Short germ insects utilize both the ancestral and derived mode of Polycomb group-mediated epigenetic silencing of Hox genes

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ABSTRACT

In insect species that undergo long germ segmentation, such as Drosophila, all segments are specified simultaneously at the early blastoderm stage. As embryogenesis progresses, the expression boundaries of Hox genes are established by repression of gap genes, which is subsequently replaced by Polycomb group (PcG) silencing. At present, however, it is not known whether patterning occurs this way in a more ancestral (short germ) mode of embryogenesis, where segments are added gradually during posterior elongation. In this study, two members of the PcG family, Enhancer of zeste (E(z)) and Suppressor of zeste 12 (Su(z)12), were analyzed in the short germ cricket, Gryllus bimaculatus. Results suggest that although stepwise negative regulation by gap and PcG genes is present in anterior members of the Hox cluster, it does not account for regulation of two posterior Hox genes, abdominal-A (abd-A) and Abdominal-B (Abd-B). Instead, abd-A and Abd-B are predominantly regulated by PcG genes, which is the mode present in vertebrates. These findings suggest that an intriguing transition of the PcG-mediated silencing of Hox genes may have occurred during animal evolution. The ancestral bilaterian state may have resembled the current vertebrate mode of regulation, where PcG-mediated silencing of Hox genes occurs before their expression is initiated and is responsible for the establishment of individual expression domains. Then, during insect evolution, the repression by transcription factors may have been acquired in anterior Hox genes of short germ insects, while PcG silencing was maintained in posterior Hox genes.

KEY WORDS: Epigenetic silencing, Gene expression, Hox genes, Insect, Polycomb group genes

INTRODUCTION

Though all insects possess highly conserved adult body plans, there are two different ways developmental patterning can be accomplished. In long germ insects, all segments are specified simultaneously at the early blastoderm stage. In contrast, in short or intermediate germ (hereafter collectively called short germ) insects, only the anterior regions are specified at the blastoderm stage. The remaining posterior segments are gradually formed from the most posterior region, termed the growth zone, during posterior elongation. While the short germ type is believed to be the ancestral mode of segmentation in arthropods (reviewed by Davis and Patel, 2002), the actual molecular mechanisms that regulate it have not been identified.

Despite operational differences, previous studies had revealed that canonical functions of segmentation genes are fundamentally conserved between long germ and short germ segmentation (Mito et al., 2005; Mito et al., 2006; Mito et al., 2007). As embryogenesis progresses, a noticeable difference is observed in the expression of Hox genes. In long germ species, such as Drosophila, all Hox genes are expressed simultaneously at the blastoderm stage (Akam, 1987; Castelli-Gair, 1998; Bae et al., 2002). In short germ insects, on the other hand, the middle Hox genes, Sex combs reduced (Scr), Antennapedia (Antp), and Ultrabithorax (Ubx), are expressed in the anterior regions preceding initiation of posterior elongation. This is followed by expression of their posterior counterparts, abdominal-A (abd-A) and Abdominal-B (Abd-B), which are associated with the formation of posterior segments (Tear et al., 1990; Kelsh et al., 1993; Shippy et al., 1998; Peterson et al., 1999; Zhang et al., 2005). These observed differences in the temporal activation of posterior Hox genes might reflect different regulatory mechanisms of Hox genes.

In Drosophila, gap genes function as repressors and provide positional information, determining the anterior border of the Hox gene expression domain. This repressed state of each Hox gene is maintained by Polycomb group (PcG) genes after decay of gap gene activity (Simon et al., 1992; Struhl and Akam, 1985; Jones and Gelbart, 1990). Previous studies reveal that the functions of gap genes as Hox gene repressors are conserved in short germ insects (reviewed by Jaeger, 2011), while the functions of PcG genes have not yet been analyzed in short germ insect development.

Functionally, PcG genes are identified as trans regulators that contribute to maintaining the expression patterns of Hox genes in Drosophila (Lewis, 1978). PcG gene products comprise 3 different types of complexes termed Polycomb repressive complex (PRC) 1 and 2 and Pleiohomeotic repressive complex (PhoRC). PhoRC, which binds specifically to Polycomb response elements (PREs), recruits PRC2 to PREs. PRC2 then trimethylates histone H3 on lysine 27 (H3K27) residues. This, in turn, provides a platform for recruiting PRC1. PRC1 catalyzes ubiquitination of lysine 119 on histone H2A, leading to silencing of target genes (Grimalda et al., 2006; Müller and Kassis, 2006; Simon and Kingston, 2009; Simon and Kingston, 2013). Drosophila PcG mutants exhibit homeotic
phenotypes, in which multiple Hox genes are activated in body regions where they should be silent (Simon et al., 1992; Soto et al., 1995). In those mutants, transformation of all segments to posterior segments occurs as a result of misexpressed Abd-B (Jones and Gelbart, 1990; Birve et al., 2001). Misexpression of Hox genes starts after establishment of normal expression domains, indicating that PcG genes are involved in maintenance of Hox gene repression but not in initial repression (Simon et al., 1992; Struhl and Akam, 1985; Jones and Gelbart, 1990). Thus, during Drosophila embryogenesis, PcG-mediated silencing maintains Hox expression boundaries after they are set in early embryos by gap gene activity (White and Lehmann, 1986; Harding and Levine, 1988; Irish et al., 1989; Reinitz and Levine, 1990; Qian et al., 1991). Concordantly, trimethylation of histone H3 on lysine 36 (H3K36me3) is first detected after germ band formation, 4–7 hours after egg laying (AEL) (Tie et al., 2009) and after the stage of assumed gap gene activity.

The PcG gene function to silence Hox genes is conserved in vertebrates. However, the establishment of Hox gene expression domains is different from that in Drosophila. In vertebrates, segments are progressively formed from anterior to posterior, along with posterior embryo growth. Hox genes are activated in time-dependent manner, during and after posterior growth, reflecting their positions in the gene cluster. This temporal and spatial collinear activation of Hox genes is accomplished through progressive demethylation of H3K27 in the gene cluster, which is silenced by PcG gene action prior to Hox gene activation (Soshnikova and Duboule, 2009). This sequential histone-demethylation process is regulated by a gradient of retinoic acid signaling (Lee et al., 2007; Agger et al., 2007). Thus, in the regulatory machinery of vertebrate Hox genes, PcG-mediated silencing occurs before Hox gene expression is initiated, and it is responsible for the establishment of individual expression domains. This patterning mechanism differs substantially from Drosophila. Because the process of posterior growth in vertebrates might be homologous to that in short germ insects with canonical Wnt signaling and the transcription factor caudal playing crucial roles (Martin and Kimelman, 2009), the regulatory machinery of the posterior Hox genes in short germ insects could be more similar to vertebrates than to Drosophila.

To examine this possibility, two members of the PcG family, the Enhancer of zeste (E(z)) and Su(z)12 (Su(z)12) genes, which are essential for histone methyltransferase activity of the PRC2 complex, were investigated in the short germ cricket Gryllus bimaculatus. To elucidate their functions in short germ insect development, RNA interference (RNAi)-based functional analyses of these genes were performed in the cricket. Here we discuss how the data provide novel insight into the key transitions and mechanisms governing regulation of Hox genes during animal evolution.

RESULTS
Suppression of Gryllus PcG genes causes a homeotic phenotype
To investigate the functions of PcG genes during embryogenesis, we cloned E(z) and Su(z)12 from Gryllus (supplementary material Fig. S1). E(z) was first detected by in situ hybridization at stage 8 in a ubiquitous pattern (supplementary material Fig. S2A,C). A parental RNAi approach was used to knock down these genes. E(z)RNAi embryos exhibited a membrane-enclosed, crescent-shaped body that lacked cuticle formation (Fig. 1B). In these embryos, dorsal closure occurred at the ventral side due to failure in katabresis, resulting in an “inside-out” morphology and 100% lethality (Fig. 1B; supplementary material Fig. S3 and Movie 1). As illustrated in Fig. 1D, the phenotype was characterized by a greatly contracted body and by transformation of antennae and mouthparts to leg-like appendages (supplementary material Fig. S5). Two different dsRNAs, Gb′E(z)1RNAi and Gb′E(z)2RNAi, produced the same morphological phenotypes, excluding the possibility of off-targeting effects by dsRNAs. Su(z)12RNAi embryos exhibited a similar but less severe phenotype (supplementary material Fig. S4C). This observation was consistent with real-time quantitative PCR (RT-qPCR) results showing the lesser reduction of Su(z)12 mRNA levels in Su(z)12RNAi embryos compared to E(z) mRNA levels in E(z)RNAi embryos (supplementary material Fig. S2D,E). For this reason, E(z)RNAi embryos were used for further detailed analyses.

The patterns of leg markers, aristalless (al) (Miyawaki et al., 2002) and Distal-less (Dll) (Niwa et al., 1997), were determined in E(z)RNAi embryos. With the exception of mandibles, the head appendages assumed leg-like expression patterns of al compared to wild type (supplementary material Fig. S5A,B). In addition, in the affected head appendages, Dll expression patterns resembled those found in thoracic legs with distal and proximal domains (supplementary material Fig. S5C,D). The number of segments was not affected, suggesting that the observed phenotypes were not caused by changes in segment specification mechanisms.

Expression of wingless (wg), a ventral side marker of legs (Niwa et al., 2000), was restricted to the ventral margin of the elongating limb buds (supplementary material Fig. S5E). However, in E(z)RNAi embryos, the wg pattern expanded to the dorsal limb margin (supplementary material Fig. S5F). These observations indicated that, in depleted embryos, head appendages (antennae and mouthparts) assume leg-like identities, which also displayed altered dorsoventral polarity.

Gryllus E(z) is involved in histone methylation
To elucidate whether the observed E(z)RNAi phenotype was caused by changes in histone methylation activity, the spatiotemporal distribution of methylated histone 3 on lysine 36 (H3K36me3) was examined. In wild type Gryllus, H3K27me3 signals were observed ubiquitously throughout development (Fig. 2, two left-most columns), starting at the early blastoderm stage and continuing through stage 8. In E(z)RNAi embryos,
H3K27me3 levels were greatly reduced at every stage, although a slight signal was observed at stages 6–8 (Fig. 2, right side), consistent with RT-qPCR results (supplementary material Fig. S2D). These results indicated that the function of E(z) in Gryllus is to activate and maintain histone methylation, and suggest that the phenotypes observed in Fig. 1B,D may be attributed to changes at the epigenetic level.

**E(z)^{RNAi} embryos show anterior misexpression of Hox genes**

To clarify the identity of transformed leg-like structures and determine whether the functions of PcG genes in regulation of Hox genes are conserved in Gryllus, the three middle and two posterior Hox genes, Scr, Antp, Ubx, and abd-A (Zhang et al., 2005), and Abd-B, were investigated. Specifically, expression was determined in wild-type and E(z)^{RNAi} embryos at stage 4 (germ band formation stage), stage 5 (just after the initiation of posterior elongation and before A1 and/or A2 are formed), stage 6 (posterior elongation stage and beginning of limb bud formation), and stage 8 (posterior elongation completed). Consistent with the transformation of appendage morphology, all Hox gene patterns were also altered in E(z)^{RNAi} embryos (Figs 3 and 4). Similar phenotypes were observed in Su(z)12^{RNAi} embryos, although the effects were much milder (supplementary material Fig. S4).

Initial expression domains of the middle genes, Scr, Antp, and Ubx, were established at stage 4 (Fig. 3A,I,Q), and throughout stage 4 and stage 5 expression domains of these three genes were identical in wild-type and E(z)^{RNAi} embryos (Fig. 3). Differences in expression were observed at stage 6 (Fig. 3G,O,W). At stage 6, E(z)^{RNAi} embryos misexpressed Scr in the prospective mandible segment, while Scr expression in the prospective labial segment was significantly reduced (Fig. 3G). Scr expression was abolished by stage 8 (Fig. 3H). Antp expression was reduced in E(z)^{RNAi} embryos at stage 5 (Fig. 3N), but it increased in intensity at stage 6 encompassing the whole embryo (Fig. 3O). Neurogenic expression began at stage 8 with anterior ectopic expression (Fig. 3P). Finally, E(z)^{RNAi} embryos expressed Ubx in the T1 and T2 limb buds at stage 6 (Fig. 3W), which was followed by expansion into the anterior region by stage 8 (Fig. 3X).

Wild-type expression of the two posterior genes, abd-A and Abd-B, first appeared at stage 5 and stage 8, respectively (Fig. 4B,K). E(z)^{RNAi} embryos exhibited anterior expansion of expression, similar to the middle Hox genes (Fig. 3), although ectopic expression of abd-A and Abd-B appeared almost simultaneously with wild-type expression. For example, in RNAi embryos, the normal (in A1 and A2, in Fig. 4B) and ectopic expression (in the lateral regions of the gnathal and thoracic segments; Fig. 4F) of abd-A appeared simultaneously. Ectopic expression continued to expand and encompassed the anterior head segments during stage 6 and stage 8 (Fig. 4G,H). This trend was even more striking in Abd-B; ectopic expression reached its full extent at the same stage as wild-type expression (Fig. 4N).

In summary, knocking down E(z) using RNAi results in anterior misexpression of all examined Hox genes, suggesting that Hox genes were epigenetically silenced through H3K27me3 in the anterior region. In addition, there is a temporal difference in the establishment of ectopic expression domains between the middle and posterior Hox genes. The process is stepwise in the former, but it is simultaneous in the latter.

**PcG genes and gap genes regulate Hox genes independently**

E(z)^{RNAi} embryos exhibited ectopic expression of abd-A in the anterior regions at stage 5 (Fig. 4F). Coincidentally, embryos treated with RNAi directed to the gap gene hunchback (hb) also exhibit ectopic abd-A expression in the prospective gnathal and thoracic segments at stage 5 (Mito et al., 2005). Since PcG genes and hb knockdowns altered the regulation of abd-A in anterior regions, the genetic relationship between these genes was investigated.

The expression patterns of two gap genes, hb and Krüppel (Kr), were investigated in E(z)^{RNAi} embryos (Fig. 5A). Results showed...
that *hb* was not affected. Expression was confined to the prospective mandibular to labial segments (Mito et al., 2005). *Kr* spatial regulation was also preserved, appearing in the labial to T3 segments (Mito et al., 2006). However, overall expression levels were reduced, possibly due to secondary effects of derepression of other genes (Fig. 5A). In summary, spatial expression of *hb* and *Kr* were not altered due to *E(z)* depletion.

Finally, both *E(z)* and *hb* were knocked down simultaneously, and the Hox genes were examined (Fig. 5B). When *hb* was targeted with RNAi, the gnathal and thoracic regions were transformed to abdominal identities due to the expansion of *Ubx* and *abd-A* expression into the gnathal regions (Fig. 5B, left column). Interestingly, *Abd-B* remained unaffected, displaying a wild type pattern. In *hb/E(z)* RNAi embryos, however, ectopic expression of *Ubx* and *abd-A* was observed in the anterior-most head region (antennal and ocular segments) as well. Furthermore, *Abd-B* expression expanded into the gnathal segments (compare Fig. 5B, bottom left and right panels). These observations revealed that the combined *hb/E(z)* RNAi embryos exhibited a combined phenotype that resembled the sum of individual *hb* and *E(z)* knockdowns, indicating that there is no genetic interaction between *hb* and *E(z)*.

### Regional autonomy in the PcG silencing of Hox genes

To elucidate whether temporal PcG-mediated silencing of Hox genes was related to posterior elongation of the embryo, the

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**Fig. 3. Effects of *E(z)* RNAi on the expression patterns of middle Hox genes.** (A–D) Expression patterns of *Scr* in wild type (wt) embryos. Initial expression was restricted to the labrum from stage (st.) 4 to 6 (A–C), after which it spread to the T1 segment at st. 8 (D). (E–H) Expression patterns of *Scr* in *E(z)* RNAi embryos. Expression was similar to wt at st. 4 (E), then it became weaker as development progressed until it disappeared completely at st. 8 (F–H). At st. 6, anterior misexpression appeared (red bracket in G). (I–L) Expression patterns of *Antp* in wt. *Antp* was strongly expressed in T1–2 at st. 4 (I), then it expanded into the abdominal segments at st. 5 and st. 6 (J,K). At st. 8, the signal was observed in both the epidermis and central nervous system (CNS) of thoracic and abdominal segments (L). (M–P) Expression patterns of *Antp* in *E(z)* RNAi embryos. (M) Expression was normal at st. 4, then it was reduced at st. 5 (N), followed by ectopic expression encompassing the whole embryo at st. 6. At st. 8, the signal in the epidermis disappeared completely, but it was maintained in the CNS throughout the A–P axis (P). Anterior ectopic expression is shown by the red brackets in O,P. (Q–T) Expression patterns of *Ubx* in wt. (Q) Expression started in the growth zone at st. 4, then it expanded into T1 and abdominal segments at st. 5–8 (R–T). (U–X) Expression of *Ubx* in *E(z)* RNAi embryos. (U,V) The pattern appeared normal until st. 5, after which it expanded into the anterior regions (red brackets in W,X). Abbreviations: Mx: maxilla; Lb: labium; T1–3: thoracic segments 1 to 3; A1: abdominal segment 1; GZ: growth zone. Scale bars: 200 μm.

**Fig. 4. Effects of *E(z)* RNAi on the posterior Hox genes expression patterns.** (A–D) Expression patterns of *abd-A* in wild type (wt). Expression started in A1–2 at stage (st.) 5 (B), then it expanded posteriorly to encompass the whole abdomen during st. 6–8 (C,D). (E–H) Expression of *abd-A* in *E(z)* RNAi embryos. *abd-A* expression was not be detected at st. 4 (E). At st. 5 and 6, *abd-A* expanded into anterior regions, as depicted with red brackets (F,G). At st. 8, the signal was observed throughout the ventral regions, the head, and thorax, but was absent from the gnathal appendages and legs (H). (I–K) Expression patterns of *Abd-B* in wt. *Abd-B* was not present until posterior elongation was completed (I,J). Expression started at st. 8 and localized to A8–10 (K). (L–N) Expression of *Abd-B* in *E(z)* RNAi embryos. *Abd-B* expression was absent at st. 5 and 6, similar to wt (L,M). At st. 8, the signal expanded ventrally into the head region and thorax (N). Abbreviations: A1–10, abdominal segments 1 to 10. Scale bars: 200 μm.
showed only anterior head morphology. Furthermore, the posterior regions (Fig. 6A–C). In severe phenotypes, embryos 

Ubx, abd-A 

Gryllus 

abd-A 

regions posterior from T2 were missing. In those embryos, phenotypes, anterior regions were formed normally, whereas the (Fig. 6). Both mild and severe phenotypes were observed. In mild phenotypes, Ubx, abd-A, and Abd-B exhibited anterior expansion compared to single E(z) RNAi embryos (Fig. 6D–F). Remarkably, this trend became even stronger in the severe phenotype. Indeed, while none of Hox genes were expressed in insects treated with the single cad RNAi, they all become overexpressed in the double RNAi mutant (Fig. 6J–L). These observations indicated that PcG-mediated silencing of Hox genes was region-specific and stage-specific, with silencing in the anterior regions occurring independently of posterior region development.

DISCUSSION

Functional conservation of the PRC2 complex in Gryllus

In the present study, Gryllus embryos treated with RNAi directed against E(z) displayed reduced H3K27me3 signals during embryogenesis (Fig. 2), suggesting that the E(z) protein plays an important role in histone methylation activity of the PRC2 complex. These observations are consistent with previous work in Drosophila (Diptera) and Bombyx (Lepidoptera) (Tie et al., 2009; Li et al., 2012). The phenotypes of insects treated with RNAi directed against Su(z)12, another component of the PRC2 complex, were similar to E(z) RNAi phenotypes, supporting the model of structural and functional conservation of the entire PRC2 complex in Gryllus (Orthoptera). Thus, our results strengthen the view that epigenetic regulation machinery involving PcG complexes may be shared among all insect lineages.

There was also a noticeable difference in the developmental dynamics of H3K27me3 in Gryllus, which was first detectable at the syncytial blastoderm stage before the germ anlage was formed (12 h AEL; corresponding to stage 4 in Drosophila) (Fig. 2). By comparison, H3K27me3 was first detected in Drosophila after germ band formation at stages 9–11 (Tie et al., 2009). At present, we do not know how E(z)-mediated temporal differences in H3K27me3 could affect early embryo development. As indicated by data (supplementary material Fig. S3), one possibility is that H3K27me3 in the early blastoderm may be involved in proper development of extraembryonic tissues and dictate katatrepsis defects observed in E(z)RNAi embryos.
Mode of establishing expression domains varies among Gryllus Hox genes

As demonstrated in Figs 3 and 4, treatment of Gryllus with E(z) RNAi resulted in anterior misexpression of Scr, Antp, Ubx, Abd-A, and Abd-B, suggesting that these Hox genes are epigenetically silenced by PcG in the region anterior to each of their individual expression domains. This anterior silencing may be essential for providing proper segment identities in embryos, as the E(z)RNAi phenotype exhibited a homeotic transformation of head appendages, with the exception of mandibles, into leg-like structures (Fig. 1). However, while anterior misexpression of those same Hox genes was reported in E(z) loss-of-function mutants in Drosophila, mutant embryos displayed very different phenotypes; all trunk segments acquired the A8 identity (Jones and Gelbart, 1990). This discrepancy may be due to the fact that ectopic expression of Abd-B in Gryllus occurs at a germband stage with well-developed leg buds (stage 8), later than the extended-germband stage in Drosophila (Simon et al., 1992). This may prevent the inhibition of leg development in Gryllus. In addition, ectopic expression of Scr, Antp, and Ubx in early and late appendage buds may activate the leg development program, leading to leg-like transformation of head appendages.

In addition to the different morphological phenotypes of E(z) loss-of-function mutants, significant differences in the patterns of Hox gene expression were observed. In Gryllus E(z)RNAi embryos, Scr expression was lost at stage 8 (Fig. 3H). On the other hand, Drosophila E(z) mutant embryos exhibited ectopic expression of Scr in the whole embryo at late stages (Soto et al., 1995). It is possible that Scr expression in Gryllus is repressed by Ubx, because Ubx is misexpressed in the whole body of late stage E(z)RNAi embryos, overlapping potential regions of Scr expression. This regulatory relationship may not be conserved in Drosophila, suggesting that there may be differences in transcriptional regulation of Hox genes between Gryllus and Drosophila.

This study revealed another critical difference in PcG silencing of posterior Hox genes (abd-A and Abd-B) between Drosophila and Gryllus. In Drosophila, the repression by gap genes determines the anterior expression boundary of each Hox gene (in both Antennapedia and Bithorax complexes). Subsequently, the role of a gap gene is replaced by epigenetic silencing from PcG genes, which, in turn, maintains anterior borders (Simon et al., 1992; Struhl and Akam, 1985; Jones and Gelbart, 1990). Such a stepwise change in the Hox repression system may also apply to regulation of Scr, Antp, and Ubx in Gryllus, as indicated by anterior expansion of expression in E(z)RNAi embryos (Fig. 3). On the other hand, Gryllus abd-A and Abd-B were misexpressed at the stage when normal expression appears (Fig. 4), suggesting that PcG silencing is involved in establishing expression domains of these genes. Indeed, hb represses abd-A expression in anterior (gnathal and thoracic) regions (Mito et al., 2005), as expected if a gap gene is involved in establishing the initial Hox expression domain. However, as shown by embryos treated with RNAi against hb and E(z), both genes seemed to act in parallel, not in a stepwise manner (Fig. 5). In addition, Abd-B is normally activated after completion of segmentation, when gap gene activity cannot be assumed.

The transcription of Gryllus posterior Hox genes seems to be activated during or after posterior embryo elongation and is epigenetically silenced by PcG in the regions outside of their normal expression as a way of establishing their anterior expression boundaries. This mechanism is reminiscent of Hox gene regulation in vertebrates. The initial state of the vertebrate Hox gene cluster is “closed (H3K27me3 positive)” via PcG silencing and subsequently “opened (H3K27me3 negative)” in a temporal manner to induce the expression of a particular Hox gene. Thus, PcG silencing is also required for establishment of the initial expression domains (Soshnikova and Duboule, 2009). This similarity between vertebrates and Gryllus with regard to dependence on PcG silencing in establishment of Hox expression domains suggests that this mode may represent the ancestral state in insects.

Activation of Abd-B in Gryllus may also be regulated in the manner similar to vertebrates. Indeed, this locus may also be silenced by PcG prior to transcription and subsequently turned into an active state when temporal and spatial patterns dictate. It should be noted, however, that inhibition of posterior elongation in Gryllus did not affect ectopic expression in the remaining embryonic regions (Fig. 6), implying the existence of autonomous mechanisms for Hox gene silencing and induction of transcriptional activators. Such a transcriptional activator may be upregulated throughout the wild type embryo at a specific developmental stage where Hox genes are expressed. This differs from vertebrates, in which intercellular signals, such as retinoic acid gradients, control where a specific Hox gene is activated or repressed (Kiecker and Lumsden, 2012). Alternatively, the Gryllus Abd-B locus might be kept “open” in prospective Abd-B-expressing cells throughout posterior embryo elongation until its activation stage, while in more anterior regions the locus might be “closed” prior to Abd-B activation. In this case, signals from the posterior growth zone, such as Wnt (Miyawaki et al., 2004), might be involved in inhibiting PcG silencing according to an activity gradient during posterior elongation.

Evolutionary transition of PcG-mediated silencing of Hox genes

Insights from the present and previous studies in vertebrates, Drosophila, and Gryllus, suggest that an intriguing transition of PcG-mediated silencing of Hox genes occurred during animal evolution (Montavon and Duboule, 2013; Bantignies and Cavalli, 2006). As illustrated in Fig. 7, the ancestral bilaterian state may have resembled the current vertebrate mode, where PcG-mediated silencing of Hox genes occurs before Hox gene expression is initiated, establishing individual expression domains. Then, during insect evolution, repression by transcription factors may have been acquired in anterior Hox genes of short germ insects, while PcG silencing was maintained in posterior Hox genes. During long germ insect evolution, the involvement of transcription factors may have spread to encompass the posterior Hox genes, resulting in the stepwise repression governed by gap and PcG genes that is observed in present day dipterans.

MATERIALS AND METHODS

Animals

Gryllus bimaculatus nymphs and adults were reared at 28–30°C with 70% humidity under a 10 light, 14 dark photoperiod, as previously described (Niwa et al., 1997). Fertilized eggs were collected with wet kitchen towels and incubated at 28°C in a plastic dish. Embryos were staged as described previously (Zhang et al., 2005).

Cloning of the Gryllus bimaculatus E(z) and Su(z)12

Partial nucleotide sequences of Gryllus bimaculatus E(z) and Su(z)12 were identified from cDNA obtained from adult ovaries (Zeng et al., 2013). Partial fragments of E(z) and Su(z)12 were PCR-amplified with gene specific primers and used as double-stranded RNA (dsRNA) templates. The primer sequences for E(z)N and E(z)C (see supplementary material Fig. S1) were 5′-ATACCTTGCCACACATCCAA-3′ (forward) and 5′-TTCCTTGGCCCTCCCTTAT-3′ (reverse) and 5′-CTTGGAGTGGA-
CTGCACTGA-3′ (forward) and 5′-CTCGCACACGAAGATAGCAG-3′ (reverse), respectively. Primer sequences for Su(z) are 5′-ATGGAACGCACCAAGAACC-3′ (forward) and 5′-ATGGGCCACATTCGAAGTGAA-3′ (reverse). The cDNA sequences of Gryllus E(z) and Su(z) were deposited in the DNA Data Bank of Japan (DDBJ) (accession numbers: AB378079; LC005751).

Parental RNAi
Cloned partial cDNAs of E(z) and Su(z) were used as templates to prepare dsRNAs. The MEGAScript Kit (Ambion) was used for in vitro synthesis of dsRNAs, which were adjusted to a concentration of 20 μM. Parental RNAi treatment was performed by injecting dsRNAs into the body cavity of adult female crickets as described previously (Mito et al., 2005).

Embryo fixation, whole mount in situ hybridization, and immunohistochemistry
Embryo fixation and whole-mount in situ hybridization with digoxigenin (DIG)-labeled antisense RNA probes were performed as previously described (Niwa et al., 2000; Zhang et al., 2005). For immunohistochemistry, embryos were fixed with the same methods as in situ hybridization (Niwa et al., 2000). Fixed embryos were rehydrated stepwise in 75%, 50%, and 25% solutions of methanol/phosphate-buffered saline + 0.1% Tween (PBT) and PBT for 5 minutes each. Next, embryos were incubated for 1 hour in 1% bovine serum albumin (BSA) (invitrogen)/PBT at room temperature and then with Alexa Fluor 488 Goat Anti-Rabbit IgG (Invitrogen) supplemented with DAPI (Sigma) diluted 1 to 1000 in PBT for 1 hour. After washing with PBT three times, embryos were counter stained with DAPI (Sigma) diluted 1 to 1000 in PBT for 10 minutes and then washed with PBT three times. PBT was then substituted by 25% and 50% glycerol/PBT to make embryos transparent for microscopy.

Real-time quantitative PCR
Total RNA was extracted from embryos using ISOGEN (Nippon-Gene). After treatment with DNaseI (Invitrogen), RNA was reverse-transcribed to cDNA using SuperScriptIII reverse transcriptase (Invitrogen). Real-time quantitative PCR was performed using the power SYBR Green PCR Master Kit (Applied Biosystems) and an ABI 7900 Real Time PCR System (Applied Biosystems), as described previously (Nakamura et al., 2008). Primer pairs were: E(z)Fw; 5′-GCGAGATGCACAAAAGCAGTGT-3′ and E(z)Rv; 5′-CTTCATGCAGGGCACGATGGA-3′; Su(z)12Fw; 5′-ACCCGTGGTGGTGTTACTT-3′ and Su(z)12Rv; 5′-GCGATAAAATCTCGGTGTTT-3′.

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Competing interests
The authors declare no competing or financial interests.

Author contributions
Y.M., T.B., S.N., and T.M. designed the work. Y.M. performed initial cloning of cDNAs used in this study, Y.M., T.B., T.W., Y.I., S.N., A.P., and T.M. analyzed experimental data. Y.M., A.P., and T.M. wrote the manuscript.

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