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Summary
In Drosophila, the morphological diversity is generated by the activation of different sets of active developmental regulatory genes in the different body subdomains. Here, we have investigated the role of the homothorax/extradenticle (hth/exd) gene pair in the elaboration of the pattern of the anterior mesothorax (notum). These two genes are active in the same regions and behave as a single functional unit. We find that their original uniform expression in the notum is downregulated during development and becomes restricted to two distinct, α and β subdomains. This modulation appears to be important for the formation of distinct patterns in the two subdomains. The regulation of hth/exd expression is achieved by the combined repressing functions of the Pax gene eyegone (eyg) and of the Dpp pathway. hth/exd is repressed in the body regions where eyg is active and that also contain high levels of Dpp activity. We also present evidence for a molecular interaction between the Hth and the Eyg proteins that may be important for the patterning of the α subdomain.

Key words: Notum patterning, hth, exd, eyg

Introduction
One major issue in developmental biology is the manner in which the different body parts are genetically subdivided. In Drosophila, several major subdivisions have been identified and characterised: notably, the appearance of anterior and posterior compartments in all body segments and the various domains defined by the Hox genes along the anteroposterior body axis (Lawrence and Morata, 1994; Lawrence and Struhl, 1996; Mann and Morata, 2000). More recently, the gene pnr has been demonstrated to subdivide all or most body segments in the dorsoventral axis (Calleja et al., 2000; Herranz and Morata, 2001). All these are general subdivisions that affect several body segments, and therefore the specific development of each body part is not determined by any of the individual genes involved but more likely by a combination of active gene in each part – a genetic address (Garcia-Bellido et al., 1979).

The dorsal mesothoracic structures are formed by the wing imaginal disc and include the mesothorax, the wing hinge and the wing blade. The mesothorax is part of the trunk and is subdivided into an anterior compartment, the notum, and a posterior one, the postnotum. The notum contains approximately 15,000 cells and is the biggest part of the thorax. It is subdivided by the pannier (pnr) gene (Calleja et al., 2000) into medial and lateral regions, which are in turn further subdivided by the Pax gene eyegone (eyg) (Aldaz et al., 2003).

All the genes involved in these subdivisions encode transcription factors, and their activities trigger the establishment in the cells of specific developmental programmes, i.e. states of determination. Experiments in which these factors are expressed ectopically, which amount to transplantation experiments, demonstrate that these products are able to induce the formation of the corresponding pattern out of the normal context (Aldaz et al., 2003; Calleja et al., 2000; Diez del Corral et al., 1999).

Among the genes involved in body patterns, a special case is the pair homothorax (hth) and extradenticle (exd), which encode related homeodomain proteins (Kurant et al., 1998; Pai et al., 1998; Rauskolb et al., 1993; Rieckhof et al., 1997). exd is expressed ubiquitously, but it is only functional when the Exd product is transported to the cell nuclei (Aspland and White, 1997; Pai et al., 1998; Rieckhof et al., 1997). hth is required for the nuclear transport of Exd, and thus acts as a positive regulator of exd. In turn the Exd nuclear activity is necessary to prevent the degradation of the Hh product (Abu-Shaar and Mann, 1998; Aspland and White, 1997; Mann and Abu-Shaar, 1996; Pai et al., 1998). Thus, the two gene products are mutually necessary. Besides, the phenotype of hth and exd mutations is similar or identical (Abu-Shaar and Mann, 1998; Azpiazu and Morata, 2002; Kurant et al., 1998; Rieckhof et al., 1997). Altogether these observations suggest that the two genes are involved in the same function to which we refer as hth/exd.

A principal role described for hth/exd is its function as cofactor of Hox products (Peifer and Wieschaus, 1990; Rieckhof et al., 1997; Ryoo et al., 1999). The Hth and Exd proteins contribute to the specificity of the Hox products by forming complexes with the different Hox products that recognise Hox-binding sites with high affinity and specificity (Chan et al., 1994; Ryoo and Mann, 1999; Ryoo et al., 1999; Van Dijk and Murre, 1994). This raises the possibility that Hth and Exd may also interact with other transcription factors.

In addition to its role as a Hox co-factor, there are hth/exd

Patterning function of homothorax/extradenticle in the thorax of Drosophila

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functions that seem to be independent of Hox activity. It is involved in the subdivision of wings and legs into proximal and distal domains (Abu-Shaar and Mann, 1998; Azpiazu and Morata, 2000; Azpiazu and Morata, 2002; Casares and Mann, 2000; Gonzalez-Crespo et al., 1998), and also has been shown to act as a selector gene in antennal development (Casares and Mann, 1998; Dong et al., 2002). That hth/exd may have this kind of function is not totally unexpected as hth and exd encode transcription factors that may regulate the transcriptional activity of specific target genes.

The notum of the fly is a region where there is no known Hox gene activity and is therefore a convenient place to examine possible hth/exd roles that are not dependent on interactions with Hox genes. Previous results have indicated that in the absence of exd activity the notum pattern is abnormal (Gonzalez-Crespo and Morata, 1995), and we have also noticed that the expression of hth and exd in the notum is not uniform, but shows a regional modulation. These two observations suggested a Hox-independent hth/exd function in the notum, which we explore in this report. We find that hth/exd is necessary to discriminate between two major parts of the notum, scutum and scutellum, and also contributes to scutellum identity. We also provide evidence for a molecular interaction between the Hth and Eyg products.

Materials and methods

Drosophila strains and clonal analysis

The following Drosophila strains were used to analyse mutant phenotypes or generate loss of function clones: exd<sup>3012</sup>, eyg<sup>332</sup>, FRT40A Mad<sup>+/FRT40AGFP</sup> (Wiersdorff et al., 1996), FRT2A eyg<sup>332</sup>/FRT2A GFP and FRT82Bhth<sup>+/FRT82BGFP</sup>. The FLP/FRT technique (Xu and Rubin, 1993), or X-rays, were used to generate loss-of-function clones. For the first, larvae of the appropriate genotype were heat shocked for 1 hour at 37°C at different larval stages. The clones were visualised in discs by loss of GFP expression. For the second, the exd<sup>3012</sup> null allele and the Minute technique were used. Larvae of the genotype y exd<sup>3012</sup>+/M(1)osb were irradiated at 24 and 48 hours after egg laying (AEL) with X-rays (1000 Rad). Mitotic recombination proximal to the forked (f) locus resulted in a clone of cells homozygous for exd<sup>3012</sup>, y and f that can be easily scored.

For gain-of-function experiments, the following Gal4 lines were used: w;flp122; act-FRT y<sup>+</sup> FRT Gal4 UAS-GFP/SM5 Tb (Ito et al., 1997), ap-Gal4 (Rincon-Limas et al., 2000), 248-Gal4 (Sanchez et al., 1997) eyg-Gal4 (Aldaz et al., 2003) and hth-Gal4 (GETDB – Gal4 Enhancer Trap Insertion Data Base). The gain-of-function clones were generated by recombination at the FRT sequences. The clones were labelled with Gal4 and GFP activity. In the adult cuticle the clones can be scored because they are mutant for P<sup>o</sup> and contain y<sup>+</sup> activity. The UAS-eyg, UAS-hth and UAS-skv<sup>00</sup> (Hoodless et al., 1996) lines used were described previously. For the apoptosis experiments we used an UAS-P35 line (Hag et al., 1994). The lacZ reporter line used was the DC-LacZ (Culi and Modolell, 1998).

Immunostaining of embryos and discs

Discs were dissected in PBS and fixed in 4% parafomaldehyde for 20 minutes at room temperature. They were subsequently washed in PBS, blocked in blocking buffer (PBS, 0.3% Triton, 1% BSA) and incubated overnight with the primary antibody: anti-β-Gal 1:2000 (rabbit), anti-Eyg 1:2000 (guinea pig), anti-En 1:10 (mouse), anti-Exd 1:200 (rat), anti-Hth 1:500 (rabbit), anti-Ara 1:200 (rabbit) and anti-pMad 1:2000 (rabbit) diluted in blocking buffer at 4°C. Washes were performed in blocking buffer, and the appropriate fluorescent secondary antibody was added for 1 hour at room temperature. Following further washes in blocking buffer, the discs were mounted in Vectashield.

Anti-Ara antibody was kindly provided by S. Campuzano, anti-pMad by T. Tabata, anti-β-Gal (rabbit) and anti-En were purchased from Cappell and from the Hybridoma Bank respectively. Images were taken in a laser MicroRadiance microscope (BioRad) and subsequently processed using Adobe Photoshop.

Protein interaction experiments

Crude Drosophila discs extracts were prepared by homogenizing 0.2 ml of third instar larvae in 0.4 ml of lysis buffer (1×PBS, 1% NP-40, 1 mM PMSF and 20 μg/ml each of peptatin and leupeptin). The homogenates were centrifuged, and the aqueous phase was mixed with the Hts-tagged, full-length Hth protein extracted under native conditions. The complexes formed were purified using the Ni-NTA agarose (Quiagen), washed five times in 1×PBS, 0.5 M NaCl and one final time in 50 mM Tris (pH 6.8). They were boiled in loading buffer and resolved by SDS-PAGE. After blotting to nitrocellulose, the filter was incubated with the anti-Eyg antibody and the signal was detected using the Amersham ECL western blotting analysis system.

Preparation of larval and adult cuticles

For good X-gal staining of adult patterns, pharates were removed from the puparium and treated as described by Calleja et al. (Calleja et al., 1996). To examine the cuticular patterns of the different genetic combinations adult flies were prepared by the standard methods for microscopic inspection. Soft parts were digested with 10% KOH, washed with alcohol and mounted in Euparal. Embryos were collected overnight and aged an additional 12 hours. First instar larvae were dechorionated in commercial bleach for 3 minutes and the vitelline membrane removed using heptano-methanol 1:1. Then, after washing with methanol and 0.1% Triton X-100, larvae were mounted in Hoyer’s lactic acid 1:1 and allowed to clear at 65°C for at least 24 hours.

Results

Expression of hth/exd

We have made use of the anti-Hth and anti-Exd polyclonal antibodies (Gonzalez-Crespo and Morata, 1995; Azpiazu and Morata, 2000), to study the expression patterns of hth and of exd in different stages of the wing disc. As hth activity is necessary for the nuclear translocation of the Exd protein, it was expected that there should be a correlation of hth expression and nuclear localisation of Exd. We have checked this by double staining mature third instar discs for hth and exd expression. The result is illustrated in Fig. 1D, which shows a near perfect co-extension of Hth with nuclear Exd. Therefore, for subsequent studies we have used the anti-Hth antibody as indicative of the expression of the two genes.

The expression of hth in the notum evolves during imaginal development. At the second instar all or nearly all the prospective notum cells express hth (Azpiazu and Morata, 2000) but by the beginning of the third instar period some modulation is already visible (Fig. 1A): hth expression is reduced in the central domain, whereas it remains at high levels in a posterior and an anterior region. Mature discs show two well-defined subdomains of expression (Fig. 1B), one located in the anterior region (subdomain α), and the other located more posteriorly (subdomain β).

We have further delimited the expression of hth with respect to that of other developmental genes that are active in the notum. Double staining with antibodies directed against the En,
Eyg and pMad (Tanimoto et al., 2000) products is shown in Fig. 1E-G. Of special interest is the comparison of the eyg and hth domains (Fig. 1F): the α subdomain of hth is included within the eyg domain, but the β subdomain abuts in its anterior border with the posterior border of eyg. This subdomain coincides with high levels of pMad (Fig. 1G), indicating that the Dpp signalling pathway is active in this domain. X-gal staining of hth-Gal4/UAS-lacZ flies (Fig. 1I) shows that the Dpp signalling is active in the notum expression domain abut and form a sharp border, but the α subdomain is included within the eyg domain. (G) Double staining with anti-Hth (red) and anti-pMad (green). The β subdomain contains high levels of Dpp signalling. (H) A schematic of hth expression in the adult thorax. (I) Thorax of an hth-Gal4 > UAS-lacZ stained with X-gal to reveal hth expression in adult structures.

Developmental function of hth/exd in the notum

We have studied the developmental role of hth/exd in the notum by examining the consequences of the loss of function and of modifying its normal spatial expression.

Notum development in the absence of hth/exd function

Null hth and exd mutants are zygotic lethal, therefore we have induced marked clones to study the behaviour of mutant cells in imaginal discs and the adult patterns they form. As their phenotype is the same, we have used indistinctly exd or hth mutant clones as convenient. For the adult cuticle we have used exd clones as they are better marked for the adult notum structures (see Materials and methods). We made use of the Minute technique (Morata and Ripoll, 1975) to induce large clones. Some of those that initiated early in development occupy a large part of the notum thus allowing the visualisation of the pattern produced in absence of hth/exd function (Fig. 2). The results obtained after having examined more than hundred clones can be summarised by saying that the loss of hth/exd does not produce a change of identity of the notum cells but gives rise to an abnormal notum pattern. It is illustrated in the cartoon of Fig. 2C, where we compare a normal notum pattern with that formed by the composite of a number of exd mutant clones. There are supernumerary macrochaetes on the presutural area (Fig. 2A), the infrascutellar suture disappears and the postalar bristles are not formed. The suture between scutum and scutellum also disappears (Fig. 2B), and the more posterior bristles tend to align along with the dorsocentral ones.

Fig. 1. Expression of hth/exd in the Drosophila notum. (A) Single staining for hth expression in a middle third instar disc. hth expression (red) covers most of the notum but some modulation is already visible. (B-D) Notum region of a mature disc doubly stained for hth (red) and exd (green). The two regions of high hth expression are the α and the β subdomains. The image in C shows only exd staining and in D the red and green channels are merged. The hth and exd expression patterns are almost identical. (E) Third instar disc doubly stained for hth (red) and en (green). Part of the β subdomain is included in the postnotum. (F) Notum part of a mature disc stained for hth (red) and eyg (green). The β subdomain and the eyg expression domain abut and form a sharp border, but the α subdomain is included within the eyg domain. (G) Double staining with anti-Hth (red) and anti-pMad (green). The β subdomain contains high levels of Dpp signalling. (H) A schematic of hth expression in the adult thorax. (I) Thorax of an hth-Gal4 > UAS-lacZ stained with X-gal to reveal hth expression in adult structures.

Fig. 2. Developmental effects of the loss of hth/exd function.

(A) Adult notum containing a exd clone (arrow) in the lateral region. The clone differentiates several macrochaetes that are not normally present in that zone. (B) A large M+ exd clone showing alterations of the bristle pattern in the scutellum region and the disappearance of the suture between the scutum and the scutellum. (C) Idealised image of the phenotype of an entire exd heminotum (right) compared with a normal heminotum (left). The two sutures are lost and the pattern of macrochaetes is different from the normal one. dc, dorsocentral; pa, postalar; s, suture; sc, scutellum. (D-F) Notum region of the disc containing several hth clones, marked black. The red staining marks the activity of the DC enhancer (see main text for details), which is expressed in the precursors of the dorsocentral bristles. The normal activity of this line is indicated in the inset in D. The clone in the posterior region (arrows in D,F) shows ectopic activity of the DC enhancer, indicating a change of the identity towards scutum.
Moreover, these clones often differentiate microchaetes in the scutellum region.

All together, these observations suggest that the loss of hth/exd function results in the formation of an abnormal notum with some scutum pattern elements, microchaetes, although not a perfect scutum pattern. This interpretation is further supported by the behaviour of hth− clones in the scutellar region of the disc. These clones often show expression of the specific DC enhancer of the scute gene (Culi and Modolell, 1998), which is normally active only in the corresponding region of the scutum (Fig. 2D-F).

Notum development with uniform hth/exd function
The previous experiment tested the functional role of hth/exd in the notum pattern. We then tried to assess the functional significance of the modulation of hth/exd activity. We have used the Gal4/UAS method to replace the normal expression pattern by a uniform pattern as driven by the Gal4 lines ap-Gal4 and 248-Gal4. As shown in Fig. 3A, the notum region of an ap-Gal4>UAS-hth wing disc presents an uniform hth activity, very different from the normal pattern – compare with Fig. 1B.

The developmental consequences of the change in the expression pattern are illustrated in Fig. 3B: the anterior part or the thorax, the scutum, is much reduced in size, and lacks most pattern elements like bristles. The effect is more pronounced in the central region, the lateral part of the notum and the scutellum are relatively less affected.

The size reduction observed in these flies seems not to be a consequence of massive apoptosis. We have checked for levels of active caspase in discs of genotype ap-Gal4>UAS-hth or 248-Gal4/UAS-hth and did not find a significant increase compared with wild-type discs. Moreover, we were not able to restore the normal size of the notum in flies of those genotypes by co-expressing the caspase inhibitor P35 (not shown).

The conclusion from the previous experiments is that hth/exd is not involved in fate specification of the notum cells: in the absence of hth/exd function the cells still differentiate notum pattern elements. However, the local modulation of hth/exd expression appears to be an important factor in the patterning process.

Regulation of hth expression
It follows from the results above that the understanding of the spatial regulation of hth/exd may provide insights into the notum patterning. As the hth expression in the notum evolves from ubiquitously to spatially restricted during the larval period, one of our aims was to identify the factors responsible for this regulation.

eyg is a negative regulator of hth
We suspected that eyg might regulate hth/exd because, as shown in Fig. 1F, hth and eyg expressions abut in some places as if they were mutually exclusive. In particular, the anterior border of the hth β subdomain abuts with the posterior border of the eyg domain.

We first examined hth expression in eygE42 homozygous discs. As shown in Fig. 4A it becomes uniform and covers most of the notum, suggesting that in absence of Eyg there is an expansion of the hth β subdomain. This result indicates that eyg can function as a negative regulator of hth/exd. However, in normal development the hth α subdomain is included within the eyg domain (Fig. 1F), suggesting that the repressive role of Eyg is effective only in part of the domain. To explore this possibility further, we induced clones of mutant eyg cells all over the notum and examined their local effect on hth/exd expression. We obtained two types of eyg− clones in respect of their effect on hth expression. Those in the α subdomain, where hth and eyg are normally co-extensive, have no effect on hth expression (not shown). However, the clones in the posterior region of the eyg domain, located between the α and β hth subdomains (Fig. 4B,C) show ectopic hth activity. This result indicates that eyg acts as a negative regulator of hth in the posterior region of its domain; the sharp border of hth in the posterior region probably reflects the repression by eyg. We have examined eyg expression in hth− clones (not shown) and found that it is not modified.

To confirm that eyg is indeed capable of repressing hth and also that it has distinct local effects, we conducted gain-of-function experiments. We generated clones of eyg-expressing cells all over the notum, and checked for hth activity in the clones (Fig. 4D-F). As expected from the loss-of-function experiments, eyg-expressing cells were only able to repress hth in the β subdomain. Clones generated in the α subdomain had no effect. Furthermore, we also ectopically expressed eyg in the majority of the notum cells using the 248-Gal4 line. In 248-Gal4>UAS-eyg discs, the β subdomain is eliminated but the α subdomain remains unaltered (Fig. 4G-I). This distinct behaviour of eyg in different parts of the notum suggests the existence of some other local factor contributing to hth regulation.

The Dpp pathway is a negative regulator of hth
Because high levels of Dpp signalling co-express with the β hth subdomain, we wanted to determine whether the Dpp pathway could be involved in hth regulation. We generated clones of cells mutant for Mothers against dpp (Mad), which are unable to transduce the Dpp signal (Newfeld et al., 1996), and examined them for hth expression.

According to their position Mad− clones have different effects on hth expression (Fig. 5): (1) those located in the α subdomain do not affect hth; (2) those located between the α and β subdomains exhibit gain of hth; and (3) the clones in the β subdomain lose hth expression. The loss of hth by the Mad− clones in the β subdomain appears to be an indirect consequence of the up regulation of eyg in absence of activity

Fig. 3. Effect of uniform hth expression in the notum pattern. (A) Uniform expression of hth in an ap-Gal4>UAS-hth notum. (B) Notum structures differentiated by the same genotype. Some scutellum structures remain but most of the scutum is lacking. There is a general lack of microchaetes and the few that remain are in the lateral region.
Eyg and the Dpp pathway act as repressors of *hth* in the inter-subdomains region. However, in both cases their activity domains are co-extensive in part with the *hth* domain; the *hth* α subdomain for Eyg and the *hth* β subdomain for the Dpp pathway. This indicates that Eyg and the Dpp pathway require additional factors to fulfill its repressing role (see Discussion).

**Interactions between the Hth and the Eyg proteins**

The α and the β subdomains differentiate distinct patterns in the adult notum (Fig. 1). The α subdomain, where *hth/exd* and *eyg* are co-extensive, gives rise to a part of the scutum and contains macrochaetes as a distinctive feature. The β subdomain, which does not contain *eyg* activity, differentiates the scutellum and part of the lateral region, which do not contain macrochaetes. This suggests that the differential expression of *hth/exd* and *eyg* may contribute to the pattern differences. To check on this possibility, we have expressed the Hth and Eyg products under the control of the same driver (*248-Gal4*), both separately and together, and compared the notum patterns obtained. In *248-Gal4>UAS-hth*, we observe (Fig. 6A) a reduction of the notum, which affects mostly the scutum territory; as a result, it differentiates into very few macrochaetes and the dorsocentral macrochaetes are missing. We have checked in discs of this genotype the expression of the specific dorsocentral enhancer of *scute* (Culí and Modolell, 1998) and found it is not expressed. In *248-Gal4>UAS-eyg* (Fig. 6B), there is a mirror image duplication of the scutum pattern in the scutellum, as reported previously (Aldaz et al., 2003). This duplication includes macrochaetes, which are part of the *eyg* domain (Aldaz et al., 2003). By comparison, the duplicated notum structures in the *248-Gal4>UAS-hth UAS-eyg* genotype do not contain macrochaetes, suggesting that the duplicated pattern corresponds to the α subdomain. This interpretation is supported by the observation that in discs of this genotype the DC enhancer of *scute* is not expressed (not shown).

The preceding results suggested a genetic interaction between *hth/exd* and *eyg* that may be responsible for the specification of the α subdomain pattern. As Hth/Exd act as co-factors of the Hox genes to confer in vivo specificity to the Hox products (Rauskolb et al., 1993; Rieckhof et al., 1997), there was the possibility that they may act in a similar manner acting as a co-factor of Eyg. Therefore, we attempted to find

**Fig. 5.** Regulation of *hth* by the Dpp pathway. (A–C) Disc containing several *Mad* clones marked by the loss of GFP (green). In the α subdomain, they do not affect *hth* (red) but those in the inter-subdomains zone (small arrows) show gain of *hth*, although not in all the cells. The clone inside the β subdomain (large arrows) shows loss of *hth*. (D–F) Several TkvΔD-containing clones marked by the gain of GFP (E). The clones in the α subdomain (arrows) show loss of *hth* (red) but the clones in the β subdomain do not affect *hth*. 

**Fig. 4.** Regulation of *hth* expression by *eyg*. (A) Mutant *eyg* disc stained with an anti-Hth antibody showing generalised *hth* expression. (B,C) A mutant *eyg* clone (arrows, labelled by the loss of GFP) in the inter-subdomains zone, exhibiting ectopic *hth* expression. (D) Notum region with many clones of *eyg*-expressing cells, marked with GFP. The clones in the α subdomain do not affect *hth* expression, in contrast to those in the β subdomain where *hth* is lost. (G–I) Disc of genotype *248-Gal4>UAS-eyg* doubly labelled with anti-Eyg (green) and anti-Hth (red), showing loss of *hth* in the β but not in the α subdomain.
Research article

Discussion

Our experiments bear on the problem of the spatial organization and pattern of the Drosophila notum, and in particular on the role of the homeobox-containing genes hth and exd. The function of hth/exd on segmental identity is well known; they mediate much of the in vivo specificity of the Hox genes (Chan et al., 1994; Chan et al., 1996; Rauskolb and Wieschaus, 1994; Ryoo et al., 1999) by forming Hth/Exd/Hox complexes that bind DNA. The vertebrate homologues of hth and exd perform a similar Hox-related function (Chang et al., 1996; Chang et al., 1994).

Fig. 7. Model for hth regulation. The two horizontal bars indicate expression of the two regulators: the Dpp signalling pathway and eyg. In the anterior (A) part of the disc, eyg is expressed but the levels of Dpp signalling are too low to repress hth. In the inter-subdomain region, eyg is present and the levels of Dpp signalling are sufficient to repress hth. Close to the posterior (P) border of the disc, high levels of Dpp signalling are present, but there is no eyg activity and hence hth is not repressed.

Additionally, hth/exd has some other roles that are not directly related to Hox gene activity. During limb development, it acts to repress the response of the proximal region to the influence of Hh/Wg/Dpp pathways, thus contributing to the subdivision of appendages along the proximodistal axis (Abu-Shaar and Mann, 1998; Azpiazu and Morata, 2000; Azpiazu and Morata, 2002; Gonzalez-Crespo et al., 1998). This function is also conserved in vertebrate development (Mercader et al., 1999).

Here, we deal with a novel hth/exd function: its patterning role in the notum. It is not related to the specification of notum identity because it is not affected by alterations of hth/exd activity. For example, in the absence of hth/exd the cells still differentiate as notum, if an abnormal one (Fig. 2). Conversely, high and uniform Hth levels also produce notum tissue but with abnormal pattern (Fig. 3). This function is only required in part of the notum and is therefore linked to the modulation of hth expression during the development of the disc. The final result of this modulation is the appearance of the α and β subdomains of hth that we report here. These two subdomains differentiate distinct notum patterns, suggesting that Hth/Exd interact with other localised products to generate these patterns.

Thus, there are two principal aspects in the patterning function of hth/exd: (1) the spatial regulation, that eventually results in the restriction of its expression to the α and β subdomains; and (2) the local interactions of Hth/Exd with other products in either of the subdomains.

Regulation of hth/exd in the notum

Although hth and exd form a single functional unit, their mode of regulation is different: exd is expressed ubiquitously but is regulated at the subcellular level by hth, which promotes Exd nuclear transport. Therefore, the key element of hth/exd regulation is the transcriptional control of hth.

Originally, hth is expressed in all the notum cells (Azpiazu and Morata, 2002) (this report) and later becomes restricted to the α and β subdomains. Consequently, the principal aspect of hth regulation is the mechanism(s) leading to its repression in the regions outside the α and β subdomains. We have identified two negative regulators: the eyg gene and the Dpp pathway, which probably acts through some unidentified downstream gene. In the notum hth behaves as a downstream target of both the Dpp pathway and eyg.

The role of Eyg as a negative regulator of hth is based on the following observations: (1) the beginning of the modulation of
hth expression in the notum at the early third instar coincides with the initiation of eyg expression (Aldaz et al., 2003); (2) in eyg mutants the hth domain is extended, extending to most of the notum (Fig. 4A); (3) mutant eyg clones show hth derepression in the inter-subdomains region (Fig. 4B, C), and conversely, ectopic eyg activity in the β subdomain represses hth (Fig. 4). The fact that it fails to affect hth in the α subdomain was expected as eyg and hth are normally co-expressed in this subdomain (Fig. 1F). In conclusion, eyg suppresses hth in the inter-subdomains region and also acts as a barrier for hth in the eyg/β-hth border.

The role of the Dpp pathway as a negative regulator of hth is based on results illustrated in Fig. 5A-C, showing that Mad mutant clones in the inter-subdomains region show activation of hth. This is in contrast to the behaviour of those clones in the α subdomain, where they have no effect, or in the β subdomain, where they show suppression of hth. We believe that the reason for the latter effect is that eyg is up regulated in those clones, as described previously (Aldaz et al., 2003), and in turn Eyg suppresses hth, as we discuss above. The lack of effect of Mad clones in the α subdomain is probably due to the low activity of Dpp in that region (see below). The observation (Fig. 5D-F) that the high activity levels generated in the TkvQD clones suppress hth in this subdomain in principle supports this view. Expectedly, TkvQD clones do not affect hth expression in the β subdomain, because it normally possesses high Dpp activity levels.

Taking all the results together, we propose the following model of hth regulation (Fig. 7). As hth is originally expressed in all trunk embryonic cells (Azpiazu and Morata, 1998) and in all the notum cells in the early disc (Azpiazu and Morata, 2002), the regulation of hth during wing disc development essentially reflects local repression in specific parts of the disc. The basic idea is that hth is repressed by the joint contribution of eyg and high/moderate levels of the Dpp pathway. Neither of these elements can repress hth individually. Although eyg appears to act uniformly in its domain, the repressing activity of Dpp is concentration dependent. Within the eyg domain, the hth α subdomain is located in the anterior region, in which the Dpp levels are too low to be effective and Eyg alone cannot repress hth/eyg. In the inter-subdomains region the Dpp levels are high enough to repress hth as here it acts together with Eyg. The β subdomain is outside the eyg domain and therefore in the absence of Eyg even the high Dpp levels are not capable of repressing hth/β-exd. The model is also supported by the experiments of overexpressing eyg. The eyg-expressing clones in the β subdomain suppress hth because the two repressors are active in the clones, while they have no effect in the α subdomain because it normally contains high eyg levels. In principle the experiments overexpressing the Dpp pathway (TkvQD clones) appear to support the model. These clones have no effect in the β subdomain, which normally possesses high Dpp activity levels, but they suppress hth in the α subdomain. However, these clones are known to suppress eyg (Aldaz et al., 2003) and therefore hth should not be repressed according to our model. It is possible that in certain circumstances the very high Dpp activity levels induced by these clones may be sufficient to down regulate hth, even in the absence of eyg.

The presence of two distinct repressors may suggest that the hth promoter region contains binding sites for Eyg and for Mad/Medea (Raferty and Sutherland, 1999) that would be responsible for the transcriptional repression. The ubiquitous expression in the absence of these two repressors may be due to a constitutive promoter.

**Interactions of Hth/Exd with other products**

The second aspect of the late patterning function of hth/eyg arises from the observation that the α and β subdomains form different patterns with similar levels of hth. This suggests the existence of interactions between Hth/Exd and products specifically localised to the different subdomains. In the case of the α subdomain, the obvious candidate for the interaction is Eyg. We show that the joint activity of hth/eyg and eyg specifies a notum pattern that is different from those specified by each of these genes alone (Fig. 6A-C).

Our finding that the Eyg and Hth proteins associate to form a complex in vitro suggest a mechanism to achieve the pattern difference between the α and the β subdomains. As it has been shown to be the case for the in vivo specificity of the Hox genes, the association of Hth/Exd with the different Hox products results in higher affinity and specificity for target sites (Ryoo et al., 1999). Here, the formation of a Eyg/Hth/Exd complex in the α subdomain may result in a constellation of gene activity different from that in the β subdomain where Eyg is not present. In the latter subdomain hth/eyg may act alone, for after all the two genes encode transcription factors. Alternatively, the Hth/Exd products may interact with some other yet unidentified co-factor.

**Genetic subdivisions of the notum**

As pointed out in the Introduction, the morphological diversity of the body is achieved by regulating the spatial expression of developmental regulatory genes. For example, the spatial deployment of the various Hox genes along the anteroposterior body axis establishes the identity of the different segments (reviewed by Lawrence and Morata, 1994; Mann and Morata, 2000). Within each segment, this process is reiterated to elaborate the identity of the anterior or posterior compartments, which requires the deployment of engrailed (Morata and Lawrence, 1975). Further genetic subdivisions establish the identity of even more discrete regions. In the notum, previous work has identified two subdivisions that appear during the development of the disc. One is established by pnr, which subdivides the notum into a medial and a lateral region (Calleja et al., 2000). The second results from the activation of the eyg gene and straddles the pnr domain, thus originating four genetically distinct regions (Aldaz et al., 2003). Here, we report a new element involved in the notum subdivision: the appearance of hth expression in two distinct subdomains. These two hth subdomains are superimposed with the genetic subdivisions established by en, pnr and eyg, and contribute to the genetic diversification of the notum and hence to the morphological diversity within it. It is part of a genetic address (Garcia-Bellido et al., 1979) that specifies the final pattern. As shown in Fig. 6C, the combination of Hth with Eyg produces a notum pattern different from that produced by Hth alone (or in combination with some unknown factor). Our demonstration that the Hth and the Eyg products form a protein complex suggests that protein-protein interactions are part of the patterning process.

One interesting aspect of the interaction of hth/exd and eyg is that it acts in two different ways. At the gene regulation level, eyg participates in the spatial control of hth/exd activity, but where the two genes are co-expressed their proteins interact,
presumably to contribute to the in vivo affinity and specificity for target genes.

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