Pax group III genes and the evolution of insect pair-rule patterning

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SUMMARY

Pair-rule genes were identified and named for their role in segmentation in embryos of the long germ insect Drosophila. Among short germ insects these genes exhibit variable expression patterns during segmentation and thus are likely to play divergent roles in this process. Understanding the details of this variation should shed light on the evolution of the genetic hierarchy responsible for segmentation in Drosophila and other insects. We have investigated the expression of homologs of the Drosophila Pax group III genes paired, gooseberry and gooseberry-neuro in short germ flour beetles and grasshoppers. During Drosophila embryogenesis, paired acts as one of several pair-rule genes that define the boundaries of future parasegments and segments, via the regulation of segment polarity genes such as gooseberry, which in turn regulates gooseberry-neuro, a gene expressed later in the developing nervous system. Using a crossreactive antibody, we show that the embryonic expression of Pax group III genes in both the flour beetle Tribolium and the grasshopper Schistocerca is remarkably similar to the pattern in Drosophila. We also show that two Pax group III genes, pairberry1 and pairberry2, are responsible for the observed protein pattern in grasshopper embryos. Both pairberry1 and pairberry2 are expressed in coincident stripes of a one-segment periodicity, in a manner reminiscent of Drosophila gooseberry and gooseberry-neuro. pairberry1, however, is also expressed in stripes of a two-segment periodicity before maturing into its segmental pattern. This early expression of pairberry1 is reminiscent of Drosophila paired and represents the first evidence for pair-rule patterning in short germ grasshoppers or any hemimetabolous insect.

Key words: Pax, Drosophila, Schistocerca, Tribolium, Grasshopper, Paired, Gooseberry, Segmentation, Pair-rule, Pattern formation

INTRODUCTION

We currently know a great deal about how the Drosophila embryo becomes progressively subdivided into its future body segments. Gradients of maternal information act at the top of a genetic hierarchy that involves the sequential activation of the zygotic gap, pair-rule, and segment polarity genes. In phylogenetically derived long germ insects such as Drosophila, this genetic hierarchy functions to define and pattern all segments almost simultaneously within the blastoderm. In short germ insects, however, only segments of the head are defined in the initial blastoderm, while the remaining segments of the thorax and abdomen form progressively from a posterior growth zone (Sander, 1976). Thus, crucial questions arise as to which components of the Drosophila segmentation hierarchy are shared by different short germ insects and how they might function in the short germ context.

To better understand segmentation in short germ insects, we have chosen here to focus on homologs of the pair-rule and segment polarity class of segmentation genes in flour beetles and grasshoppers. Segment polarity genes were originally defined by their loss-of-function phenotypes in Drosophila, which reveal patterning defects within each segment of the embryonic cuticle (Nüsslein-Volhard and Wieschaus, 1980). Consistent with their phenotypes, most of these genes are expressed in Drosophila just before and throughout the morphologically segmented germ band stage in a segmentally reiterated pattern. The segment polarity genes that have been most widely studied in other insects are engrailed (en) and wingless (wg). In Drosophila, each is expressed as a single ectodermal stripe within each individual segment, defining the anterior and posterior boundaries, respectively, of each parasegment. These same patterns have thus far been found in all insects examined (reviewed by Patel, 1994a; Dearden and Akam, 2001), suggesting that segment polarity genes constitute part of the ancestral insect segmentation system. Indeed the role of these genes in patterning segments is likely to be ancient, as they are also expressed in segmental stripes in embryos of non-insect arthropods such as crustaceans (reviewed by Patel, 1994b; Nulsen and Nagy, 1999) and spiders (Damen et al., 1998).

In contrast to segment polarity genes, pair-rule homologues tend to exhibit more divergent patterns. Pair-rule genes were also originally defined by their loss-of-function phenotypes in Drosophila, in which regions of the embryonic cuticle are deleted with a two-segment periodicity (Nüsslein-Volhard and
Wieschaus, 1980). The three that have been widely studied outside of Drosophila are even-skipped (eve), hairy (h), and fushi-tarazu (ftz). In Drosophila, all three of these genes are expressed in stripes of a two-segment periodicity before the onset of gastrulation. After gastrulation, eve is expressed segmentally with refined late stripes in odd-numbered parasegments and weaker so-called minor stripes in even-numbered parasegments (Frasch et al., 1987). The expression of all three of these genes is conserved in the short germ flour beetle Tribolium (reviewed by Patel, 1994a). In the case of eve, its pair-rule function appears to be conserved as well, in that chromophore-assisted laser inactivation of Eve protein results in a pair-rule phenotype (Schröder et al., 1999).

A deletional mutant of the Tribolium Hox complex that includes the ftz ortholog, however, does not exhibit any pair-rule defects (Stuart et al., 1991), indicating that despite its two-segment periodicity, this gene appears to be functioning differently from its Drosophila ortholog. Additionally, genetic screens in Tribolium have produced at least two, possibly three, mutants that display pair-rule phenotypes (Maderspacher et al., 1998; Sulston and Anderson, 1996; Sulston and Anderson, 1998).

In the short germ grasshopper Schistocerca – a more distant relative of Drosophila – evidence of pair-rule patterning has instead proven elusive. eve and ftz orthologs are reportedly not expressed in periodic stripes in the early embryo, but in broad posterior domains (Dawes et al., 1994; Patel et al., 1992). This suggests that eve and ftz might play altogether different roles in grasshoppers, and raises the possibility that these insects might manage to define and pattern their segments without the use of pair-rule patterning. Alternatively, grasshoppers might use a form of pair-rule patterning that uses only some of the Drosophila pair-rule genes.

We have investigated the embryonic expression of homologs of the Drosophila pair-rule gene paired (prd), the segment polarity gene gooseberry (gsb) and gooseberry-neuro (gsbn), a gene that is expressed in the developing nervous system, but whose function has not yet been defined (reviewed by Noll, 1993). These three fly genes are the products of two duplication events, the first of which gave rise to prd and an ancestral gsb/gsbn gene, which then subsequently duplicated, giving rise to gsb and gsbn. Together with their vertebrate homologues Pax5 and Pax7, the three genes belong to Pax group III (PgIII), one of at least four subgroups of the Pax family of transcription factors (Balczarek et al., 1997) whose members all possess both a paired domain (PD) and an extended S80 paired-like homeodomain (HD).

In spite of their different roles in Drosophila, the Prd, Gsb and Gsbn proteins appear to be interchangeable with regard to patterning the embryonic cuticle and nervous system. The ubiquitous expression of each gene results in a similar cuticular phenotype. Furthermore, when placed under the control of gsb cis-regulatory elements, the coding region of prd is capable of rescuing gsb- defects in both the cuticle and the expression of target genes (Li and Noll, 1994). The coding region of gsb, when placed under the control of prd cis-regulatory elements, is likewise able to rescue a prd deficiency (Xue and Noll, 1996). Thus, differences in the roles played by prd and gsb in segmentation (as well as gsb in the developing nervous system) appear to derive solely from their different cis-regulatory systems and their resulting differential expression.

In Drosophila, Prd protein is found in seven primary stripes of a two-segment periodicity at the onset of cellularization,
consistent with its role as a pair-rule gene (Gutjahr et al., 1993a). The stripes, each approximately six cell rows wide, are centered on even-numbered parasegments and extend across both anterior and posterior parasegmental boundaries (Fig. 1L). By mid-cellularization the protein is upregulated in the posterior region of stripes 2-7, resulting in a step pattern within each primary stripe. Beginning at mid-gastrulation repression of prd in the middle two cell rows of stripes 2-7 results in the ‘splitting’ of these stripes. Before germ band extension, this splitting process, together with the narrowing of stripe 1 and the addition of an eighth posterior stripe, results in 14 secondary stripes of alternating intensity, each approximately two cell rows wide (Fig. 1M). These secondary prd stripes correspond to parasegmental boundaries: the anterior cell row expresses wg, while the posterior cell row expresses en (Gutjahr et al., 1993a).

Consistent with this pattern of co-expression, prd is required for the activation of both wg and en in the odd-numbered stripes (DiNardo and O’Farrell, 1987; Ingham and Hidalgo, 1993). prd is also required for the activation of the odd-numbered stripes of gsb (Baurmann et al., 1987).

gsb was originally identified for its role in patterning the epidermis, as evidenced by the loss of naked cuticle in mutant embryos (Nüsslein-Volhard and Wieschaus, 1980). This cuticle phenotype appears to be mediated almost entirely by wg, which requires gsb for its maintenance after stage 11 (Li and Noll, 1993). Gsb protein is first detected at the end of cellularization and by the onset of germ band extension is found in 14 segmental stripes at the posterior of each parasegment, consistent with the role of gsb as a segment polarity gene (Gutjahr et al., 1993b; Fig. 1U). At the end of germ band extension, stripes 4-14 undergo restriction to the ventral neuroectoderm (Fig. 1, compare W with Y). At this stage, gsb expression includes the Wg domain and extends across the parasegmental boundary one to two cell rows into the anterior portion of the En domain. The neuroectodermal stripes of gsb are required for the proper patterning of neuroblasts of rows 5 and 6, plus the most medial neuroblast of row 7 (Duman-Scheel et al., 1997). gsb is also responsible for the subsequent expression of gsb in a subset of the ganglion mother cell and neuronal progeny of the gsb-expressing neuroblasts (Gutjahr et al., 1993b, Fig. 1BB-EE).

To better understand the role PgIII genes play in the segmentation of short germ insects, we have focused on both flour beetles, in which expression of pair-rule and segment polarity homologs have thus far been found to resemble Drosophila, and grasshoppers, in which an expression pattern consistent with pair-rule function has not yet been reported. Our approach has been to develop a polyclonal antibody that has allowed us to visualize the products of PgIII genes in embryos of these insects. In both flour beetle and grasshopper embryos, we find that the expression pattern of PgIII genes resembles the pattern in Drosophila. Although these data are consistent with previous results for flour beetles, we show for the first time that a grasshopper segmentation gene is expressed in stripes of a two-segment periodicity, suggesting the existence of a pair-rule prepattern in this insect. To identify the PgIII genes responsible for the observed expression in grasshoppers, we isolated cDNAs of two PgIII genes, pairberry1 (pby1) and pairberry2 (pby2). We describe the structure of these genes as well as their expression patterns in grasshopper embryos.

MATERIALS AND METHODS

Antibody production

The Drosophila-specific mouse anti-Prd monoclonal antibody (mAb) DP201 and the crossreactive rat anti-Pairberry polyclonal antibody (anti-Pby) were generated by injection of full-length Drosophila Prd (derived from the cDNA c7340.1, kindly provided by Marcus Noll) fused to the product of the TrpE gene using PATH expression vectors (Koerner et al., 1991). Bacterial expression and purification were carried out as previously described (Papel et al., 1992). Affinity purification of anti-Pby serum was carried out as previously described (Papel et al., 1992), using a column bound with a portion of Gsbn fused to the product of the TrpE gene. The region of Gsbn used for purification was the C-terminal 289 amino acids that contained the Gsbn HD, but not the PD or the octapeptide (derived from cDNA bsh4c4, kindly provided by Marcus Noll).

Immunohistochemistry

Embryos of Drosophila melanogaster were prepared according to the standard protocol (Papel, 1994c). Embryos of Tribolium castaneum were prepared as previously described (Papel et al., 1994). Embryos of Schistocerca americana were prepared as previously described (Papel et al., 1989b), except that embryos were fixed in FEM-FA for 15 minutes, and then washed immediately with PT-NGS, followed by overnight incubation with primary antibody at 4°C.

In general, staining was completed as previously described (Papel et al., 1989b; Papel, 1994c). In addition to anti-Pby serum and MAb DP201, staining was performed with mAbs 4D9 (anti-En; Papel et al., 1989b), 2B8 (anti-Eve; Papel, 1994) and P7C11 (anti-Hb, Papel et al., 2001), as well as 16F12 (anti-Gsb) and 9A1 (anti-Gsbn), which were kindly provided by Bob Holmgren.

Cloning and sequence analysis

Total RNA was isolated with TRIzol Reagent (Gibco BRL) from three collections of embryos of the grasshopper Schistocerca americana at ~20-25%, 25-30% and 30-35% of development (Bentley et al., 1979; Patel et al., 1989a). Three separate pools of cDNA were then generated from these RNA collections with the SuperScript Preamplication System (Gibco BRL) and used for initial PCR screens using nested degenerate primers (first, 5’-GGN GGN GTN TTY ATH AAY GG-3’ and 5’-RTT NSW RAA CCA NAC YTG-3’, then 5’-MAR ATH GTN GAR ATG GC-3’ and 5’-RTA NCT NGG RTA YTG-3’) based on the PD and HD of Drosophila and mouse PgIII genes. The three cDNA pools were sampled with seven independent PCR reactions from which 87 clones were sequenced. No PgIII genes other than pby1 and pby2 were found.

Additional sequence 3’ of the HD of pby1 and pby2 was obtained using 3’ RACE (Gibco BRL). Phylogenetic trees are based on an amino acid alignment of a partial PD (98 amino acids) or both a partial PD plus the HD (63 amino acids; see Fig. 3A). The optimality criterion was maximum parsimony using the ProtPars step matrix (PHYLIP (Phylogeny Inference Package), J. Felsenstein, 1993) and searches were performed in PAUP* v 4.0b8 (Swofford, 2001) using the branch and bound algorithm.

In situ hybridization

Whole-mount in situ hybridization using a digoxigenin-labeled RNA probe was performed as previously described (Papel, 1996) with the following changes. Embryos of Schistocerca americana were fixed for 15-20 minutes in 3.7% formaldehyde after dissection in 1x phosphate-buffered saline (PBS; pH=7.4) and were then dehydrated stepwise in methanol before storing them at 4°C. Riboprobes for pby (1500bp) and pby2 (~700bp) were generated by digesting cDNA plasmids with BpiI and NdeI, respectively, such that only non-conserved regions 3’ of the HD were transcribed. Fixed embryos were not treated with xylene or proteinase K, and the hybridization was
carried out overnight at 65°C in an sodium dodecyl sulfate (SDS) hybridization solution (SDS-Hyb; 50% formamide, 5x saline sodium citrate (pH 4.5), 0.1% Tween-20, 0.3% SDS, 50 μg/ml heparin, and 100 μg/ml sonicated salmon sperm DNA).

The embryos were then washed at 65°C in the following solutions of SDS-Hyb and 1× PBS containing 0.1% Tween-20 (PTw): 2×20 minutes (80% SDS-Hyb/20% PTw); 2×20 minutes and 2×1 hour (50% SDS-Hyb/50% PTw); 2×20 minutes in (20% SDS-Hyb/80% PTw); then 2×20 minutes (100% PTw). Finally, embryos were washed at room temperature for 2×20 minutes in 1× PBS with 0.1% bovine serum albumin and 0.1% Triton X-100 (PBT) before adding sheep anti-digoxigenin-AP diluted 1:3000 in PBT, and incubating at 4°C overnight. The next day, embryos were washed 4×20 minutes and 2×60 minutes in PBT before performing the color reaction.

RESULTS

Antiseras raised to Drosophila Paired crossreact to Gooseberry and Gooseberry-Neuro

Antisera raised against Drosophila Prd protein have previously shown reactivity not only to Prd, but also to Gsb and Gsbn (Gutjahr et al., 1993a). We thus considered it likely that such antisera would contain antibodies to epitopes shared by all three proteins, as well as the homologous proteins of other insects. We therefore raised antiseras to Prd and enriched for crossreactivity by positive adsorption to an affinity column made with the HD of Gsbn. The resulting polyclonal antibody reveals a combined pattern of Prd, Gsb and Gsbn in stained Drosophila embryos, confirming that the reagent recognizes the products of all three genes (Fig. 1A-J). The antibody additionally recognizes the products of other genes possessing paired-like homeodomains, such as aristalest and repo (see below). Because such genes are expressed in non-stripe patterns later in development, this additional crossreactivity did not interfere with our analysis of segmentation.

When applied to embryos of other insects the affinity-purified antibody reveals striped patterns similar to those in Drosophila, suggesting that it recognizes the products of PgIII genes more generally. In light of this crossreactivity, we refer to this polyclonal antibody as anti-Pairberry (anti-Pby), and to the pattern it reveals as the Pairberry (Pby) pattern.

Expression of Pax group III genes in Tribolium mimics the pattern in Drosophila

The expression of segment polarity and pair-rule homologs in the flour beetle Tribolium have thus far been shown to be similar to Drosophila (reviewed by Patel, 1994a; see Brown et al., 1994a; Brown et al., 1994b). Tribolium probably also possesses at least three PgIII genes (Wim Damen and Martin Klingler, personal communication). We thus predicted that the Pby pattern in Tribolium should closely mimic the combined pattern of Prd, Gsb and Gsbn in Drosophila.

As with Drosophila Prd, the Pby pattern (the sum product of presumptive PgIII genes) in Tribolium castaneum appears in the blastoderm as a broad anterior domain, corresponding in Tribolium to the presumptive serosa (Fig. 2A,B). Concurrently, Eve protein is found in a broad posterior domain (Fig. 2C). Before gastrulation, a Pby stripe corresponding to the mandibular segment appears de novo (Fig. 2D,E). The stripe is positioned just anterior to the first of two broad Eve stripes, which form sequentially from the posterior domain before gastrulation (Fig. 2F). Like the mandibular stripe of Prd in Drosophila, this Pby stripe does not split.

As the amnion fold advances (Fig. 2H, asterisk shows initial amnion fold), a broad Pby stripe appears de novo between the two broad Eve stripes (Fig. 2J, arrowhead). The relative positions of these domains mimic expression in Drosophila, where primary Prd and Eve stripes are centered on even- and odd-numbered parasegments, respectively. In Tribolium, broad Pby stripes continue to appear de novo in sequential fashion between broad Eve stripes at the posterior (Fig. 2L,M,O,P, arrowheads). In that the broad Eve stripes have previously been shown to be stripes of a two-segment periodicity (Patel et al., 1994), the complementary Pby stripes are likewise of a two-segment periodicity.

As the Tribolium germband continues to extend posteriorly, the broad primary Pby stripes, like the early Prd stripes of Drosophila, split by loss of expression in the center of each stripe (Fig. 2J-N). Of the resulting two secondary stripes, the anterior stripe is transiently narrower than the posterior stripe. This is similar to the splitting of broad primary Eve stripes in this insect, though in the case of Eve it is the posterior secondary stripe that is transiently narrower and the primary stripes originate from a posterior domain, rather than appearing de novo (Patel et al., 1994). As in Drosophila, this splitting process is followed by the appearance of stripes of En, which partially overlap the posterior of the now segmental secondary Pby stripes (Fig. 2M-S). After the appearance of En, the secondary Pby stripes undergo restriction to the neuroectoderm in a manner similar to Drosophila Gsb (Fig. 2, compare R with Q). Later, during Tribolium neurogenesis, the Pby pattern is similar to the neural pattern for Drosophila Gsb and Gsbn (not shown). These observations suggest that anti-Pby recognizes the products of PgIII genes generally, as well as demonstrating that the expression pattern of these genes in Tribolium closely mimics their pattern in Drosophila.

Schistocerca possesses at least two Pax group III genes

Anti-Pby also revealed a striped pattern in embryos of the grasshopper Schistocerca americana. Like Tribolium, this pattern is similar to the pattern in Drosophila, but with some important differences. In order to identify the PgIII genes responsible for the grasshopper Pby pattern, we screened embryonic cDNA pools for PgIII genes by degenerate PCR followed by 3’ RACE. Our screen yielded two unique partial cDNAs, which we named pairberry1 (pby1) and pairberry2 (pby2).

The cDNA sequences of pby1 and pby2 predict proteins that each possess a PD plus an extended S0 domain-like HD and terminate 39 and 148 amino acids, respectively, after the HD (Fig. 3A,B). Within the PD and HD, the grasshopper genes are highly similar to one another and to Drosophila prd, gsb and gsn, yet lack significant sequence similarity C-terminal to the HD. Both pby1 and pby2 also possess the octapeptide sequence shared by gsb, gsn, pax-3 and pax-7, but not by prd (Frigerio et al., 1986). Finally, we were able to detect alternatively spliced forms not reported for any of the Drosophila genes. The alternate splice forms result in the insertion of five amino acids in the PD of Pby1 and the deletion of three amino acids from the HD of Pby2 (Fig. 3A). The pby1 splice site is shared by gsn but not by gsb or prd. The splice site in pby2 appears to be unique among insect PgIII genes.
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Phylogenetic analysis supports the inclusion of **pby1** and **pby2** within PgIII, but fails to resolve their relationship to the fly genes (Fig. 3C). The PD and HD amino acid and nucleotide sequence for **pby1** and **pby2** show >80% identity to each other and >60% identity to each of the three fly genes. Thus, **pby1** and **pby2** may be more closely related to each other than either is to **prd**, **gsb**, or **gsbn**. Finally, the combined distribution of **pby1** and **pby2** mRNA fully accounts for the striped Pby pattern in grasshopper embryos (Fig. 4). Thus, while we cannot rule-out the existence of additional homologs, we believe that we have found all of the PgIII genes in *Schistocerca*.

The combined expression of **pairberry1** and **pairberry2** fully accounts for the striped Pairberry pattern in *Schistocerca*

While possessing important differences, the overall Pby pattern in *Schistocerca*, like *Tribolium*, is similar to the combined pattern of Prd, Gsb and Gsbn in *Drosophila*. At ~35% of development, the grasshopper Pby pattern, as well as the pattern of **pby1** and **pby2** mRNA, includes 19 segmentally reiterated stripes corresponding to the antennal (An), intercalary (Ic), mandibular (Mn), maxillary (Mx), labial (La), thoracic (T1-3) and abdominal (A1-11) segments (Fig. 4K,L,N). The combined expression of **pby1** and **pby2**, then, fully accounts for the 19 stripes of protein observed with anti-Pby. That anti-Pby indeed reacts to the protein products of both **pby1** and **pby2** was confirmed by western blots of recombinant protein (not shown).
Before ~20%, pby1 is transcribed in a complex pattern that culminates in seven segmental stripes of the head and thorax (An, Mn, Mx, La, T1-3; Fig. 4A). Transcripts of pby2, however, are not detectable at these stages (Fig. 4B). As the pattern of Pby stripes mimics the pattern of pby1 stripes at these stages (Fig. 4A,D), we presume that these Pby stripes are the product of pby1 and not pby2. In 20-27% embryos, abdominal pby1 stripes appear at least four segmental stripes more posterior of the most posterior pby2 and En stripes (Fig. 4F-H). Thus, in the abdomen, as in the head and thorax, pby1 is transcribed before pby2. As the pattern of posterior abdominal Pby stripes is identical to the pattern of posterior abdominal pby1 stripes at these stages (Fig. 4F,I), we also presume that the Pby stripes in the posterior pre-En region of the embryo are the product of pby1 and not pby2, while Pby stripes in the anterior post-En region reflect the protein products of both genes.

In addition to these 19 stripes, the Pby pattern also includes repeating patterns of neural expression and various non-stripe domains in the pre-antennal region of the head, in appendage primordia, in lateral ectoderm of the abdomen and in the telson (Figs 4K-O, 5H). Most of these non-stripe domains are found in the mRNA pattern of either pby1 or pby2, or both, and the majority do not appear until after ~30%, well after segmentation is complete. The portions of the Pby pattern that are not due to either pby1 or pby2 are probably due to crossreactivity to proteins possessing paired-like homeodomains, such as aristaeless and repo.
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Striped expression of pairberry

Head and thoracic stripes

*pby1* is first expressed in the grasshopper embryo shortly after gastrulation at ~40 hours after oviposition. At this point, anti-Pby reveals low levels of Pby1 protein in a posterior domain spanning six to ten cells along the anteroposterior axis (Figs 5B, 6B, 9%). As the embryo begins to extend posteriorly, a second, more anterior, domain appears medially and spreads laterally to form an arc of expression spanning ~ten cells along the anteroposterior axis (Fig. 5C, arrowhead; Fig. 6B, 10-11%). This early arc corresponds to the region of the future gnathal segments (Mn, Mx and La) and is thus referred to as the ‘gnathal arc’. As the embryo continues to extend (~12–13%), the posterior domain disappears while the gnathal arc persists. At ~15% of development, a de novo stripe spanning ~four cell rows arises ~ten cells posterior to the gnathal arc and expands posteriorly, becoming a broad domain spanning ~15 cell rows, which comprises the future stripes of both T2 and T3 (Figs 5D, 6B, 15-16%).

After the T2/T3 broad domain appears, the gnathal arc begins to split. The split results from loss of Pby1 protein in the middle six cell rows of the arc, leaving two stripes corresponding to regions of the future Mn and La segments (Fig. 5E, black staining; Fig. 6B, 15-16%). As the gnathal arc splits, expression in the more posterior portion of the T2/T3 broad domain diminishes, while expression levels increase in the most anterior two cell rows, forming the T2 stripe (Fig. 5E, black staining). Concurrently, the T3 stripe, which spans ~four cell rows, appears...
Fig. 5. Early Pairberry pattern in *Shistocerca*. (A-D) Anti-Pby immunostaining of early grasshopper embryos. (A) Dapi stain of embryo, ~9% of development. (B) Same embryo, showing weak posterior Pby domain also observed with *phy1* mRNA (not shown). (~11% embryo showing gnathal arc (black arrowhead). The amniotic fold has been left intact (asterisk). (D) ~15% embryo showing gnathal arc (black arrowhead) and T2/T3 broad domain with higher levels at the anterior edge where the T2 Pby stripe will form (open arrowhead). (E-G) Anti-Pby (black) and anti-Hb (brown) immunostaining of ~16-17% embryos. (E) At ~16% the Mn, La and T2 Pby stripes have formed, while T1 is just beginning to appear. The strong subdomain of Hb protein extends from the Mn Pby stripe to just posterior of the La Pby stripe, where the weak subdomain continues through the T1 Pby stripe. Low levels of Hb are also found throughout the more anterior head lobes (asterisk). (F) Slightly later, the Mx Pby stripe has formed while the Hb domain remains static. (G) At ~18%, extension results in the concomitant separation of Pby stripes and increased length of the Hb domain, particularly in T1. (H) ~17% embryo after the split of the gnathal arc and intercalation of the Mx and T1 Pby stripes, plus addition of antennal (red arrowhead) and T3 Pby stripes. Open arrowhead indicates position of T2 Pby stripe. Embryo also shows several pre-antennal domains, which include the eyespot present in the *phy1* mRNA pattern (red arrow) and domains not seen in either the *phy1* or *phy2* pattern (black arrows). Scale bar: 300 μm for A-D,H; and 170 μm for E-G.

near the posterior edge of the previous broad domain (not shown). After the formation of the Mn, La, T2 and T3 stripes, stripes of expression corresponding to the Mx and T1 segments intercalate de novo (Fig. 5E-G, black staining; Fig. 7B, 16-17%).

This early segmental Pby1 pattern allowed us to determine more precisely the position and modulation pattern of the early anterior gap domain of *hunchback* (*hb*) (Patel et al., 2001). At 10% (~50 hours AEL), this domain of Hb protein comprises both weak expression in the head lobes and a strong band of expression lying just posterior. The strong band then modulates into a step-pattern that consists of a strong anterior subdomain and weaker posterior subdomain. While we have mapped the position of the these subdomains by double labeling for En (Patel et al., 2001), double labeling with anti-Pby confirms that the formation of the step-pattern occurs via reduction of expression in the most posterior portion of the original band. Embryos stained for both Pby1 and Hb protein reveal that from the outset this modulated Hb stripe (in brown) extends from the posterior edge of the Mn Pby1 stripe through to the Pby1 stripe of T1 (Fig. 5E). Within this larger stripe, the boundary between the strong and weak subdomains lies just posterior to the La Pby1 stripe (Figs 5F-G, 6C). Importantly, this reveals that the apparent ‘expansion’ of the weak subdomain is due to differential growth within T1 (compare Fig. 5F with 5G), while domain boundaries are maintained.

After the appearance of the gnathal and thoracic Pby1 stripes, anti-Pby reveals a bilateral pair of stripes in the An segment (Fig. 5H, red arrowhead). A bilateral pair of En stripes arises just posterior to the An Pby1 stripes (Figs 4C-E, 6B, 17%). En stripes then appear in the Mn, T1 and T2 segments. Each En stripe lies posterior to a Pby1 stripe, the two stripes overlapping by one to two cell rows (Fig. 4F-J). This ordering of the appearance of En stripes (An at ~17%, followed by Mn, T1 and T2 at ~18%, Fig. 6A) differs from the order previously reported for this species (Patel et al., 1989a), suggesting that the timing of En stripes may be polymorphic. The only remaining anterior Pby1 stripe, that of the Ic segment, does not appear until ~20-21%, just before the Ic En stripe (Figs 4F, 6B). After the appearance of adjacent En stripes, both the gnathal and thoracic Pby1 stripes undergo restriction to the ventral neuroectoderm (Figs 4F, 6B, 20-22%), in a manner similar to *Drosophila gsb*.

Abdominal stripes

The origin of the T2 and T3 stripes from within a single broad domain of expression suggests a transient two-segment periodicity for the stripes of *phy1* in the thorax. In the abdomen as well, this process – two adjacent stripes arising from within an initially broad domain – is repeated five times, reminiscent of the process by which *prd* acquires its segmental pattern in *Drosophila*. The process in grasshoppers consists of the following steps: (1) appearance of a broad domain (10–15 cells wide) near the extending posterior end; (2) increased expression in a stripe (~four cells wide) at the anterior edge of the broad domain with a concomitant decrease in expression levels in the posterior portion; and (3) appearance of a second posterior stripe (~four cells wide) arising from within the fading posterior portion of the broad domain (Fig. 7). An essential observation in this regard is that broad domains are only observed posterior to stripes of even-numbered abdominal segments. Hence, abdominal Pby1 stripes emerge from the following broad domains: A1/A2, A3/A4, A5/A6, A7/A8 and A9/A10. At least at the protein level, broad domains typically appear less refined at their posterior edge, so that low levels of
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protein often extend to the posterior tip of the embryo. In general, low levels of protein are also observed between nascent stripes, but these interstripe regions are quickly cleared as the stripes mature, as can be seen in more anterior segments (Fig. 7B). Finally, the last stripe to appear – that of A11 – appears in restricted form at ~35% and is not associated with an En stripe (Fig. 4K-O), as is the case for the A11 Gsb stripe in *Drosophila* (Gutjahr et al., 1993b).
Fig. 7. Early pby1 stripes are of a two-segment periodicity. (A) The posterior portion of ~18-20% grasshopper embryos stained for pby1 mRNA are shown. A1 and A2 pby1 stripes arise from within an initial A1/A2 broad domain, comprising the future pby1 stripes of A1 and A2. Note residual expression connecting A1 and A2 stripes during the individuation process (red arrow), as well as the low level of expression posterior to the A1 stripe through to the posterior tip. The individuation of stripes A1 and A2 is accompanied by the appearance of the A3/A4 broad domain, which will later refine into stripes A3 and A4. (B) The extending abdomens of ~21-24% embryos immunostained for Pby (black) and En (brown) are shown. A5 and A6 Pby stripes arise from within the broad ‘A5/A6’ domain and A7 and A8 Pby stripes from within the broad ‘A7/A8’ domain. As in A, note the low level of expression throughout the posterior beginning from the most recently individuated anterior stripes. Also note that En stripes appear before the restriction of Pby stripes to the ventral neuroectoderm: the third embryo from the left shows both a restricted stripe (arrowhead, A2) with En and an unrestricted stripe (arrow, A3) posterior to which an En stripe is just beginning to appear. Although some broad domains appear after the previous (more anterior) broad domain has split (A), other broad domains appear before the anterior nascent stripes have fully individuated (B), though this may reflect a difference in the turnover rates of transcript versus protein. Scale bar: 100 μm. Embryos in A have swelled somewhat as a result of the in situ protocol.

After forming, each of the segmental abdominal stripes narrows along the anterior-posterior axis to span only 2-3 cell rows. This narrowing is followed by the appearance of an En stripe posterior to the Pby1 stripe, such that the two stripes overlap by ~one cell row (Fig. 4, 23%; Fig. 7B). In part owing to their early appearance, stripes of Pby1 protein, unlike En, appear to keep pace with the extending posterior tip (Fig. 6B). After the appearance of an adjacent En stripe, each abdominal Pby1 stripe, like the gnathal and thoracic stripes, undergoes restriction to the ventral neuroectoderm and then expands to span four to five cell rows (Fig. 4, 23%). Unlike the segmental secondary stripes of Drosophila Prd, in which the posterior prd-expressing cell also expresses en (Gutjahr et al., 1993a), nascent En stripes are not situated entirely within Pby1 stripes. Pby1 stripes instead behave more like Gsb in this respect, overlapping En stripes by just one cell row.

Striped expression of pairberry2

The distribution of pby2 mRNA reveals that this gene is expressed in a pattern spatially coincident with, but temporally delayed with respect to, pby1. In particular, pby2 is expressed exclusively in stripes coincident with mature (i.e., ventrally restricted) pby1 stripes and these stripes appear at approximately the same time as stripes of En protein and slightly before stripes of Pby1 protein become ventrally restricted (Fig. 4G). The earliest pby2 stripes appear at ~19-21% in the An, thoracic and gnathal segments, followed by the Ic and abdominal stripes, the latter appearing in strict anterior to posterior progression (Fig. 6A,B). Based on its spatial and temporal dynamics, pby2 expression is reminiscent of Drosophila gsbm and late gsb expression.

The expression of pairberry1 and pairberry2 partially account for the non-stripped Pairberry pattern in Schistocerca

As pby1 and pby2 were the only grasshopper PgIII genes found in our screen, we reasoned that these genes together should be responsible for most, if not all, of the Pby pattern in this insect. Surprisingly, pby1 expression alone recapitulates the entire striped Pby pattern (Fig. 4). pby1 also recapitulates some (but not all) of the Pby domains in the pre-antennal region of the head, the earliest of which (Fig. 4A,D,E, brown arrows; Fig. 5E, red arrow) is found in the eye lobe and is likely to be coincident with a similar domain of wg (Dearden and Akam, 2001; Friedrich and Benzer, 2000). At ~23%, pby1 mRNA is found in two separate domains in the eye lobe (Fig. 4F), while at 35% the pre-antennal domains of pby1 are located more anteriorly (Fig. 4K). pby1 is also expressed in at least one of three circumferential rings in the limb primordia (Fig. 4K,N,O, red arrows) and these rings are also part of the Tribolium Pby pattern (Fig. 2S).

pby2 expression also recapitulates some non-stripe features of the Pby pattern. After ~30% pby2 joins pby1 in apparently coincident pre-antennal domains (Fig. 4L) and by ~40% in at least one limb ring (not shown). pby2 is also expressed in the mandibles and in the maxilla and labium primordia (corresponding to the emerging galea, lacinia and lingula) (Fig. 4L,N,O, red arrowheads) and at later stages (>40%) pby1 mRNA is found in these domains as well (not shown). This late gnathal expression is also part of the Tribolium Pby pattern (Fig. 2S) and is reminiscent of the late expression of Drosophila prd, which is also found at the base of the embryonic gnathal protuberances (Fig. 1Q-T).

Although pby1 and pby2 account for most of the Pby pattern in Schistocerca, some non-stripe features of the Pby pattern are apparently not due to either of these genes. These Pby domains are instead probably due to crossreactivity to additional proteins possessing the putative epitope shared by the products of PgIII genes. These non-PgIII Pby patterns include: (1) staining in the amnion (not shown); (2) pre-antennal domains that initially lie more anterior than pby1 (Fig. 4D,E, brown arrowheads; Fig. 5H, black arrows); (3) additional staining in the mandibles (Fig. 4L,N,O, asterisk) plus the distal tips of the maxillary and labial palps, limb primordia, lateral
abdominal ectoderm (Fig. 4N,O) and the telson (Fig. 4N,O, black arrowheads); and (4) glia of the developing central and peripheral nervous system (not shown). All four of these patterns are also observed in *Tribolium* and the latter three in *Drosophila* (not shown). The source of Pby staining in the amnion of *Schistocerca* and *Tribolium* is unknown, but staining in the pre-antennal region of all three insects is probably due to one or several of the paired-like homeodomain proteins known to be expressed in the developing brain and eye of *Drosophila*. Pby domains in the mandibles and the tips of the maxillary and labial palps, limb primordia, lateral abdominal ectoderm and the telson are probably due to *aristaless*, as this gene is expressed in analogous domains in *Drosophila* and possesses a paired-like homeodomain. Furthermore, anti-Pby staining of *Drosophila* wing and leg imaginal discs matches the published description of *aristaless* (Schneitz et al., 1993, not shown). The Pby staining in glia is almost certainly due to *repo*, as the product of this gene also possesses a paired-like homeodomain and is found in the glia of *Drosophila* and *Schistocerca* embryos (Halter et al., 1995). Consistent with this, the Pby glial pattern is observed in wild-type *Drosophila* embryos, but lost in repo<sup>1</sup> embryos (Xiong et al., 1994, not shown). The non-PgIII crossreactivity of anti-Pby should be useful in comparing the expression of these additional genes between various arthropods.

**DISCUSSION**

Using a crossreactive antibody (anti-Pby), we have observed that the pattern of presumptive PgIII gene products (the Pby pattern) in flour beetle and grasshopper embryos closely resembles the combined pattern of *prd, gsb* and *gsbn* in *Drosophila* (Figs 1, 2, 4). Importantly, Pby stripes in grasshopper embryos appear before the segment polarity gene *en* and exhibit a 2-segment periodicity, indicating that pair-rule patterning is a facet of segmentation in this insect. In order to identify the genes responsible for the Pby pattern in grasshoppers, we conducted a screen for *Schistocerca* PgIII genes. The screen resulted in two genes whose expression accounts for the entire striped Pby pattern. We discuss the evolution, expression and possible regulatory interactions of these two genes. We then reflect on how these data shape our picture of the ancestral insect segmentation system.

**pairberry1 and pairberry2 may be the result of duplication of the ancestral PgIII gene**

With the exception of possible nematode homologs (reviewed by Hobert and Ruvkun, 1999), protostome PgIII genes have thus far not been reported outside *Drosophila*. We have isolated two PgIII genes from *Schistocerca*, which we have named *pairberry1* (*pby1*) and *pairberry2* (*pby2*). Each gene possesses both a paired box and an extended S<sub>50</sub> paired-like homeobox (Fig. 3A,B). Phylogenetic analysis and high sequence similarity to *Drosophila prd, gsb* and *gsbn* supports the inclusion of *pby1* and *pby2* within PgIII (Fig. 3C). Additionally, *pby1* and *pby2* appear to be more closely related to each other than either is to *prd, gsb* or *gsbn*, suggesting they may be the result of an independent duplication (Fig. 3C). This conclusion is tempered, however, by the possibility of homogenization of *pby1* and *pby2* via gene conversion.

Although the two grasshopper genes may be closely related, we were unable to unequivocally resolve their relationship to the fly genes (Fig. 3C). Although it is possible that *pby1* and *pby2* result from the duplication of the ancestral *gsb/gsbn* gene along the lineage leading to *Schistocerca* after its split with *Drosophila*, this scenario implies that a grasshopper *prd* ortholog either exists and has not been found, or was subsequently lost. As the expression patterns of both *pby1* and *pby2* include elements similar to the expression of each of the three *Drosophila* genes, we think it more likely that *pby1* and *pby2* result from an independent duplication of a single ancestral insect PgIII (*prd/gsb/gsbn*) gene.

**The early expression of pairberry1 constitutes evidence for pair-rule patterning in *Schistocerca* and is reminiscent of *Drosophila* paired**

The early transcript and protein expression patterns of *pby1* provide, for the first time, evidence of pair-rule patterning in the grasshopper *Schistocerca*. Indirect evidence is provided by the order of appearance of the gnathal and thoracic Pby1 stripes. In particular, the onset of the Mx and T1 stripes is delayed relative to their adjacent stripes (Figs 5F-H, 6B, 16-17%). Thus, like many segment polarity genes in *Drosophila*, the order of appearance of these segmental stripes follows a two-segment periodicity. This may reflect, as it does in *Drosophila*, regulation by an underlying pair-rule patterning mechanism.

Stronger evidence for pair-rule patterning lies with the early domains of *pby1* expression from T2 to A10. Stripes of these segments originate as broad domains of a two-segment periodicity at the extending posterior tip, each of which subsequently splits into a pair of adjacent segmental stripes. Thus, adjacent stripes arise by subtly different means. The segmental stripes of T2, A1, A3, A5, A7 and A9 resolve from the anterior edge of sequentially appearing broad domains. By contrast, the segmental stripes of T3, A2, A4, A6, A8 and A10 resolve from within the posterior portions of the same respective broad domains (Figs 6B, 7). This resolution of broad domains into adjacent pairs of segmental stripes is analogous to the process by which *Drosophila* *prd* acquires its segmental pattern from initial stripes of a two-segment periodicity (Fig. 1B,C).

Although similar to *Drosophila* and flour beetles, the broad domains in grasshopper exhibit at least one notable difference. When compared with either *Drosophila* or flour beetles, the pairing of stripes in grasshoppers is shifted by one segment. For example, in grasshoppers, the Pby1 stripes of A1 and A2 derive from a single A1/A2 broad domain, while in flies and flour beetles the segmental Pby stripes of A1 and A2 derive from the T3/A1 and A2/A3 broad domains (primary Prd stripes 4 and 5 in *Drosophila*). The shift in phasing of stripe pairs in *Schistocerca* when compared with *Tribolium* and *Drosophila* is reflected in the fact that the grasshopper A11 Pby1 stripe (Fig. 4K), which appears relatively late, arises without a sister stripe. Such variation in phasing is likely to reflect a spatial shift in the expression of upstream components of the segmentation hierarchy.

An additional similarity of early *pby1* expression to *Drosophila* *prd* is its timing relative to segment polarity genes. In *Drosophila*, *prd* is expressed before *en* and *wg*. In *Schistocerca*, *pby1* is expressed before En protein by
approximately four to five stripes from ~20-27% (Figs 4A,C,F,H, 7B). *pby1* is, hence, also likely to be expressed ahead of *wg*, as in *Schistocerca gregaria*, *wg* transcript appears only two to three stripes ahead of En protein (Dearden and Akam, 2001; C. J. and N. P., unpublished ). Another feature shared by the early *pby1* pattern and that of *Drosophila prd* is the gnathal arc. This early domain comprises the future *pby1* stripes of the Mn, Mx and La segments (Figs 5C,D,E, 7B, 10-16%). In *Drosophila*, *prd* is also expressed as a single broad stripe before splitting into primary Prd stripes 1 and 2 at the onset of cellularization, just as stripes 3-7 begin to appear (Gutjahr et al., 1993a; Fig. 1A,B,K,L). Primary stripes 1 and 2 in turn give rise to the future Mn, Mx and La secondary stripes of Prd. This early Prd domain in flies is thus remarkably similar to the *pby1* gnathal arc in grasshoppers. We were not able to detect a similar pattern in flour beetle embryos, as the Mn Pby stripe appears de novo (Fig. 2D-F).

**The late expression of pairberry1 and pairberry2 is reminiscent of *Drosophila* gooseberry and gooseberry-neuro**

The position of *Pby1* stripes just anterior to En with an overlap of ~one cell row, along with their subsequent restriction to the neuroectoderm (Fig. 5B), is reminiscent of *gsb* expression in *Drosophila* (Fig. 1U-Y). Similarly, the delayed appearance of *Pby2* stripes, their restricted form, and their coincident expression with *Pby1* anterior to En (Figs 4F-J, 6) is reminiscent of late *gsb* expression (Fig. 1X,Y). Additionally, the striped neural expression of both *pby1* and *pby2* as late as 40% (not shown) is reminiscent of *gsbn* expression (Fig. 1BB-EE). Thus, only one of two PgIII genes identified in *Schistocerca*, *pby1*, is potentially functioning in the capacity of one of all three PgIII genes in *Drosophila* (*prd*, *gsb* and *gsbn*), while *pby2* is potentially functioning in the capacity of one, or perhaps two, of the *Drosophila* genes (*gsb* and *gsb-n*). Finally, although the behavior *pby2* is most similar to *Drosophila* *gsb* and *gsbn*, the late expression of both *pby1* and *pby2* at the base of the developing gnathal appendages is reminiscent of the late expression of *prd* at the base of the gnathal protuberances in *Drosophila* embryos (Figs 1Q-T, 4K-O).

**pairberry1 may regulate the expression of pairberry2 and segment polarity genes**

During *Drosophila* embryogenesis, the pair-rule gene *prd* activates the segment polarity gene *gsb*, which, in turn, activates *gsbn*. Additionally, the products of these three genes are for the most part functionally interchangeable (Li and Noll, 1994; Xue and Noll, 1996). Given both their similarity to the three fly genes and their coincident expression, *pby1* may be required for the activation of *pby2*.

In *Drosophila*, *prd* is also required for the activation of odd-numbered *wg* stripes (Ingham and Hidalgo, 1993). Thus, *Pby1* may be required for activation of *wg* in *Schistocerca americana*. The temporal dynamics of *wg* mRNA in the closely related grasshopper *Schistocerca gregaria* are consistent with this suggestion (Dearden and Akam, 2001). In *Drosophila*, *prd* is also responsible for activating and defining the posterior border of odd-numbered En stripes. This is suggested by the absence of odd-numbered En stripes in *prd*-negative embryos (DiNardo and O’Farrell, 1987), as well as their posterior expansion in heat shocked *prd* embryos (Morrissey et al., 1991). Consistent with this role, the posterior borders of secondary Prd stripes in *Drosophila* are coincident with the posterior borders of En stripes (Gutjahr et al., 1993a). In *Schistocerca*, however, *Pby1* does not simultaneously share a posterior border with En. Instead, nascent segmental stripes spanning four cell rows narrow to two cell rows just before the appearance of an adjacent En stripe, which overlaps by only a single row of cells. This lack of temporally coincident expression does not, however, rule out a possible role in activating *en*, for it is conceivable that the four-cell row domain of *Pby1* may activate *en* before narrowing, with the result that En appears specifically in cells that were previously expressing *pby1*. A similar situation may hold true for *Drosophila*, as it has been proposed that, despite the coincident expression of secondary Prd stripes and En, it is instead the earlier primary stripes of Prd that are responsible for the activation of *en* (Fujioja et al., 1995). Finally, it is important to note that a fully functioning pair-rule mechanism in grasshoppers may well require genes in addition to *pby1* that exhibit pair-rule like expression patterns.

**The evolution of insect pair-rule patterning**

Based on widespread conservation of expression patterns, it seems likely that the *Drosophila* segment polarity genes functioned as such in the context of the ancestral insect segmentation system. The picture is less clear for pair-rule genes. In light of the more basal phylogenetic position of *Schistocerca*, it is tempting to view the posterior expression domains of *eve* and *ftz* as ancestral for insects, existing before the evolutionary recruitment of these genes to play a role in segmentation (Dawes et al., 1994; Patel et al., 1992). In support of this conjecture, vertebrate orthologs of *eve* are linked to the Hox clusters and expressed in broad Hox-like domains (Bastian and Gruss, 1990; D’Esposito et al., 1991; Dolle et al., 1994; Ruiz i Altaba and Melton, 1989), while the *C. elegans* *eve* ortholog, *val-7*, is both expressed in a broad posterior domain and required for posterior cell fates (Ahringer, 1996). *ftz*, a gene closely related to the *Antp*-class Hox genes, is likewise expressed in a broad Hox-like domain in mites (Helford, 2000).

However, grasshoppers in some respects are likely to represent a derived state for insects. This is probably the case for *eve*, as this gene is expressed in stripes in spiders (Damen et al., 2000). Thus, it is possible that *eve* was primitively expressed in both stripes and a posterior domain, but somewhere along the lineage leading to *Schistocerca*, the gene lost its striped expression. Our observation that a PgIII gene is expressed in stripes of a two-segment periodicity in grasshoppers suggests that pair-rule patterning is part of the ancestral insect segmentation system. However, confirmation of this claim will require closer examination of the striped expression of pair-rule orthologs in primitive insects and non-insect arthropods.

An additional consequence of the molecular data presented here is that *Tribolium* and *Schistocerca* appear more similar in their embryology than previously appreciated. Before this study, the non-striped expression of *eve* and *ftz* did not allow comparison with the striped expression of pair-rule genes in other insects. The Pby pattern, however, allows such a comparison. In the case of *Tribolium*, only one Pby stripe, that of the mandibular segment, has formed before the onset of
gastrulation (Fig. 2D); *eve* and *fitz* stripes at this stage have likewise not formed posterior to the gnathal region (Brown et al., 1994a; Patel et al., 1994). In *Schistocerca*, we have been unable to detect any *pby1* expression before the onset of gastrulation (~36 hours AEL), and the first stripe associated with segmentation (the gnathal arc) does not appear until 10% (~50 hours AEL), well after gastrulation has begun (Fig. 5C). Thus, neither *Tribolium* nor *Schistocerca* has specified segmental or parasegmental boundaries posterior to the head at the start of gastrulation, conforming to the classical idea of short (as opposed to intermediate) germ embryogenesis (Sander, 1976).

*Drosophila* prd is at the bottom of the genetic hierarchy of pair-rule genes and this fact, coupled with its later segmental expression, have led some to suggest that in flies prd acts as a bridge between the pair-rule and segment polarity levels of the segmentation hierarchy (Baumgartner and Noll, 1991). If pair-rule patterning is an evolutionarily recent specialization of prd, then the segmental secondary Prd stripes of *Drosophila* are best seen as the remnants of an ancestral dual function as a pair-rule and segment polarity gene. It is perhaps not surprising then, that *pby1* – a PgIII gene from a more phylogenetically primitive insect – is expressed in both a pair-rule and segment polarity fashion. As one of only two PgIII genes in *Schistocerca,* *pby1* is expressed in a manner reminiscent of the combined pattern of all three PgIII genes in *Drosophila.* In lacking the specialized expression of the *Drosophila* genes, *pby1* may be our closest approximation of the ancestral insect PgIII gene.

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