2002). The sequences from the *Abd-B* and *abd-A* promoters do not match these consensus sites (mismatches shown in red). In addition, neither of the homeotic promoters contains a recognizable TATA box, suggesting that the core promoter elements at *Abd-B(m)* and *abd-A* are not distinctive. *Abd-B(m)*, morphogenetic transcript.

matching sequence for the weakly defined consensus sites for these elements (Fig. 1C). A weakly defined consensus site allows for more variation in the nucleotides present at any particular position within the site. Any variation from a weakly defined site is indicative that the site is not present. It is, therefore, unlikely that a promoter competition model accounts for the specific enhancer-promoter interactions in the BX-C. In order for long-range activation of *Abd-B* expression to occur, IAB5 has to bypass at least two known insulator sequences, *Fab-7* and *Fab-8*, that have enhancer-blocking activity (Fig. 1B) (Barges et al., 2000; Hagstrom et al., 1996; Zhou et al., 1999; Zhou et al., 1996). One characterized mechanism for IAB5 to bypass these insulator elements involves a novel class of regulatory elements known as the promoter targeting sequences (PTS). Two PTS elements have been characterized; PTS-7, which is located adjacent to *Fab-8*, and PTS-6, which is located adjacent to *Fab-7* (Chen et al., 2005). The PTS elements are thought to function as anti-insulators, facilitating the correct promoter-enhancer interactions. In addition, earlier studies suggested that genomic regions 5′ of the *Abd-B* promoter may be capable of recruiting enhancers in trans (Sipos et al., 1998). In this study we examined whether this 5′ upstream region was able to direct IAB5 to *Abd-B* in cis. In vivo analysis of transgenes identified a 255 bp DNA element that facilitates IAB5-*Abd-B* interactions. This regulatory DNA is located 40 bp 5′ of the *Abd-B* transcription start site and permits IAB5 to activate a distal *Abd-B-CAT* reporter gene in preference to a more proximal *abd-A-lacZ* reporter. This element is also sufficient to direct IAB5 to an ectopic promoter in competition assays. Deletion of this element results in the redirection of enhancer-promoter interactions on transgenes. We suggest that the 255 bp cis-regulatory sequence is a promoter-tethering element (PTE) capable of selectively recruiting enhancers from the *iab* regions, including the IAB5 enhancer, to the *Abd-B* promoter at the endogenous locus.

MATERIALS AND METHODS
Preparation of genomic regions
Genomic regions from the bithorax complex of *Drosophila melanogaster* were PCR amplified using conventional methods and cloned into either a modified pBluescript or pGemTEasy vectors. The *Abd-B* promoter region for the class A transcript (Martin et al., 1995) was isolated from genomic DNA as a 1522 bp PCR fragment (48,905-50,427 in EMBL:DM31961), which includes 294 bp of 5′ flanking sequence and 1228 bp of 3′ sequence. The *abd-A* promoter region was isolated as a 957 bp PCR fragment (152,853-153,810) which includes 538 bp of 5′ flanking sequence and 419 bp of 3′ sequence. The IAB5 enhancer (Ohtsuki et al., 1998) was isolated as a 1026 bp PCR fragment (104,011-105,037). The IAB2 enhancer (Shimell et al., 2000) was isolated as a 1969 bp PCR fragment (171,019-172,988). The PTE was isolated as a 255 bp PCR fragment that extends from –294 bp to –40 bp relative to the *Abd-B* transcription start site. The Fab-8 insulator element was isolated as a 743 bp PCR fragment (63,627-64,370) and specifically designed to exclude the adjacent PTS7 element. The *Abd-B*$^{\Delta PTE}$ region was isolated as a 1268 bp PCR fragment (49,159-50,427).

Construction of P-element transgenes
The P-transformation vector used in this study is a modified pCaSpeR and contains divergently transcribed *white*, *CAT* and *lacZ* reporter genes (Ohtsuki et al., 1998). Genomic promoter regions from the Bithorax complex were PCR amplified using conventional methods and cloned as *Asc*I-*Bam*HI fragments in a modified pBluescript at the 5′ end of either the *lacZ* or *CAT* reporter genes (Calhoun et al., 2002). The *abd-A-lacZ* fusion gene was isolated as an *Asc*I-*Xba*I fragment and used to replace the *Asc*I-*Xba*I *lacZ* fragment in the pCaSpeR vector. The *Abd-B-CAT* fusion gene was isolated as an *Asc*I-*Not*I fragment and used to replace the *Asc*I-*Not*I *CAT* fragment in pCaSpeR. The IAB5 enhancer was isolated as a *Pst*I fragment and cloned into the pCaSpeR vector in the unique *Pst*I site 3′ of *lacZ*. The IAB2 enhancer was isolated as a *Not*I fragment and cloned into the unique
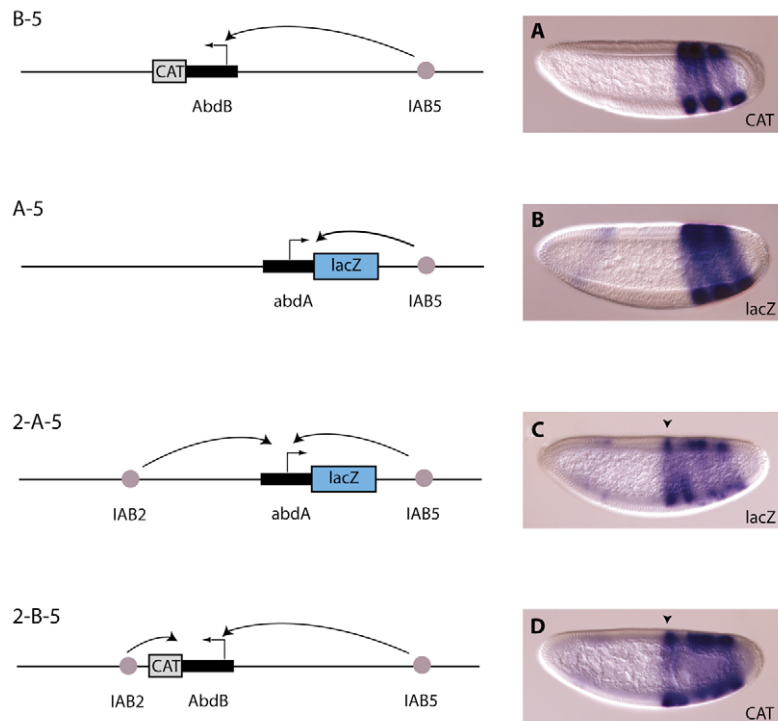
Fig. 2. Enhancer-promoter interactions at the BX-C.
Transgenic embryos were hybridized with digoxigenin-labeled antisense RNA probes (diagrams on left). The embryos shown on the right are at blastoderm stage and orientated with anterior to the left and dorsal up. (**A**) On the B-5 construct the IAB5 enhancer directs expression of the *Abd-B-CAT* reporter gene in three characteristic stripes in presumptive abdominal segments 5, 7 and 9. (**B**) IAB5 is also able to interact with the *abd-A* promoter in the absence of a competing promoter, as it activates transcription from the *abd-A-lacZ* reporter gene. Ectopic expression of the *lacZ* and *CAT* reporter genes is also detected in the anterior of some transgenic embryos, as previously described (Ohtsuki et al., 1998; Zhou et al., 1999). (**C,D**) IAB2 and IAB5 will simultaneously activate expression from the *abd-A* or *Abd-B* promoter, indicated by a broad band of expression extending from presumptive abdominal segment 2 (indicated by black arrowhead) towards the posterior in 2-A-5 (C) and 2-B-5 (D) transgenic embryos. These expression patterns indicate that, in the absence of competing promoters, both homeotic gene promoters are responsive to interaction with the enhancers from the BX-C.

*Not*I site 3′ of *CAT*. The *Fab-8* insulator element was isolated as an *Asc*I fragment and cloned into the unique *Asc*I site between the *Abd-A-lacZ* and *Abd-B-CAT* fusion genes. The previously described 1.6 kb spacer from bacteriophage λ alone was sub-cloned into the *Asc*I site in pCaSpeR (Calhoun et al., 2002). The PTE element was isolated as an *Asc*I fragment and cloned into the unique *Asc*I site 5′ of *eve-lacZ* and its orientation was determined by sequencing. The *eve-lacZ* gene used was as previously described (Ohtsuki et al., 1998). The *Abd-B*^ΔPTE promoter was isolated as an *Asc*I-*Not*I fragment and used to replace the *Asc*I-*Not*I *CAT* fragment in pCaSpeR.

P transformation assays and in situ hybridization
Reporter transgenes were introduced into the *Drosophila* germline using standard methods (Small et al., 1992). Multiple transgenic lines were generated for each construct and at least three independent lines were analyzed by in situ hybridization. Embryos were collected, fixed and hybridized with digoxigenin-labeled *lacZ* or *CAT* probe as previously described (Bae et al., 2002).

Bioinformatic analysis
Levels of sequence conservation were calculated using VISTA (Frazer et al., 2004) for the PTE (chr3R:12,760,005-12,760,259), PTE 5′ (chr3R:12,760,259-12,760,513), PTE 3′ (chr3R:12,759,751-12,760,005), BX-C (chr3R: 12,470,945-12,809,178) and *iab5-iab8* (chr3R: 12,695,347-12,755,125) regions of the *D. melanogaster* genome (April 2004) using the following parameters: calc window, 24 bp; cons window, 24 bp; cons identity, 80%. Absolute levels of conservation were obtained by comparing the number of perfectly aligned base pairs to the total length of the promoter-tethering element in *D. melanogaster*.

RESULTS
Dissecting promoter-enhancer interactions at the BX-C
On transgenic reporter constructs, IAB5 activates expression only from the *Abd-B* promoter in parasegments 10, 12 and 14 (presumptive abdominal segments 5, 7 and 9) in the developing embryo (Fig. 1B) (Drewell et al., 2002a; Ohtsuki et al., 1998). To identify the cis-regulatory elements responsible for this specificity, an *Abd-B* promoter was attached to a *CAT* reporter gene. The *Abd-*

B promoter region is 1.5 kb in length and includes 294 bp of 5′ flanking sequence and approximately 1.2 kb of 3′ sequence. On a reporter transgene the IAB5 enhancer is able to direct strong *CAT* expression from the *Abd-B* promoter in the characteristic three posterior abdominal stripes in blastoderm-stage embryos (Fig. 2A). One possible mechanism by which promoter-enhancer specificity is established at the BX-C could be the existence of promoter-proximal elements, which inhibit enhancers from interacting with specific promoters. For example, IAB5 may be prevented from interacting with the *abd-A* promoter by a negative regulatory element close to the *abd-A* transcription start site. However, this does not appear to be the case, as IAB5 is able to interact strongly with a 1 kb *abd-A* promoter-*lacZ* reporter gene when located close to the *abd-A* promoter and in the absence of any other competing promoters (Fig. 2B). If the IAB2 enhancer is also added to this transgenic construct, a much broader band of *lacZ* expression expanding towards the anterior of the blastoderm-stage embryo is seen (Fig. 2C), indicating that IAB2 and IAB5 are both able to drive expression from the *abd-A* promoter. On transgenic constructs, IAB2 directs expression from the *abd-A* promoter predominantly in parasegments 7 and 9 (presumptive abdominal segments 2 and 4) and more weakly in parasegments 11 and 13 (segments 6 and 8), as previously described for a *Ubx-lacZ* reporter gene (Shimell et al., 2000). However, on transgenes the *Abd-B* promoter is also capable of interacting with the IAB2 enhancer. When the IAB2 and IAB5 enhancers are present on the same construct, bands of *CAT* expression are detected extending from presumptive abdominal segment 2 towards the posterior of the blastoderm-stage embryo (Fig. 2D). The promoters from the BX-C, therefore, appear to be responsive to both of the enhancers tested, indicating that the promoter regions themselves are not able to inhibit enhancer-promoter interactions.

It is a formal possibility that promoter-enhancer specificity at the BX-C is established as a result of the endogenous enhancers interacting with promoters in an orientation-dependent manner. This is unlikely to be a general rule as the enhancers in the IAB3 and
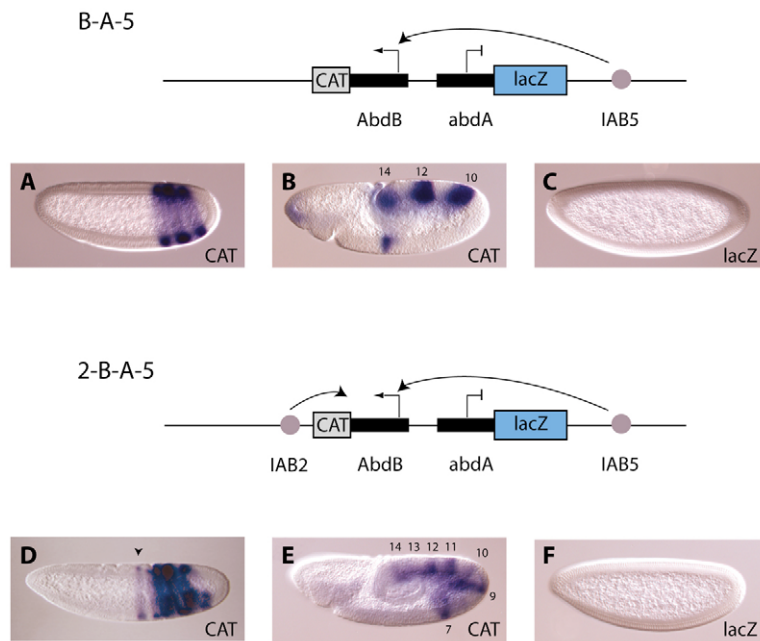
B-A-5

Fig. 3. Regulatory specificity determines cis-interactions at the BX-C. On the B-A-5 construct (top diagram), the IAB5 enhancer was placed 3′ of the proximal *abd-A-lacZ* reporter gene. The distal *CAT* gene is under the control of the *Abd-B* promoter. In this configuration the IAB5 enhancer selects *Abd-B* over *abd-A*, so that the *Abd-B-CAT* reporter exhibits a three-stripe IAB5 expression pattern in parasegments 10, 12 and 14; this is readily detected in blastoderm-stage embryos (**A**) and germband-elongation-stage embryos (**B**), whereas *abd-A-lacZ* is silent (**C**). By contrast, the IAB2 enhancer on the 2-B-A-5 construct (lower diagram) does not interact with its normal endogenous target (*abd-A*), but directs expression from the *Abd-B-CAT* gene in parasegments 7 (black arrow), 9, 11 and 13. In blastoderm-stage (**D**) and germ band elongation-stage embryos (**E**), a composite IAB2-IAB5-driven expression pattern is detected. The inactivity of the *lacZ* reporter on this construct (**F**) suggests that IAB2 only interacts with the most proximal promoter.

IAB4 regions must activate the *abd-A* promoter in the 3′ direction, while IAB5 and IAB2 both interact with their respective target promoters in the 5′ direction (see Fig. 1B). To test whether the enhancer activities are directional we also reversed the orientation of IAB2 and IAB5 relative to their target promoters on the transgenic constructs. This failed to disrupt enhancer-driven expression of the reporter genes (data not shown). Therefore, the enhancers from the BX-C appear to be orientation independent and promiscuous, able to activate any promoter. In addition, the homeotic gene promoters do not appear to harbor inhibitory regulatory elements capable of repressing activation from either enhancer. As a result, when only a single promoter is present, both IAB2 and IAB5 will drive expression strongly from either *abd-A-lacZ* or *Abd-B-CAT*.

The *Abd-B* promoter contains a tethering element

In order to determine if the *Abd-B* and *abd-A* promoters are able to specifically recruit either the IAB5 or IAB2 enhancers in competition with another promoter, we introduced the two promoters in tandem on transgenic constructs. On the B-A-5 construct, the IAB5 enhancer is placed 3′ of the *abd-A-lacZ* gene. In this stringent test, IAB5 fails to activate the proximal *abd-A-lacZ* gene (Fig. 3C) but directs strong expression of the more distal *Abd-B-CAT* gene in both blastoderm-stage (Fig. 3A) and germband-elongation-stage embryos (Fig. 3B). These staining patterns mimic the endogenous IAB5-driven activation pattern in parasegments 10, 12 and 14 and indicate that the 1.5 kb *Abd-B* promoter region is sufficient to selectively recruit the IAB5 enhancer. To test whether the *abd-A* promoter has a similar tethering activity for an endogenous enhancer, IAB2 was placed 3′ of the *Abd-B-CAT* gene on the 2-B-A-5 construct. However, unlike IAB5, IAB2 is not directed to its endogenous target promoter but is instead recruited to the proximal *Abd-B* promoter. This was shown by broad stripes of *CAT* staining in transgenic embryos in parasegments 7, 9, 11 and 13 driven from IAB2 and 10, 12 and 14 driven from IAB5 (Fig. 3D,E), while no *abd-A-lacZ* expression was observed (Fig. 3F). This result indicates that the *abd-A* promoter does not contain a regulatory element sufficient to

tether the IAB2 enhancer. It is possible that at the endogenous locus there is no requirement for this activity, as the *abd-A* promoter is relatively close to IAB2 and therefore may not have to compete for the enhancer. As discussed earlier, in contrast to IAB2, IAB5 is roughly equidistant from both homeotic promoters in the BX-C but is selectively recruited only to *Abd-B* over 55 kb of intervening DNA sequence.

Anti-insulator activity in the *Abd-B* promoter

In order to activate *Abd-B* expression at the endogenous gene complex, IAB5 has to bypass at least two known insulator sequences, *Fab-7* and *Fab-8*, that have enhancer-blocking activity (Fig. 1B) (Hagstrom et al., 1996; Zhou et al., 1999; Zhou et al., 1996). These insulator elements have previously been shown to disrupt promoter-enhancer interactions when placed between a promoter and enhancer on transgenes (Barges et al., 2000; Zhou et al., 1999; Zhou et al., 1996; Zhou and Levine, 1999). To further characterize the IAB5-*Abd-B* interaction, we therefore needed to test the interaction in the presence of an insulator from the BX-C. The 2-B-Fab-8-A-5 construct was created in which the previously characterized *Fab-8* insulator element (Zhou and Levine, 1999) was placed between the homeotic promoter elements. The *Fab-8* insulator sequence was specifically designed to exclude the adjacent PTS7 element. The addition of the *Fab-8* insulator sequence did not disrupt the IAB5-*Abd-B* interaction, as strong CAT expression was detected in posterior stripes in blastoderm-stage embryos (Fig. 4A) whereas no *abd-A-lacZ* expression was detected (Fig. 4B). To confirm that the CAT expression in these embryos was not solely an IAB2-driven pattern, we generated transgenic lines carrying the B-Fab-8-A-5 transgene, from which the IAB2 enhancer was removed. In these embryos the IAB5 enhancer was recruited to the *Abd-B* promoter, as strong IAB5-driven expression was detected for the *Abd-B-CAT* gene (Fig. 4C) and no *abd-A-lacZ* expression was observed (Fig. 4D). To ensure that altering the enhancer-promoter spacing would not modulate the IAB5-*Abd-B* interaction, we created the 2-B-1.6λ-A-5 construct. To generate this construct, a 1.6 kb lambda DNA fragment (Calhoun et al., 2002) was inserted between the promoter
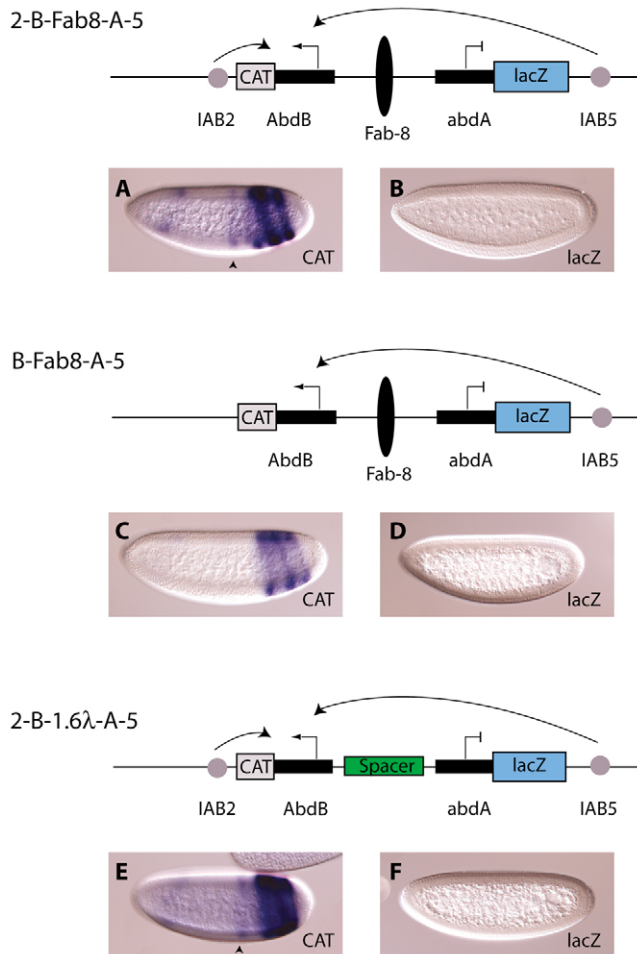
Fig. 4. Anti-insulator activity in the Abd-B promoter. On the 2-B-Fab-8-A-5 construct (top diagram), the *Fab-8* insulator was inserted between the two homeotic promoters. In this configuration both the IAB2 and IAB5 enhancers activate the *Abd-B* promoter, as *CAT* is expressed in the broad stripes, extending from parasegment 7 (black arrowhead) towards the posterior of the embryo (**A**), whereas no *lacZ* expression can be detected (**B**). To verify that IAB5 is activating expression from the *Abd-B* promoter, the IAB2 enhancer was removed to generate the B-Fab-8-A-5 construct (middle diagram). Transgenic embryos confirmed that IAB5 is indeed recruited the *Abd-B* promoter as CAT expression can be seen in a distinctive IAB5 pattern (**C**), whereas *lacZ* is not activated (**D**). To examine whether spacing had an effect on these interactions, a 1.6 kb λ-spacer DNA was placed between the two homeotic promoters on the 2-B-1.6λ-A-5 construct (bottom diagram). The addition of this λ-spacer did not modulate the activation of expression from the *Abd-B* promoter by the IAB2 and IAB5 enhancers (**E**) and no *lacZ* expression is detected (**F**).

Fig. 5. Identification of the promoter-tethering element. On the B-A-5 construct (top diagram), the IAB5 enhancer specifically bypasses the *abd-A* promoter (**B**) to activate expression from the *Abd-B* promoter (**A**). When the 255 bp region extending from –40 to –294 bp relative to the transcription start site is removed from the *Abd-B* promoter (B^ΔPTE-A-5 construct; middle diagram), the IAB5 enhancer is now re-directed to the *abd-A* promoter, as no *CAT* expression is detected (**C**) and strong *lacZ* expression is detected (**D**) in the majority of embryos. Extremely weak *CAT* expression in an IAB5-directed pattern was detected in a few transgenic embryos (data not shown). The integrity of the *Abd-B^ΔPTE* promoter was confirmed by insertion of the IAB2 enhancer 3′ of the *Abd-B^ΔPTE-CAT* reporter gene on the 2-B^ΔPTE-A-5 construct (bottom diagram). This resulted in IAB2 activation of the *Abd-B^ΔPTE* promoter indicated by an IAB2-driven *CAT* expression pattern in parasegments 7 (black arrowhead), 9, 11 and 13 in transgenic embryos (**E**), whereas *lacZ* is activated in an IAB5-driven expression pattern in the more posterior parasegments 10, 12 and 14 (**F**). Embryos exhibiting weaker staining are shown to clearly demonstrate the different expression patterns driven by the two IAB enhancers, although overall the expression in the 2-B^ΔPTE-A-5 embryos was comparable to other transgenic lines analyzed in this study.

regions on the 2-B-A-5 construct (Fig. 3). The addition of the spacer had no effect on the IAB5-*Abd-B* interaction, as strong *CAT* expression in a composite IAB2-IAB5-driven pattern was observed (Fig. 4E) whereas no *lacZ* expression was detected (Fig. 4F). These results indicate that the *Abd-B* promoter may contain a tethering activity that allows the IAB5 enhancer to drive expression of *Abd-B-CAT* across the *Fab-8* insulator. This anti-insulator activity is important in the context of the endogenous BX-C, as IAB5 must bypass at least two insulators to interact with the *Abd-B* promoter.
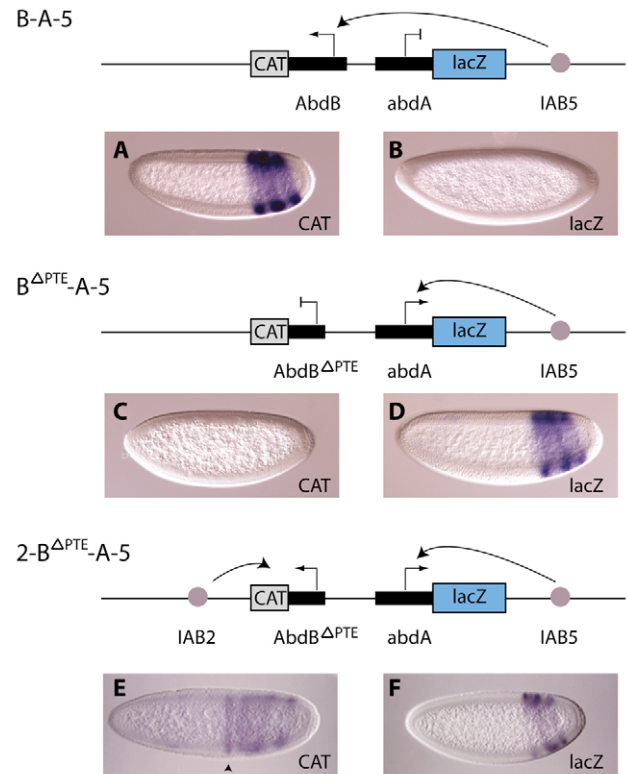
Identification of the promoter-tethering element

In an effort to identify the region in the *Abd-B* promoter responsible for the tethering of IAB5 to the *Abd-B* promoter, a 255 bp DNA sequence from –40 to –294 bp 5′ of the *Abd-B* transcription start site was deleted from the *Abd-B* promoter. Although no consensus core elements are present at the *Abd-B* promoter, this region was selected to exclude the possibility of including any potential core promoter sequences (Butler and Kadonaga, 2002) close to the transcriptional start site but leaving the promoter region capable of activating transcription. This 255 bp sequence also overlaps with the 5′ region

previously shown to be functionally important in regulating promoter-enhancer communication at the BX-C in trans (Sipos et al., 1998).

When comparing *CAT* reporter gene expression in transgenic embryos containing the full-length *Abd-B* promoter (Fig. 5A) to those in which the 255 bp sequence is deleted (Fig. 5C), it appears that this deletion abrogates recruitment of the IAB5 enhancer to the *Abd-B* promoter. In fact, deletion of the 255 bp sequence in the $B^{\Delta PTE}$-A-5 construct resulted in re-direction of IAB5-driven expression from the *Abd-B* promoter (Fig. 5C) to the *abd-A* promoter directing *lacZ* expression (Fig. 5D) in transgenic embryos. We therefore named the 5′ 255 bp sequence the promoter-tethering element (PTE). In a few transgenic lines carrying the $B^{\Delta PTE}$-A-5 construct very weak IAB5-driven expression of the $B^{\Delta PTE}$-CAT reporter gene was observed (data not shown), probably because of position effects. This experiment indicates that the *Abd-B* promoter is functional in this configuration, but only at certain integration points in the genome. It is possible that the lack of expression of the *CAT* reporter gene on these constructs could simply be a result of a non-functional *Abd-B* promoter, caused by the truncation of the promoter. To verify that the $Abd\text{-}B^{\Delta PTE}$ promoter was still functional in a non-competitive situation, IAB2 was inserted 1 kb 3′ of the $Abd\text{-}B^{\Delta PTE}$ promoter to generate the 2-$B^{\Delta PTE}$-A-5 construct. This resulted in IAB2-driven activation of the $Abd\text{-}B^{\Delta PTE}$ promoter (Fig. 5G), indicating that this promoter is still functional, whereas IAB5 was solely recruited to the *abd-A* promoter. (Fig. 5H). The level of expression detected from the truncated $Abd\text{-}B^{\Delta PTE}$ promoter was comparable to other transgenic lines analyzed in this study, suggesting the promoter is fully active. In addition, these embryos clearly demonstrate the different expression patterns driven by the two IAB enhancers (Fig. 5G,H). The deletion of the PTE, therefore, confirms that this cis-regulatory sequence is necessary for the recruitment of IAB5 to the *Abd-B* promoter on transgenes.

PTE can regulate ectopic enhancer-promoter interactions

To further analyze the functional activity of the PTE in *Drosophila* embryos, the W-5-EZ construct was created in which the IAB5 enhancer was positioned between the *mini-white* reporter gene and an *even-skipped-lacZ* fusion reporter gene. As previously described, in this configuration the IAB5 enhancer has a strong preference for the TATA-box-containing *even-skipped* (*eve*) promoter in transgenic blastoderm-stage embryos and only weakly activates *white* (Fig. 6A,B) (Ohtsuki et al., 1998). Insertion of the 255 bp PTE adjacent to the *eve-lacZ* gene on the W-5-PTE-EZ transgenic construct resulted in redirection of the IAB5 enhancer-driven expression solely to the *eve* promoter as *lacZ* was expressed in the three characteristic posterior abdominal stripes (Fig. 6D), whereas no *white* expression was detected (Fig. 6C). The expression patterns from these constructs demonstrate that the PTE from 5′ of *Abd-B* will regulate ectopic promoter-enhancer interactions. The regulatory switch induced by the juxtapositioning of the PTE with the *eve* promoter indicates that the tethering of IAB5 is not promoter-specific. This fits with the regulatory logic required at the endogenous locus as a PTE in a gene complex will only be required to recruit specific enhancers to the promoter at which it is located.

Bioinformatic analysis of the PTE sequence in different *Drosophila* species

Our transgenic studies indicate that the PTE is a functional element in the BX-C. One potential model for the tethering function of this regulatory sequence is that it may contain binding sites for trans
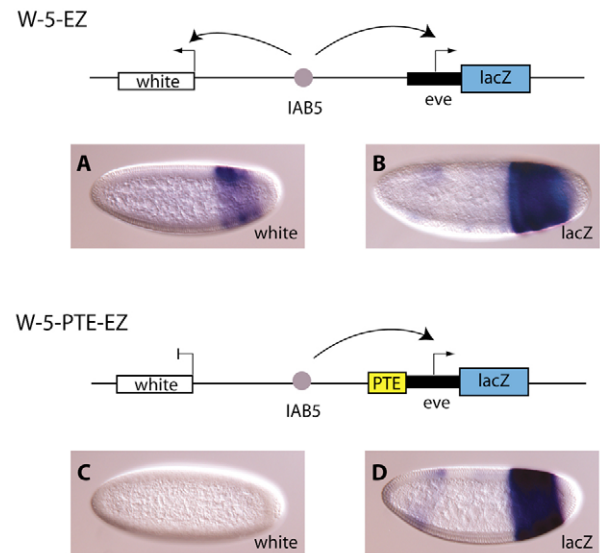

Fig. 6. The PTE is able to regulate expression of an ectopic promoter. In the W-5-EZ construct (top diagram), the IAB5 enhancer is located between the *white* and *even-skipped* (*eve*) promoters. In this configuration, IAB5 is able to drive expression from *white* (**A**) and *eve-lacZ* (**B**). Insertion of the 255 bp PTE sequence adjacent to the *eve-lacZ* promoter in the W-5-PTE-EZ construct (bottom diagram) resulted in strong expression of *lacZ* (**D**) and an absence of expression of *white* (**C**), indicating that IAB5 is now exclusively activating the *eve-lacZ* promoter.

factors that directly interact with the enhancers in the BX-C to bring them into close proximity with the *Abd-B* promoter. A prediction of this model is that the putative binding sites in the PTE should be conserved in different *Drosophila* species. As a result it should be possible to identify a high level of conservation for short stretches of sequence within the PTE that contain binding sites. To test this we carried out bioinformatic studies across seven different *Drosophila* species (Fig. 7A). The PTE sequence as a whole does not demonstrate a significantly higher level of conservation in the different species when compared to other sequences from the BX-C, including the IAB5 enhancer with known regulatory activity (Fig. 7B). However, within the PTE there are two short sequences that are more highly conserved: a 24-mer and a 27-mer (Fig. 7B,C). It is therefore possible that these short sequences represent conserved protein binding sites and that the trans factors involved in the functional activity of the PTE interact specifically with these conserved sequences (see Discussion).

DISCUSSION

Previous genetic studies demonstrated that genomic regions 5′ of the *Abd-B* promoter are capable of recruiting the enhancers from the BX-C in trans (Sipos et al., 1998). At the endogenous BX-C, the IAB5 enhancer specifically directs expression from the *Abd-B* promoter in cis, although it is located slightly closer to the *abd-A* promoter and is separated from the target promoter by at least two known insulator sequences. The present study provides evidence that a novel promoter-tethering element (PTE), located –40 to –294 bp relative to the *Abd-B* transcription start site, is responsible for mediating these regulatory interactions and consequently plays a critical role in controlling promoter-enhancer communication at the BX-C.
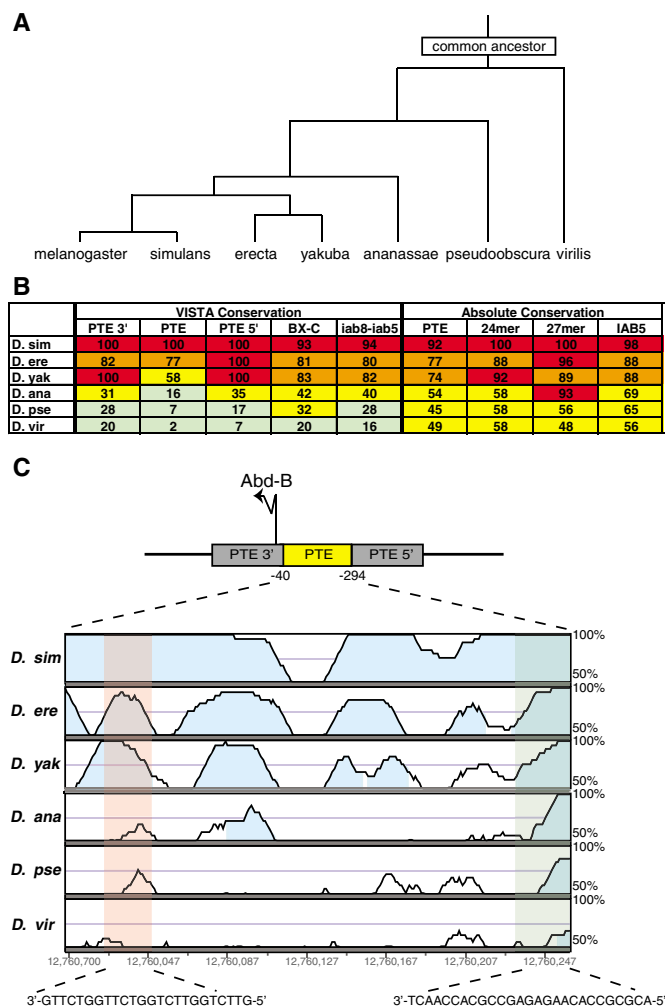
Fig. 7. Conservation of the PTE sequence across *Drosophila* species. (**A**) An informal consensus tree (Crosby et al., 2007) illustrating evolutionary relationships among *Drosophila* species. (**B**) Sequence conservation levels for the 255 bp PTE and PTE 5′ and PTE 3′ (which represent the 255 bp regions 5′ and 3′ of the PTE with respect to *Abd-B*). For comparison, the conservation within the entire bithorax complex (BX-C) and the complete chromosomal control regions that direct *Abdominal-B* gene expression (*iab8-iab5*) and the IAB5 enhancer are also shown. Level of conservation between *D. melanogaster* and six other *Drosophila* species is indicated by color code: >90% red, 70-89% orange, 30-69% yellow, <30% green for different sequences. Conservation values were calculated using VISTA genome browser (see Materials and methods). Absolute conservation is the total percentage of *D. melanogaster* nucleotides that were conserved in the homologous region identified by VISTA alignment from the other species examined. (**C**) VISTA plots of the alignments indicate that the level of conservation is variable across the length of the PTE sequence. Overall, the PTE is less highly conserved than neighboring sequences or the non-genic regions in the BX-C, but there are two short, highly conserved sequences within it, a 24-mer (pink) and a 27-mer (green). The height of the peaks in the plots represents the level of conservation over a 24 bp window. Regions at least 24 bp long that are >80% conserved are indicated in cyan.

Functional properties of the PTE

A 1.5 kb *Abd-B* promoter specifically recruits the IAB5 enhancer on reporter transgenes. The tethering activity contained in the *Abd-B* promoter region is able to interact with IAB5 over a long distance (>5 kb) and is capable of facilitating the bypass of an intervening promoter (*abd-A*) from the BX-C (see Figs 3 and 4). Deletion of a 255 bp sequence located in the 5′ region of the *Abd-B* promoter reveals the existence of a novel cis-element responsible for tethering of the IAB5 enhancer to the promoter. Removal of this PTE sequence from the *Abd-B* promoter is sufficient to redirect the IAB5 enhancer to the adjacent *abd-A* promoter on transgenes (see Fig. 5). In addition, fusion of the PTE sequence to an ectopic promoter results in complete recruitment of the IAB5 enhancer to the promoter (Fig. 6).

PTE mediated cis-regulatory interactions in the BX-C

The transgenic experiments presented here demonstrate that the 255 bp DNA sequence located 5′ of the *Abd-B* promoter contains a promoter-tethering element (PTE) that serves a key regulatory function by specifically recruiting the IAB5 enhancer to the *Abd-B* promoter. It is conceivable that at the endogenous complex the PTE may be involved in recruiting multiple intergenic enhancers to the *Abd-B* promoter, such as IAB6 and IAB7. Although this has yet to be tested on transgenes, the available genetic evidence supports this idea, as a relatively small deletion in the *Abd-B* upstream region is sufficient to disrupt activation by the IAB7 enhancer in trans (Sipos et al., 1998). By contrast, the IAB8 enhancer may not require a tethering element to activate the *Abd-B* promoter, possibly due to the close proximity of this enhancer to the *Abd-B* promoter and the fact that there are no intervening insulator elements (see Fig. 1B).

Previous studies demonstrated that a deletion 5′ of the *Abd-B* promoter region, which included the PTE, resulted in reduced IAB enhancer-*Abd-B* promoter interactions in trans (Sipos et al., 1998). As larger deletions were made, the interactions between the IAB7 enhancer and the target *Abd-B* promoter became increasingly weaker. One explanation for this observation could be the existence of additional elements in the extended 5′ promoter sequence which may play a role in the tethering of the IAB enhancers to the *Abd-B* gene at the endogenous BX-C. Our bioinformatic studies across different *Drosophila* species support this idea. The neighboring sequence 5′ of the PTE is highly conserved; suggesting that part of this upstream region may also contain sequences that aid in the tethering activity (Fig. 7). In this case, the critical in vivo function of the PTE may be supported by, as yet unidentified, additional cis-regulatory sequences capable of facilitating promoter-enhancer tethering. Transgenic constructs containing a PTE sequence extended to include part of this 5′ region will be important in determining the function of this region.

The PTE may also function in conjunction with a different class of anti-insulator elements at the BX-C, the promoter targeting sequences (PTS), which are known to facilitate promoter-enhancer interactions (Chen et al., 2005). Future transgenic and genetic experimental approaches will help to unravel the combinatorial regulatory activities of these complex cis-elements. However, it is clear that the promoter-enhancer interactions facilitated by the PTE are relatively strong, as neither spacer DNA nor endogenous insulator elements were capable of disrupting these interactions in our transgenic assays. These results provide insight into the regulatory requirements at the endogenous locus. It seems likely that these strong interactions are necessary for the IAB5 enhancer element to bypass the two known insulator elements to activate the *Abd-B* promoter approximately 55 kb away in cis.

The precise molecular mechanism by which the tethering element functions is not clear. It is possible that common trans factors may bind to both the IAB5 enhancer and PTE and establish

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protein-protein interactions, although the *Abd-B* PTE and IAB5 enhancer do not share any extensive sequence homology. There is, however, a precedent for this type of interaction as Sp1 has been shown to form DNA loops between binding sites proximal to promoter sequences and distant binding sites to mediate an increased concentration of activator protein at the promoter (Mastrangelo et al., 1991). Bioinformatic analysis reveals two separate short sequences within the PTE that are highly conserved in different *Drosophila* species, when compared to the other sequences in the PTE (Fig. 7). It is possible that these sequences harbor binding sites critical for the recruitment of the trans factors involved in the molecular function of the PTE. As previously proposed, it is possible that a mechanism involving the IAB enhancers looping to interact with the PTE and drive expression from the target *Abd-B* promoter could be facilitated by specific chromatin structures in the BX-C (Akbari et al., 2006; Sipos and Gyurkovics, 2005). A similar spatial nuclear organization has also been suggested as a global regulator of developmental gene expression in higher eukaryotes (de Laat and Grosveld, 2003). More recent studies have demonstrated that there are indeed physical interactions between distant regulatory regions with the BX-C (Cleard et al., 2006), although the details remain to be fully elucidated. This model would explain the necessity of a functional PTE in the BX-C, as the disruption of this element would prevent the formation of the chromatin loop structures essential for promoter-enhancer communication, leaving the *Abd-B* target promoter inactive.

Implications for regulatory specificity in gene complexes

Promoter-tethering elements represent a precise mechanism for regulating specific enhancer-promoter interactions in gene complexes. Other mechanisms of cis-regulation may be less flexible. Recent studies have identified enhancers in the *Drosophila* genome capable of interacting only with distinct sub-sets of promoters. Some enhancers will only interact with DPE-containing promoters, whereas others only interact with TATA-containing promoters (Butler and Kadonaga, 2001). At the BX-C this may not be a feasible method for regulating enhancer-promoter interactions as the addition of a TATA box to one promoter, for example, may result in recruitment of all the enhancers in the complex. However, the PTE may function similarly to promoter competition in some respects, as the specific IAB5-*Abd-B* interaction it mediates appears to predominantly prevent the enhancer from activating other promoters.

The existence of a tethering element capable of specifically recruiting the distal T1 enhancer to the *Scr* gene promoter at the antennapedia *Hox* gene complex in *Drosophila* (Calhoun et al., 2002) suggests that promoter-tethering elements may represent a common mechanism for regulating enhancer-promoter interactions at complex loci. The ability of the IAB5 enhancer to activate *Abd-B* across insulator DNAs provides an intriguing model for tethering activities at other gene complexes. An example is the well characterized insulator at the mouse *H19* imprinting control region which separates 5′ enhancers from the *H19* promoter (Bell and Felsenfeld, 2000; Drewell et al., 2002b; Hark et al., 2000; Szabo et al., 2000). It is possible that a tethering element is required to selectively recruit these 5′ enhancers to the target promoter. The identification of an enhancer-containing global control region at the mouse *Hoxd* complex (Spitz et al., 2003) raises the possibility that promoter tethering over long distances may also be required at mammalian Hox genes.

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