The establishment of segmentation in the Drosophila leg

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SUMMARY
Segmentation is a developmental mechanism that subdivides a tissue into repeating functional units, which can then be further elaborated upon during development. In contrast to embryonic segmentation, Drosophila leg segmentation occurs in a tissue that is rapidly growing in size and thus segmentation must be coordinated with tissue growth. I demonstrate that segmentation of the Drosophila leg, as assayed by expression of the key regulators of segmentation, the Notch ligands and fringe, occurs progressively and I define the sequence in which the initial segmental subdivisions arise. I further demonstrate that the proximal-distal patterning genes homothorax and dachshund are positively required, while Distal-less is unexpectedly negatively required, to establish the segmental pattern of Notch ligand and fringe expression. Two Serrate enhancers that respond to regulation by dachshund are also identified. Together, these studies provide evidence that distinct combinations of the proximal-distal patterning genes independently regulate each segmental ring of Notch ligand and fringe expression and that this regulation occurs through distinct enhancers. These studies thus provide a molecular framework for understanding how segmentation during tissue growth is accomplished.

Key words: Leg development, Segmentation, Drosophila, Serrate, Delta, fringe, homothorax, dachshund, Distal-less

INTRODUCTION
Segmentation is a developmental mechanism common to a large number of animal species, including insects and vertebrates (Kornberg and Tabata, 1993; McGrew and Pourquie, 1998; Pick, 1998). Segmentation subdivides a tissue into a series of repeating units, whereupon each basic unit can then be further elaborated upon during development. The best-studied example of segmentation is that of the Drosophila embryo, where the molecular mechanisms are now well understood (Kornberg and Tabata, 1993; Pick, 1998; Small and Levine, 1991). However, segmentation of the Drosophila embryo differs substantially from other organisms, in that segmentation subdivides the entire embryo at once, without accompanying changes in tissue size. By contrast, segmentation of the insect leg, and of the body axes of short germ band insects and vertebrates, is fundamentally different in that segmentation occurs in a tissue that is rapidly growing in size (Bishop et al., 1999; de Celis et al., 1998; Gossler and Hrabe de Angelis, 1998; McGrew and Pourquie, 1998; Pick, 1998; Rauskolb and Irvine, 1999). Knowledge of the molecular mechanisms involved in the segmentation of these tissues is more limited.

Most insects have visibly segmented legs. Drosophila legs are composed of nine segments; from proximal (closest to the body wall) to distal (tip of the leg) they are the coxa, trochanter, femur, tibia and tarsal segments 1-5 (Fristrom and Chihara, 1978). Each segment is separated from the next by a flexible joint. In recent years, early steps in Drosophila leg development have been elucidated, and key genes involved in leg segmentation have been identified (Bishop et al., 1999; de Celis et al., 1998; Rauskolb and Irvine, 1999). Yet, it has remained unclear how a repeating segmental pattern is generated during leg development.

The adult Drosophila leg develops during larval stages from a cluster of undifferentiated cells, the leg imaginal disc. The leg disc is divided into anterior and posterior compartments. Signaling from the posterior to anterior compartment induces the expression of Decapentaplegic (DPP) in dorsal anterior cells and Wingless (WG) in ventral anterior cells, with their expression intersecting at the center of the disc (Basler and Struhl, 1994). DPP and WG encode secreted signaling molecules that specify dorsal and ventral cell fates, respectively (Baker, 1988; Brook and Cohen, 1996; Diaz-Benjumea et al., 1994; Held et al., 1994; Struhl and Basler, 1993).

The leg imaginal disc also has a proximal-distal axis. The center of the disc will give rise to the future distal tip of the leg, while progressively more peripheral regions of the disc will give rise to more proximal leg structures (Schubiger, 1971). Importantly, WG and DPP also direct proximal-distal patterning, and act together to regulate the expression of transcription factors expressed in broad domains along the proximal-distal axis of the leg disc, including homothorax (hth), dachshund (dac) and Distal-less (Dll) (Abu-Shaar and Mann, 1998; Diaz-Benjumea et al., 1994; Lecuit and Cohen, 1997; Milan and Cohen, 2000; Wu and Cohen, 1999). Leg development is dynamic and the expression profiles of these
genes change as development proceeds (Abu-Shaar and Mann, 1998; Campbell and Tomlinson, 1998; Diaz-Benjumea et al., 1994; Gorlinskii et al., 1997; Lecuit and Cohen, 1997; Wu and Cohen, 1999). At second instar, the leg disc is divided into two domains: a proximal domain defined by HTH expression and a distal domain defined by DLL expression. At early third instar (~72 hours after egg-laying, AEL) a population of cells expressing DAC arise that lie at an intermediate position between the DLL- and HTH-expressing cells. At mid third instar (~96 hours AEL) clear overlap between the DLL and DAC expression domains is observed. Finally, by late third instar (~120 hours AEL), there is a thin band of cells expressing all three genes, corresponding to the future trochanter.

Importantly, the expression of hth, dac andDll roughly corresponds to the regions of the leg affected by their absence. Absence of hth function results in deletion of proximal leg segments, absence of dac function results in deletion of intermediate leg segments, and reduced Dll function results in deletion of distal leg segments (Wu and Cohen, 1999; Campbell and Tomlinson, 1998; Cohen and Jurgens, 1989; Gorlinskii et al., 1997; Mardon et al., 1994). Given that mutations in these broadly expressed genes result in deletions (gaps) of leg segments, and by analogy with embryonic segmentation, they will be referred to, hereafter, as the leg gap genes.

While the function of each leg gap gene spans across several leg segments, localized Notch signaling is required within each leg segment to promote the formation of the boundaries that separate each leg segment and to induce leg growth. Notch is a transmembrane receptor protein (Artavanis-Tsakonas et al., 1999). There are two ligands for Notch in Drosophila, Serrate (SER) and Delta (DL) (Artavanis-Tsakonas et al., 1999). In addition, Fringe, a glycosyltransferase, functions to modulate Notch signaling by inhibiting the ability of a cell to respond to SER and potentiating the ability of a cell to respond to DL (Bruckner et al., 2000; Fleming et al., 1997; Moloney et al., 2000; Panin et al., 1997).

SER, DL, and fringe are expressed in a segmentally repeated pattern during leg development (Bishop et al., 1999; de Celis et al., 1998; Rauskolb and Irvine, 1999). At late stages of leg development they are expressed in a series of concentric rings within each of the future leg segments, proximal to cells destined to form the segment boundary (i.e. the actual joint). Through mutant clone analysis and ectopic expression studies it has been shown that Notch signaling has a key role in leg segmentation. Clones of cells mutant for Notch, Notch ligands or fringe result in fusions between leg segments and reduced leg growth (de Celis et al., 1998; Rauskolb and Irvine, 1999). Notch signaling also is sufficient to promote segmentation and growth as ectopic segment borders (joints) and local cell growth are induced when Notch is activated at ectopic sites within the leg (Bishop et al., 1999; de Celis et al., 1998; Rauskolb and Irvine, 1999).

Importantly, Notch activation must be restricted to a narrow region within each segment for proper leg development. If a constitutively activated form of Notch is expressed continuously across the length of several segments, legs lack segmentation and are shorter (de Celis et al., 1998; Rauskolb and Irvine, 1999). The requirement for a segmentally repeated pattern of Notch activation highlights the importance of establishing appropriately patterned expression of the regulators of Notch activation.

I have identified mechanisms that are responsible for establishing the segmentally repeated expression of the Notch ligands and fringe. My results demonstrate that leg segmentation occurs progressively as the leg disc grows, and I establish the temporal and spatial pattern of early steps in segmentation. I further demonstrate that the leg gap genes are key regulators of the segmental pattern of Notch ligand and fringe expression, and identify two Serrate enhancers that respond to regulation by a leg gap gene. These studies begin to elucidate the molecular mechanisms involved in establishing the repeating segmentation that occurs during Drosophila leg development.

**MATERIALS AND METHODS**

**Drosophila strains and generation of clones**

Mutant dac clones were induced in larvae (48-72 hours AEL at 25°C) of the genotype: y w hsFLP/++; dac<sup>-</sup> FRT40A/2<sup>M</sup>Myc FRT40A or, for clones in adult legs, y w hsFLP/++; dac<sup>-</sup> FRT40A/y<sup>+</sup> FRT40A (Mardon et al., 1994). Homozygous dac mutant leg discs were examined in dac<sup>-</sup> FRT40A/dac<sup>-</sup> FRT40A larvae. Mutant Dll clones were induced in larvae (60-84 hours AEL at 25°C) of the genotype y w hsFLP/++; FRT42 Dll<sup>flsa</sup>/FRT42 arm-lacZ<sup>M</sup> (Abu-Shaar and Mann, 1998).

For ectopic expression studies, ptcGAL4 UASGFP flies were crossed to UASdac<sup>7c4</sup> (Shen and Mardon, 1997), UASdll, or UASfringe2 (Pai et al., 1998), reared at 18°C, and then early to mid third instar larvae were dissected. SerlacZ1.9 and SerlacZ2.2 (originally called pCAB70-V-1.9 and pCAB70-I-2.2, respectively) (Bachmann and Knust, 1998) were used to make the stocks SerlacZ1.9 UASdac<sup>21M5</sup>/TM6b and SerlacZ2.2; UASdac<sup>21M5</sup>/L14 for the FLP-out experiments. FLP-out clones were generated as described previously (Rauskolb et al., 1999; Rauskolb and Irvine, 1999), using AγGAL4 UASGFP, with clones induced at 48-72 hours AEL at 25°C.

**Histology**

The following antibodies were used: mouse anti-DAC (DSHB), mouse anti-DLL (Duncan et al., 1998), rat anti-DLL (Wu and Cohen, 2000), rabbit anti-HTH (Kurant et al., 1998), rabbit anti-SER (Thomas et al., 1991), rat anti-SER (Papayannopoulos et al., 1998), mouse anti-DL (DSHB), goat anti-β-gal (Biogenesis) and rabbit anti-MYC (Santa Cruz Biotechnology). Antibody staining was performed as described (Panin et al., 1997; Rauskolb and Irvine, 1999). fringe expression was detected by in situ hybridization to mRNA (Rauskolb and Irvine, 1999).

**RESULTS**

**SER expression during leg development is progressive**

In theory, nine segmental units could be established at one time once leg growth is complete, similar to segmentation of the Drosophila embryo. However, several observations suggest that leg segmentation may be progressive. First, temperature-shifts of a conditional Notch allele at different stages of development interfere with the formation of distinct joints (Shellenberger and Mohler, 1978). Second, the rings of expression of a reporter gene construct that responds to Notch activation are established sequentially during leg development (de Celis et al., 1998). Although these studies indicate a
Leg gap genes regulate Notch ligand expression

To determine whether leg segmentation is initiated progressively upstream of Notch activation, I examined the expression of SER, DL and fringe, the earliest known indicators of a segmental pattern and the key regulators of Notch activation and leg segmentation. The initial focus has been on SER because a good antibody is available and because SerlacZ reporter gene constructs that represent a fraction of the SER expression profile exist. SER expression at different developmental time points was compared with that of the leg gap genes, because their expression has been well described and their relationship to presumptive leg segments established. In most cases, this made it possible to ascribe the rings of SER expression to particular leg segments. Moreover, these comparative expression studies suggested regulatory relationships that were then tested experimentally.

At ~72 hours AEL (early third instar) there is a single proximal ring of SER expression. This ring of expression arises within the presumptive coxa, as it lies just proximal to DAC-expressing cells, and within cells expressing HTH (Fig. 1A; Fig. 2A,B). A few hours later, at ~78 hours AEL, a second ring of SER expression arises just distal to the first (Fig. 1B). This expression arises within the femur, within cells expressing DAC; however, not all DAC-expressing cells express SER – only proximal ones near the HTH expression domain (Fig. 2C).

By ~84 hours AEL, two additional sites of SER expression are detectable, both within DLL-expressing cells of the presumptive tarsus (Fig. 1C). The more proximal of these is a...
ring of expression within the DLL domain, immediately distal to cells expressing DAC (Fig. 2D,E). I have tentatively assigned this ring to tarsal segment 2, based on the reported expression domains of DAC and DLL later in development (Milan and Cohen, 2000). SER expression is also observed in a central spot in the most distal region of the leg disc, in tarsal segment 5 (Fig. 1C; Fig. 2D,E). By ~96 hours AEL (mid third instar) six sites of SER expression are detectable; a tibia ring has been added as well as an additional tarsal ring (Fig. 1D). The tibia ring of expression arises in cells expressing both DAC and DLL (Fig. 2F). Late in larval development (~120 hours AEL; late third instar) there appears to be a ring of SER expression in each of the prospective leg segments (Fig. 1E) (Bishop et al., 1999; de Celis et al., 1998; Rauskolb and Irvine, 1999), with expression continuing to pupal stages (Fig. 1F) (Bishop et al., 1999; de Celis et al., 1998; Rauskolb and Irvine, 1999).

Early SER expression is regulated by the leg gap genes
Mutation of hth, dac or Dll results in deletion of leg segments (Campbell and Tomlinson, 1998; Cohen and Jurgens, 1989; Mardon et al., 1994; Wu and Cohen, 1999). Moreover, clones of cells mutant for any of these genes can be associated with leg segment fusions (Fig. 3D,G) (Campbell and Tomlinson, 1998; Wu and Cohen, 1999). Although the mechanism by which mutation of a leg gap gene results in leg segment fusions and tissue loss is not known, one possibility is that it reflects the requirement for these genes in establishing the striped expression of the Notch ligands and fringe. To test this hypothesis, I examined the influence of ectopic or absence of expression of DAC, HTH and DLL on SER expression during leg development.

DAC positively regulates SER expression
The femur ring of SER expression arises within cells expressing DAC. dac mutant flies survive to adulthood (Mardon et al., 1994), and thus SER expression could be examined in leg discs from larvae entirely mutant for dac. After 78 hours of development, when the femur ring of SER expression is normally present, SER expression in the coxa ring is unaffected, but expression in the femur ring is greatly reduced (Fig. 3F). To rule out the possibility that the femur ring is simply absent because these cells are missing in dac mutants (Mardon et al., 1994), I also analyzed dac mutant clones for their effects on femur SER expression. dac mutant clones are of comparable size with wild-type twin clones, indicating that dac mutant cells do not have a growth disadvantage (data not shown). Importantly, SER expression is cell-autonomously eliminated from dac mutant cells located in the femur (Fig. 3C). Moreover, dac is required autonomously for expression of SER in the tibia, although some nonautonomous rescue by neighboring wild-type cells is also observed (Fig. 3E). The absence of SER expression in dac mutant clones in the femur and tibia is consistent with the segment fusions observed in dac mutant clones in adult legs (Fig. 3D and data not shown). Together, these results demonstrate that DAC is an important positive regulator of SER expression in the femur and tibia. However, as SER is not expressed by all DAC-expressing cells, other factors must also influence SER expression within the DAC domain.

To determine whether DAC is also sufficient to promote SER expression, DAC was ectopically expressed along the anteroposterior (AP) axis of the developing leg (ptcGAL4 UASdac). At ~78 hours AEL, when SER is normally expressed in two proximal rings, ectopic expression of DAC cell-autonomously induces SER expression along the entire AP axis of the leg disc (compare Fig. 3A with Fig. 1B), resulting in leg...
segment fusions in the adult leg (Fig. 3B). Thus, DAC positively regulates SER expression during early leg development. It was initially surprising to observe ectopic SER expression induced in the domain of the leg where DAC is already expressed; however, ptcGAL4 drives the expression of DAC well above endogenous levels (Fig. 3A). Importantly, this indicates that the effect of DAC on SER expression is not mediated simply by repression of HTH or DLL by DAC, as these genes are not expressed significantly in the DAC domain at this stage. Together, these studies demonstrate that DAC is necessary and sufficient to establish SER expression in intermediate segments during leg development.

HTH autonomously represses and nonautonomously induces early SER expression

HTH is required for the formation of the most proximal leg segments and is expressed in the coxa and trochanter (Abu-Shaar and Mann, 1998; Wu and Cohen, 1999). The first ring of SER expression arises in the coxa and is the first sign of segmentation of the leg disc (Fig. 1A, Fig. 2A,B). To examine the influence of HTH on SER expression, HTH was ectopically expressed along the AP axis of the developing leg (ptcGAL4 UAS\textit{hth}).

Overexpression of HTH in proximal cells has no effect on the coxa ring of SER expression (Fig. 4A), consistent with the observation that the coxa ring of SER arises in cells that already express HTH. By contrast, ectopic HTH represses the expression of the femur ring of SER, and induces SER expression in neighboring cells in more distal regions of the leg (Fig. 4B). The phenotypic consequence of this is that the leg field is now split in two, with two rings of SER forming side by side and resulting in bifurcated adult legs (Fig. 4B,C). It has been reported that HTH can inhibit DAC and DLL expression cell autonomously, and HTH can induce DAC expression nonautonomously (Abu-Shaar and Mann, 1998; Goto and Hayashi, 1999; Wu and Cohen, 1999). Thus, the regulation of femur SER expression by HTH may be an indirect consequence of its effects on DAC expression. Indeed, in those cells in which femur SER expression is autonomously repressed, DAC expression is also repressed (Fig. 4D). As \textit{dac} is positively required for SER expression in the femur (Fig. 3C), this can account for the autonomous repression of SER by HTH. The nonautonomous induction of SER expression by HTH appears more complicated. On the anterior side of the ptcGAL4 stripe, DAC expression is induced, which could thus account for the induction of SER (Fig. 4D). By contrast, on the posterior side of the ptcGAL4 stripe, DAC expression is not detectably induced in the cells ectopically expressing SER (Fig. 4D). Thus, in this instance, SER expression appears to be induced nonautonomously by HTH in a DAC-independent manner.

DLL represses tarsal SER expression

The distal rings of SER expression arise within cells expressing DLL. To determine whether DLL regulates SER expression, I examined the expression of SER in \textit{Dll} mutant clones in early leg discs. \textit{Dll} mutant clones will sort out to proximal regions of the disc as \textit{Dll} also affects cell adhesive properties, but occasionally mutant cell will become ‘trapped’ in distal regions of the leg (Wu and Cohen, 1999). Strikingly, I observed that SER expression was derepressed cell autonomously in \textit{Dll} mutant clones located anywhere within the DLL domain (Fig. 4D; data not shown). Thus, DLL must normally act to repress SER expression, an unexpected result given that SER is normally expressed in the tarsus.

To further examine the repression of SER expression by DLL, I assayed the consequences of ectopic DLL expression. Expression of DLL along the AP axis of the developing leg (ptcGAL4 UAS\textit{Dll}) disrupts the femur ring of SER (Fig. 5A). The repression of SER expression in the femur is likely to be indirect, however, as a concomitant repression of DAC expression occurs (Fig. 5A). Similarly, DLL can repress SER expression in the coxa, but this effect may also be indirect through effects of DLL on HTH expression (Fig. 5B; data not shown) (Abu-Shaar and Mann, 1998). Importantly though, SER expression is also repressed by DLL in tarsal cells, outside the normal HTH and DAC expression domains (Fig. 5B).
expression of DLL along the AP axis of the leg also results in segment fusions throughout the tarsus (Fig. 5C). Thus, DLL is both necessary and sufficient to repress SER expression, and it appears that high levels of DLL expression can override positive regulators of SER expression within the tarsus.

**DAC acts through sequences present in minimal SER reporter gene constructs**

The results presented above establish that all of the known leg gap genes, HTH, DAC and DLL, are key regulators of SER expression. To begin to identify the actual sequences through which the upstream regulators act, I have begun to investigate the regulation of SER reporter gene constructs, identified previously by Bachmann and Knust (Bachmann and Knust, 1998), and reported to give SER-like expression in proximal versus distal domains of the leg disc. The sequences in these reporter constructs are from non-overlapping regions of the Ser locus (Fig. 6A) (Bachmann and Knust, 1998).

**SerlacZ1.9**

SeralcZ1.9 contains 1.9 kb from the Ser locus fused to lacZ

(Bachmann and Knust, 1998). SeralcZ1.9 expression is first detected at early third instar in a single ring (Fig. 6B), which corresponds to the femur ring of endogenous SER, as it lies just distal to the HTH domain and within the DAC domain (Fig. 6B). Thus, this reporter gene construct appears to contain the sequences required for SER expression in the femur, but lacks the sequences necessary for expression in the coxa. Moreover, because of the overlap with DAC expression,
SerlacZ1.9 may contain the sequences required for Ser regulation by DAC. By the end of the third instar, expression of SerlacZ1.9 continues in the femur but is also detected in a segmentally repeated pattern in most leg segments (data not shown).

To test whether early SerlacZ1.9 expression is regulated by DAC, I examined the effects of ectopic DAC expression. Clones of cells ectopically expressing DAC express SerlacZ1.9 at high levels in all regions of the disc, including where endogenous DAC is expressed (Fig. 6C; data not shown). These results argue that SerlacZ1.9 is a Ser enhancer containing regulatory elements that are responsive to positive regulation by DAC.

**SeralcZ2.2**

SeralcZ2.2 contains 2.2kb from the Ser locus fused to lacZ (Bachmann and Knust, 1998). Expression is restricted to the distal region of the developing leg in a ring in each of tarsal segments 1-4 (Fig. 6D) (Bachmann and Knust, 1998; Buckles et al., 2001). SeralcZ2.2 expression begins at mid third instar, later than SerlacZ1.9 expression is initially detected (data not shown). The expression of SeralcZ2.2 and DAC are complementary; SeralcZ2.2 is expressed entirely within the DLL domain (data not shown).

Surprisingly, a comparison of SeralcZ2.2 and SER expression at both mid third instar and pupal stages has revealed that expression of SeralcZ2.2 is complementary to the endogenous SER pattern in the distal leg (Fig. 6D) (Buckles et al., 2001). Thus, although SeralcZ2.2 contains the sequences necessary for restricting expression to the distal leg, sequences required for directing expression to the appropriate domain of each leg segment appear absent.

To investigate whether DAC acts to restrict SeralcZ2.2 expression to the distal regions of the leg, I examined FLP-out clones of cells ectopically expressing DAC. Indeed, DAC represses SeralcZ2.2 expression in the distal leg (Fig. 6E) and has no effect on SeralcZ2.2 expression elsewhere. This observation contrasts with the results obtained with SER expression in the femur and SerlacZ1.9, which are both positively regulated by DAC.

**DL and fringe expression occur progressively during leg development and are regulated by DAC**

Like SER, DL and fringe are expressed in a series of segmentally repeated rings during leg development. Late in leg development, DL expression overlaps that of SER, but also extends, in some segments, somewhat into regions of the disc where SER is not expressed (Bishop et al., 1999; de Celis et al., 1998; Rauskolb and Irvine, 1999). fringe expression appears coincident with SER expression in all leg segments (Rauskolb and Irvine, 1999). However, the expression of DL and fringe has not been characterized at early stages of leg development.

To determine whether DL and fringe expression are, like SER, progressive during leg development and how their profile compares with that of SER, their expression was examined at various stages. Indeed, both DL and fringe expression arise progressively, in a similar step-wise sequence as that observed for SER (Fig. 7A-C,G,H and data not shown). Interestingly, SER and DL expression in the coxa are coincident in early third instar leg discs (Fig. 7D). Thus, even at the earliest stages of leg development, the cells express both Notch ligands. This suggests that these genes overlap in expression throughout all of leg development, as they have been observed to do in most segments at late stages (Bishop et al., 1999; de Celis et al., 1998; Rauskolb and Irvine, 1999). The only notable difference among DL, SER and fringe is that SER and fringe expression arises in the most distal region of tarsal segment 5, which will ultimately give rise to the pretarsus, while DL expression encircles this domain (Fig. 7B and data not shown) (de Celis et al., 1998; Rauskolb and Irvine, 1999). The nearly identical expression patterns suggest that DL and fringe may also be regulated by the leg gap genes. Indeed, when DAC was ectopically expressed along the AP axis of the developing leg (ptcGAL4 UASdac), both DL and fringe expression were induced in an apparently cell autonomous fashion (Fig. 7E,F,I), paralleling the positive regulation of SER by DAC (Fig. 3).
DISCUSSION

Progressive segmentation of the *Drosophila* leg

In recent years the key role of the Notch signaling pathway in the segmentation and growth of the *Drosophila* leg has been established. Notch signaling must be localized within each leg segment to promote the formation of boundaries (joints) that separate each leg segment and to induce leg growth. This requirement for a segmentally repeated pattern of Notch activation is accomplished by restricting the expression of the regulators of Notch activation, SER, DL and *fringe*, to one ring per segment. By examining the expression of the Notch ligands and *fringe* during leg development, it has been possible to determine the progressive order in which leg segmentation is established (summarized in Fig. 8). At early third instar, a single ring of SER, DL and *fringe* expression is present within the coxa. The next ring to arise is located within the presumptive femur. At mid third instar, expression arises within presumptive tarsal segments 2 and 5. Subsequent expression is observed in the tibia and more tarsal segments, such that ultimately, by the end of third instar, a ring of expression is present in each presumptive leg segment, adjacent to each prospective leg segment border. Thus, segmentation of the *Drosophila* leg occurs progressively and in a reproducible pattern.

Previous studies investigating the expression of a reporter gene (E(spl)mβ-CD2) regulated downstream of Notch activation led to the conclusion that the first segment boundary to form was between tarsal segments 4 and 5 (de Celis et al., 1998). Additional rings of expression were then observed in the tarsus and then eventually in all leg segments. This led to the suggestion that the first segmental boundaries to form correspond to the most distal segments. However, further examination of this reporter gene indicates that expression is observed in proximal cells prior to expression within the tarsus (i.e. fig. 7 in de Celis et al. (de Celis et al., 1998)). Moreover, temperature shifts of a conditional Notch allele at different stages of development demonstrated that the temperature-sensitive period for Notch in proximal segmentation occurs before that in tarsal segmentation (Shellenbarger and Mohler, 1978). These studies and the data presented here lead to the conclusion that leg segmentation does not occur in a simple distal to proximal order, nor proximal to distal order, nor are the most proximal and distal segments established first and other segments added by intercalation, as has been previously

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**Fig. 8.** Summary model for the establishment of segmentation in the *Drosophila* leg. Although SER and leg gap gene expression occurs within the same cells, their expression is depicted here as two separate bars. For each panel, the top bar indicates the expression of the leg gap genes and the bottom bar denotes where SER expression (in red) is induced relative to this expression, with proximal on the left and distal on the right. Expression of HTH is in dark blue; DLL in yellow; DAC in light blue; DAC and DLL overlap in green; and HTH, DAC and DLL overlap in purple. Position of eventual leg segment borders shown in gray. Similar regulatory interactions are thought to induce segmental DL and *fringe* expression. Note that the model, as drawn here, depicts an increase in leg disc size during development, but the amount of growth and expression domains are not necessarily to scale. See text for further details of model.

(A) Early third instar (~72 hours AEL). HTH induces SER expression within the coxa, while DLL represses SER expression in more distal regions. (B) Early third instar (~78 hours AEL). DAC induces SER expression within the femur, while HTH-expressing cells produce a signal (X) that nonautonomously induces SER within the femur. (C) Early-mid third instar (~84 hours AEL). DLL represses SER expression, yet two sites of expression are observed within the tarsus. Other genes expressed within the tarsus (tarsal factors, TF), such as SS and/or BAB, may induce expression here. At early third instar SS expression overlaps with DLL, while later DLL expression extends more proximally. BAB has graded expression in tarsal segments 1-4. (D) Mid third instar (~96 hours AEL). DAC induces SER expression within the tibia, perhaps by overcoming repressive effects of DLL. New tarsal rings are also induced, depicted here in tarsal segment three; however, the precise segmental order in which tarsal expression arises is not known. (E) Late third instar (~120 hours AEL). HTH, DAC and DLL are hypothesized to function together to induce SER within the trochanter. All tarsal segments also now express SER. (F) Adult leg, with leg segment borders shown relative to the schematic shown in E. Leg segment borders (the joints) form just distal to the sites of Notch ligand expression, and do not always correspond to boundaries of leg gap gene expression. co, coxa; fe, femur; ta1-5, tarsal segments 1-5; ti, tibia; tr, trochanter. The claw forms at the distal tip of the leg.
Establishment of segmentation by the leg gap genes

A general theme in patterning during development is the subdivision of tissues initially by genes expressed in broad, partially overlapping domains, which through combinatorial control, subsequently regulate the expression of downstream genes to generate a repeating pattern (Irvin and Rauskolb, 2001; Lawrence and Struhl, 1996). The studies presented here demonstrate that leg segmentation follows this same theme. The ‘leg gap genes’ HTH, DAC, and DLL are expressed in broad domains in the leg disc that encompass more than a single segment (Abu-Shaar and Mann, 1998; Lecuit and Cohen, 1997; Wu and Cohen, 1999). Initially expression of these genes is largely nonoverlapping, but as the leg disc grows, the expression patterns of the leg gap genes change such that five different domains of gene expression are established (Fig. 8). The analysis of the regulation of Notch ligand and fringe expression during leg development reveals two fundamental aspects of leg development. First, these leg gap genes are key components in regulating the expression of the molecules controlling segmentation. Indeed, the effect of these leg gap genes on leg segmentation and growth can be accounted for by their regulation of SER, DL and fringe expression. Second, the expression of each ring of SER, DL and fringe is controlled by its own unique combination of regulators, apparently acting through independent enhancers.

How do these three transcription factors regulate the formation of nine segments? As the requirements for and the expression of the leg gap genes encompasses all leg segments, I think it unlikely that there are additional leg gap genes yet to be identified. Rather, a collection of distinct combinatorial approaches is used to establish a segmental pattern of SER, DL and fringe expression (Fig. 8).

In early third instar leg discs, there are two domains of gene expression, proximal cells express HTH and distal cells express DLL. HTH autonomously promotes the expression of SER, while DLL may prevent expression more distally, giving rise to a ring of expression in the coxa (Fig. 8A). Additionally, DLL-expressing cells may signal to the HTH-expressing cells to restrict SER expression to the distal edge of the HTH domain. As the leg disc grows, cells in an intermediate position, lying between the HTH and DLL domains, begin to express DAC (Abu-Shaar and Mann, 1998; Lecuit and Cohen, 1997; Wu and Cohen, 1999). DAC, as shown here, is both necessary and sufficient to induce the expression of SER, DL and fringe within the femur (Fig. 8B). As they are not expressed in all DAC-expressing cells, other factors appear to be required to promote their expression in the proximal femur. The nonautonomous induction of SER expression by HTH suggests that this may be accomplished by a signal (X) emanating from the neighboring HTH-expressing cells (Fig. 8B). By mid third instar stages, expression of SER, DL and fringe is also observed in tarsal segments 2 and 5, within cells expressing DLL but not DAC. Given that DLL is necessary and sufficient to repress their expression, SER, DL and fringe expression within the tarsus appears to be induced by a mechanism that overrides the repressive effects of DLL (Fig. 8C). Subsequently, expression of SER, DL and fringe is observed within the tibia, in cells expressing both DAC and DLL (Fig. 8D). DAC is necessary for expression of SER within the tibia, and its role here may be to overcome the repressive effects of DLL. It is also worth noting that the tibia ring of expression is not established at the time when cells first express both DAC and DLL (compare Fig. 2C with 2F). This may be because DAC levels may not be sufficiently high enough to overcome the repression by DLL. Clearly levels of DAC expression are critical because simply increasing DAC levels, as in the ptcGAL4 UASdac experiments, is sufficient to promote SER expression in cells already expressing endogenous levels of DAC (Fig. 3A). This observation can be explained if high levels of DAC expression in cells already expressing DAC override the function of inhibitory regulators of SER expression, such as DLL, where the expression of these genes overlap. Although I have not investigated late stages of leg segmentation, it has been noted that HTH, DAC and DLL are co-expressed in the presumptive trochanter late in leg development (Abu-Shaar and Mann, 1998; Wu and Cohen, 1999). I thus hypothesize that SER, DL and fringe expression is established by the combined activities of the three leg gap genes in the trochanter (Fig. 8E).

Although the studies presented here have focused on the regulation of SER expression, I think that not only SER, but also DL and fringe, receive primary regulatory input from the leg gap genes. I have shown that DL and fringe expression, like SER, is positively regulated by DAC. Moreover, DL and fringe mutants have stronger leg segmentation phenotypes than Ser mutants, and thus DL and fringe expression cannot simply be regulated downstream of Ser. The identification of two separate Ser enhancers, directing expression in the proximal versus distal leg, argues against SER being regulated downstream of DL and fringe. Thus, the simplest model is that expression of all three genes is regulated directly by the leg gap genes. The regulation of SER, DL and fringe expression in each segment appears to occur through independent and separable enhancer elements, supported by the analysis of the Ser reporter genes. This is reminiscent of what occurs during Drosophila embryonic segmentation, where separable enhancer elements direct different stripes of pair-rule gene expression (Pick, 1998; Small and Levine, 1991).

Importantly, Notch signaling may actually coordinate progressive segmentation of the leg with leg growth. For example, in early leg discs there is a single ring of SER expression within the coxa, in HTH-expressing cells immediately adjacent to DAC-expressing cells (Fig. 2A,B). However, by the time the femur ring arises, the coxa ring of SER expression has been displaced and is no longer within cells immediately adjacent to the DAC-expressing cells; rather, there are HTH-expressing cells lying in between that do not express SER (Fig. 2C). Thus, I postulate that once SER, DL and fringe expression is established within the coxa, Notch is activated, which promotes local cell proliferation, thereby displacing the coxa ring. This then allows for the femur ring of expression to be established in cells that are not immediately adjacent to the coxa expression ring. This mechanism also requires that once a ring of ligand expression is established in a particular segment, this expression must be maintained such that it is not influenced by later alterations in relation to leg gap gene expression. This maintenance could be accomplished by a feedback loop between Notch activation and ligand
expression, similar to what has been observed during late wing development, where Notch activation cell autonomously represses ligand expression and nonautonomously induces ligand expression in flanking cells by regulating the expression of a signaling molecule (Irvine and Vogt, 1997). Preliminary studies have indicated that Notch activation can influence Notch ligand expression in the developing leg (C.R., unpublished observations).

**Tarsal segmentation**

Most of the tarsus of the *Drosophila* leg derives from cells expressing DLL, but not DAC or HTH (Campbell and Tomlinson, 1998; Gorfinikel et al., 1997; Lecuit and Cohen, 1997). The studies presented here have surprisingly shown that DLL actually represses Notch ligand expression. This negative regulatory role for DLL contrasts with the positive promoting role of DAC and HTH, and further indicates that a distinct molecular mechanism must promote segmentation within the tarsus. One key gene is *spinless- aristapedia* (ss), as simple, unsegmented tarsi develop in *ss* mutant flies (Duncan et al., 1998). Moreover, *ss* regulates the expression of *bric-à-brac* (*bab*), which is also required for the subdivision of the tarsus into individual segments (Duncan et al., 1998; Godt et al., 1993). Together, *ss* and *bab* must, in some way, ultimately overcome the repression of Notch ligand and *fringe* expression by DLL. If the sole function of *ss* and *bab* is to overcome the inhibitory effects of DLL, then in the absence of *ss* and/or *bab*, SER expression is expected to remain repressed.

Intriguingly, the only notable variation between insect species is in the number of tarsal segments, with an unsegmented tarsus believed to be the ancestral state (Boudreaux, 1987). Thus, the combinatorial regulation of segmentation by the leg gap genes may represent an ancient mechanism common to all insect species, a hypothesis supported by the conserved expression of HTH, DAC and DLL segmentation by the leg gap genes may represent an ancient molecular mechanism must promote segmentation within the limb. One key gene is *spinless-aristapedia* (ss), as simple, unsegmented tarsi develop in *ss* mutant flies (Duncan et al., 1998). Moreover, *ss* regulates the expression of *bric-à-brac* (*bab*), which is also required for the subdivision of the tarsus into individual segments (Duncan et al., 1998; Godt et al., 1993). Together, *ss* and *bab* must, in some way, ultimately overcome the repression of Notch ligand and *fringe* expression by DLL. If the sole function of *ss* and *bab* is to overcome the inhibitory effects of DLL, then in the absence of *ss* and/or *bab*, SER expression is expected to remain repressed.

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