Variation in the number of activated torso receptors correlates with differential gene expression

Marc Furriols¹, Frank Sprenger² and Jordi Casanova¹

¹Centre d’Investigació i Desenvolupament (CSIC) C/ Jordi Girona 18-26, 08034 Barcelona, Spain
²Department of Biochemistry and Biophysics, University of California, San Francisco, California 94143-0448, USA

SUMMARY

Activation of receptor tyrosine kinases triggers many developmental decisions, yet we do not understand how activation of a single receptor can be transduced into different cell responses. The torso pathway in Drosophila provides a model to address this issue since it generates more than one response in the embryo. The torso receptor tyrosine kinase is activated at the embryonic poles under the control of trunk, a protein with similarities to several types of extracellular growth factors. Activation of torso is responsible for the development of a variety of structures, whose appearance can be correlated with activation of at least two different genes along the terminal region. In this study we have analyzed mutations in torso and trunk that express low levels of the respective proteins. We show that different amounts of torso or trunk molecules correlate with the expression of different zygotic genes, implicating changes in the number of activated torso molecules as one of the mechanisms defining differential gene expression. We suggest that variation in the number of activated receptors at the cell surface is a general mechanism that leads to differential gene expression and thus the generation of different cell responses.

Key words: torso, trunk, signal transduction, gene expression, Drosophila, receptor tyrosinase kinase

INTRODUCTION

Receptor tyrosine kinases are involved in many developmental processes where they can elicit a variety of responses. A basic question in trying to understand their role in development is how activation of a single receptor can be transduced into different cell responses in terms of gene activation (for a review, see Marshall, 1995). The torso pathway in Drosophila is a particularly appropriate model with which to address this issue owing to its ability to generate more than one response in the embryo. The torso receptor tyrosine kinase is distributed along all the surface of the Drosophila embryo but is only activated at the poles, where it specifies development of its terminal structures (Schüpbach and Wieschaus, 1986; Klinger et al., 1988; Casanova and Struhl, 1989; Sprenger et al., 1989). Activation of the torso receptor has been shown to depend on a diffusible extracellular ligand generated at each pole that is trapped by the receptor, thereby impeding further diffusion (Sprenger and Nüsslein-Volhard, 1992; Casanova and Struhl, 1993). Recently, we have cloned trunk (trk), one of the genes required for torso activation, and have shown that it codes for a protein with similarities to several types of extracellular growth factors, which is likely to be the torso ligand (Casanova et al., 1995).

Activation of the torso signal transduction pathway is responsible for the activation of tailless (tll) and huckebein (hkb) at the posterior end of the embryo (Weigel et al., 1990). However, while tll is expressed in all this region, hkb expression is activated only in its most terminal part (Pignoni et al., 1990; Brönner and Jäckle, 1991). One mechanism allowing differential gene expression could be an instructive torso activity gradient. Using mutations in torso in which activation is ligand-independent it has been possible to correlate distinct levels of torso signaling with differential gene activation (Casanova and Struhl, 1989): low levels of the constitutive torso activity are able to activate tll gene expression whereas only high levels can activate hkb expression. However, it remains an open question whether such a mechanism is also used during normal development when wild-type torso is only activated at the poles. Alternatively, a gradient of torso receptor activity may not be responsible for organizing the terminal pattern. Instead, a sharp step function of active torso receptor at the cell surface could generate one or more gradients of activated intracellular substrates that could diffuse within the cytoplasm and specify the distinct elements of the terminal pattern (Casanova and Struhl, 1989).

Extra copies of either the torso gene or the trk gene do not alter the embryonic pattern, as judged by monitoring the expression of zygotic genes (Casanova and Struhl, 1989; our own unpublished observations), indicating that in those conditions they are not limiting factors. The molecular analysis of trk is consistent with this observation since it suggests that the trk protein, as many growth factors, needs to be processed to be active (Casanova et al., 1995). Overexpression of unprocessed trk could lead to minor changes in the amount of active trk only relevant in situations or domains where the torso receptor is a limiting factor.
To investigate whether variations in the number of activated tor receptors at the cell surface might be responsible for distinct gene activation, we have generated situations in which the number of receptors or ligand molecules could be limiting. In particular, we have identified mutations that would give rise to low levels of either wild-type trk molecules secreted by the embryo or wild-type tor receptors at the cell surface, and have characterized their phenotypes. We used these mutations to demonstrate that different amounts of torso or trunk molecules correlate with expression of different zygotic genes, implicating changes in the number of activated torso molecules as one of the mechanisms defining differential gene expression.

MATERIALS AND METHODS

Stocks

trk1, trk4, trk5 and torHM are EMS mutations induced by Trudi Schüpbach (Lindsley and Zimm). trk1 results from a premature stop codon and behaves as a null allele (Casanova et al., 1995). torXR1 is a small deficiency that deletes the tor gene (Sprenger et al., 1989). Df(2L)J77 is a deficiency spanning from 31C to 31F (T. Schüpbach, personal communication) that uncovers the trk gene. TR-11 is a third chromosome carrying a 6 kb genomic fragment that fully rescues the loss-of-function mutations in the trk gene. Egg laying took place at 25°C.

RNA analysis

Poly(A)+ RNA was obtained from embryos with the PolyATract System (Promega), run in a 1.2% agarose gel containing formaldehyde and transferred to Hybond N (Amersham). Hybridization was performed with a trk-specific riboprobe derived from the antisense strand of the pR3 trk cDNA at 60°C in 50% formamide.

Sequencing

Genomic DNAs from trk4, trk5 and torHM alleles, as well as genomic DNA from the isogenic stocks in which the mutations were induced, were PCR-amplified and sequenced. Two independent PCR products were sequenced in all the coding regions for each mutant strain and were PCR-amplified and sequenced. Two independent PCR products DNA from the isogenic stocks in which the mutations were induced, Genomic DNAs from trk cDNA at 60ºC in 50% formamide.

Sequencing

Genomic DNAs from trk4, trk5 and torHM alleles, as well as genomic DNA from the isogenic stocks in which the mutations were induced, were PCR-amplified and sequenced. Two independent PCR products were sequenced in all the coding regions for each mutant strain and compared to the parental wild-type DNA in which the mutations were induced. For trk4, the only change that resulted in an amino acid substitution affected the codon for amino acid 18, which was changed from GGG (glycine) to AGG (arginine). No change was observed between the trk5 DNA and the parental wild-type DNA. In the torHM allele, the only mutation that resulted in an amino acid change affected the codon for amino acid 11, which was changed from ATC (isoleucine) to AAC (asparagine).

Plasmid constructions

pBtor

pBtor has been described by Sprenger and Nüsslein-Volhard (1992).

pBHM

The mutation detected in the torHM allele was introduced into the pBtor cDNA by PCR. Using the oligos FS41 TTCATGGT-TATTTCTATGCGAAGTACGCATTTAACCT and FS2 CCAATTCAGATTTGGCTCCTGCC and pBtor as a template, a 1750 bp fragment was amplified, cut with NcoI and BstXI, and the resulting 528 bp fragment exchanged with the corresponding fragment of pBtor, yielding pBHM. In this vector the PCR-derived fragment was sequenced to exclude PCR-induced base changes.

TR11

A BarHI-EcoRI genomic fragment of around 6 kb from the trk region was inserted into the P(ry+) transformation vector C20. This genomic fragment fully rescues the phenotype associated with the trk mutations.

In situ hybridization

til and hh probes were generated from cDNA clones provided by J. Lengyel and H. Jäckle, respectively. Whole-mount in situ hybridizations were done following the method of Tautz and Pfeifle (1989) with minor modifications.

Western analysis

Protein extracts were separated by SDS-PAGE, transferred to Immobilon membrane, and probed with anti-torso antibodies as described (Sprenger and Nüsslein-Volhard, 1992). Each lane contains material from approximately 20 eggs.

RESULTS

Different amounts of the trk product can trigger different embryonic responses

trk5 is a hypomorphic mutant allele. Embryos from trk5 females display a gradation of phenotypes ranging from trk-null phenotypes to almost wild-type phenotypes. It is worth noting that those embryos with partial terminal development always lack the most terminal structures, those that are thought to require higher levels of terminal signaling. We have sequenced the DNA of the trk coding region from this mutant and have not found any change when compared to the wild-

Table 1. Dose-dependence of trk5 and torHM phenotypes

<table>
<thead>
<tr>
<th>Maternal genotype</th>
<th>A7 segment</th>
<th>A8 segment</th>
<th>More terminal</th>
<th>n</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 copy of trk5</td>
<td>22</td>
<td>76</td>
<td>1</td>
<td>143</td>
</tr>
<tr>
<td>2 copies of trk5</td>
<td>12</td>
<td>37</td>
<td>51</td>
<td>65</td>
</tr>
<tr>
<td>1 copy of torHM</td>
<td>76</td>
<td>24</td>
<td>0</td>
<td>41</td>
</tr>
<tr>
<td>2 copies of torHM</td>
<td>46</td>
<td>41</td>
<td>14</td>
<td>37</td>
</tr>
</tbody>
</table>

torHM phenotypes are dependent on the dose of trk

| Maternal genotype | A7 segment | A8 segment | More terminal |
|-------------------|------------|------------|---------------|-------------|
| Copies of torHM   | Copies of trk5 | Percentage of embryos whose most posterior structures belong to | |
| 1                 | 1          | 98         | 2            | 0           | 48          |
| 1                 | 2          | 76         | 24           | 0           | 41          |
| 1                 | 3          | 61         | 39           | 0           | 41          |
| 2                 | 1          | 42         | 53           | 6           | 36          |
| 2                 | 2          | 46         | 41           | 14          | 37          |
| 2                 | 3          | 9          | 14           | 77          | 37          |

Cuticles from embryos derived from females of the appropriate genotypes were examined and classified according to whether their more terminal structures belonged to the seventh abdominal segment (A7), to the eighth abdominal segment (A8), or were of more terminal origin such as the anal pads and tuft. n, number of embryos analysed for every genotype. Egg laying took place at 25°C. The actual genotypes for each combination are as follows:

1. copy of trk5: trk5/Df Ider 77 (similar results were obtained for trk5/trk5).
2. copies of trk5: trk5 homozygous.
3. copy of torHM and 1 copy of trk5: torHM/trk5XR1.
4. copy of torHM and 2 copies of trk5: trk5/torHM/Tr11.
5. copy of torHM and 3 copies of trk5: torHM/torHM/Tr11.
6. copies of torHM and 2 copies of trk5: torHM/torHM/Tr11.
7. copies of torHM and 3 copies of trk5: torHM/Tr11.
expression is detected in some embryos from trk than those from females with just one copy of the ligand diffusing from the poles. Thus, the amount of fewer tor receptors have been activated by the product from two copies of trk is often reduced in those embryos, suggesting that expression but not hkb expression is detected in some embryos from females carrying two copies of trk homozygous females (Fig. 2G,H), only (see Table 1). However, while trk product from two copies of trk can trigger tor signaling to the levels required to activate till but not hkb. Conversely, the amount of trk product from two copies of trk can trigger tor signaling to the levels required to activate both till and hkb.

Different numbers of tor receptors activated at the cell surface can originate diverse terminal structures

torHM is a temperature-sensitive allele in which no terminal structures are present when embryos are raised at high temperatures (27°C). At 18°C, on the other hand, terminal structures are present (Sprenger, 1991). torHM encodes a protein with a single amino acid substitution of an asparagine for isoleucine at position 11 in the signal sequence. This change results in a significant alteration of the hydrophobicity of the leader peptide. In western blots the majority of torHM migrates differently from the mature wild-type protein that is glycrosylated (F. S., unpublished data) and with an electrophoretic mobility that compares to the non-glycosylated form (Fig. 3) (for details see legend to Fig. 3). When embryos are developed at lower temperatures, in which terminal structures are present, small amounts of torHM protein can be

type gene. However, a northern blot reveals that the trk message is hardly detectable in embryos from trk females (Fig. 1), which suggests that a reduced amount of otherwise wild-type product is causing the mutant phenotype associated with the trk allele. Interestingly, the range of terminal deletions is dependent on the number of copies of the trk allele: embryos from females carrying two copies of the trk allele tend to have more terminal structures than those from females with just one copy of the trk allele (Table 1; see table legend for exact phenotypes). Hence, we can correlate the amount of trk product with the appearance of different terminal structures and therefore with the level of tor signaling. Similar results were obtained with trk, another hypomorphic mutant allele with a single amino acid substitution of a glycine for arginine at position 18 in the putative signal sequence (data not shown).

To extend this correlation to differential gene activation we have examined the activity of tor and hkb in those embryos by in situ hybridization. As mentioned before, tor signaling is solely responsible for activating the expression of the genes till and hkb at the posterior end of the embryo (Weigel et al., 1990). Accordingly neither till nor hkb expression is detected at the posterior pole of trk embryos (Fig. 2C,D), as it occurs in tor embryos (Brömmö and Jäckle, 1991). We have examined independently hkb and till expression in embryos from trk/trk and trk homozygous females. Embryos from mothers of the same mutant genotype (either trk or trk homozygous) exhibit some variability in their pattern of till and hkb expression, in agreement with the variability observed in the cuticle structures that they develop (see Table 1). However, while till and hkb expression is detected in some embryos from trk homozygous females (Fig. 2G,H), only till expression but not hkb expression is detected in some embryos from trk/trk females (Fig. 2E,F). It is worth noting that the domain of till expression is often reduced in those embryos, suggesting that fewer tor receptors have been activated by the ligand diffusing from the poles. Thus, the amount of trk product from one copy of trk can trigger tor signaling to the levels required to activate till but not hkb. Conversely, the amount of trk product from two copies of trk can trigger tor signaling to the levels required to activate both till and hkb.

Number of activated torso receptors and gene expression

![Fig. 1](image1.png) Analysis of trk message from the trk mutants. Northern blot of poly(A)+ RNA from wild-type and trk mutant embryos from 0 to 3 hours after fertilisation hybridised with a labelled riboprobe derived from the antisense strand of trk cDNA. In trk embryos the trk transcripts (Casanova et al., 1995) are barely detectable. The blot was also probed for rp49 transcripts to confirm the integrity of each RNA sample.

![Fig. 2](image2.png) till and hkb expression in trk mutant embryos. till (A,C,E,G) and hkb (B,D,F,H) expression, as monitored by in situ hybridisation. (A,B) At the blastoderm stage, till and hkb are expressed at both poles of the embryo. (C,D) In embryos from trk mothers, neither till nor hkb expression is detected in the posterior pole; expression remains in the anterior domain, since at the anterior end the terminal signal acts in conjunction with the anterior system. (E,F) Embryos from females with one copy of the trk allele (trk/trk1). till expression is detected in some of those embryos; however, hkb expression is not detected. (G,H) Embryos from females with two copies of the trk allele (trk homozygous); both till and hkb expression can be detected among those embryos.
observed, similar to embryos, the torHM produced from the injected RNA migrated with RNA injected into embryos that lack endogenous torso. In these cDNA, the resulting cDNA (pBHM) transcribed in vitro and the HM phenotype, the mutation was introduced into the pBtor torso. The approximate size of this torHM protein (arrow) compares mothers migrates with faster electrophoretic mobility than wild-type HM 27°C, 0-3 hour eggs from homozygous mothers developed at 27°C. HM 18°C, 0-4 hour eggs from homozygous mothers at 27°C. XR1, 0-3 hour eggs (22°C) from XR1 homozygous mothers that lack torso protein. XR1 pBtor, 0-1 hour eggs from torXR1 homozygous mothers were injected with 1 mg/ml pBtor mRNA, encoding wild-type torso protein, and incubated for 2 hours at 22°C. XR1 pBHM, 0-1 hour eggs from torXR1 homozygous mothers were injected with 1 mg/ml pBHM mRNA, encoding the torHM protein, and incubated for 2 hours at 22°C. Most of the torso protein of embryos from torHM homozygous mothers migrates with faster electrophoretic mobility than wild-type torso. The approximate size of this torHM protein (arrow) compares to the non-glycosylated form of torso. However, at 18°C, a little bit of wild-type sized torso can be detected (arrowhead). To show that the change found in the sequence of torHM is solely responsible for the torHM phenotype, the mutation was introduced into the pBtor cDNA, the resulting cDNA (pBHM) transcribed in vitro and the RNA injected into embryos that lack endogenous torso. In these embryos, the torHM produced from the injected RNA migrated with the same electrophoretic mobility as torso from embryos mutant for torHM. In addition, only a little induction of terminal structures was observed, similar to torHM mutant embryos developed at 22°C (not shown).

detected that migrate with the same electrophoretic mobility as wild-type torso. However, the majority of the torHM protein still migrates like non-glycosylated wild-type torso molecules. This suggests that the first amino acids of the torHM molecule are a very poor leader peptide. The majority of protein does therefore not get glycosylated and does not get incorporated into the cytoplasmic membrane. Only at lower temperatures is a small fraction of torHM apparently glycosylated and presumably reaches the cytoplasmic membrane.

The torHM mutant phenotype, similar to the trk5 mutation, is dose-sensitive (Table 1). Interestingly, the torHM phenotype is very sensitive to the dose of the trk gene. We have analyzed the phenotype of embryos from females at 25°C carrying either one or two copies of the torHM gene and varying doses of the trk gene (Table 1). For a given number of tor receptors, an increase in the doses of trk results in the appearance of more terminal structures, indicating that a higher level of terminal signaling is being generated. Under these experimental conditions, the sole variation lies in the number of tor or trk molecules, implying that it is the different number of activated tor receptors that dictates the expression of the distinct genes responsible for the determination of diverse terminal structures.

**DISCUSSION**

**The torso signal transduction and generation of pattern**

Activation of the torso pathway is responsible for specifying the terminal portions of the embryo, which include a variety of structures that appear in an organized pattern. The generation of this pattern involves the activation of at least two different genes along the terminal region. An open question is how activation of the torso receptor can lead to differential gene expression. By using mutations coding for constitutive torso receptors it has been possible to show that the level of active tor protein can be causally related to the specification of particular portions of the terminal pattern (Casanova and Struhl, 1989). However, it has been pointed out that these results should be interpreted with caution, as mutant proteins with altered activity may represent unique situations that a wild-type form of the tor protein may not be capable of achieving (Duffy and Perrimon, 1994). Here we report the identification of mutations that either reduce the amount of trk molecules or that lower the amount of tor receptors at the cell surface. These mutations allow us to show that variation in the number of activated torso receptors can be correlated with differential expression of the distinct genes responsible for the determination of diverse terminal structures. Probably other factors are also involved in translating the tor signal into the proper pattern. For instance, diffusion of intracellular phosphorylated substrates could also generate an instructive gradient specifying different pattern elements. Moreover, many experiments suggest that uniform levels of ubiquitous tor activity (Casanova and Struhl, 1989) or uniform levels of signal transducers (Casanova et al., 1994) can generate organized pattern. These observations suggest that the terminal signal can also be modulated by its interaction with other molecules present in the embryo (e.g. gap gene products) to give rise to differential gene expression. In wild-type development all these mechanisms might cooperate to translate the terminal signal into distinct domains of gene expression responsible for organization of the terminal pattern.

**Variation in the number of activated receptors at the cell surface: a general mechanism to elicit distinct responses from cells?**

In this report, we have shown that by modulating the amount of receptor and activating molecules we can elicit different responses in cells, in terms of their gene activation. Recently, results have been reported showing that stimulation of over-expressed EGF receptor can mimic the cellular response to activation of the NGF receptor (Traverse et al., 1994). Conversely, reduction in the amount of the NGF receptor can mimic the cellular response to EGF receptor activation (Schlessinger and Bar-Sagi, 1995). This behavior has been interpreted as a quantitative difference in ERK activation that is translated into a qualitative difference in transcription factor activation, but a limitation of this model is that it is based wholly on ‘in vitro’ experiments with PC12 cells (Marshall, 1995). In addition, many other transducing signaling pathways operating in development have been shown to generate graded responses. This is the case for the dorsoventral patterning in Drosophila (Roth et al., 1989; Rushlow et al., 1989; Steward, 1989; Chasan and Anderson, 1993), embryonic ventral
ectoderm determination also in *Drosophila* (Schweitzer et al., 1995) and for patterning of vulval fates in *Caenorhabditis elegans* (Stemberg and Horvitz, 1986; Hill and Stemberg, 1993). Here we document the case of the terminal system where activation of a unique transduction pathway can elicit at least two responses in terms of gene activation and we show this by altering the number of activated receptors at the cell surface. We would like to suggest that variation in the number of activated receptors, by changes either in ligand concentration or in the amount of receptor present at the cell surface, could represent a general mechanism to elicit distinct responses from cells.

We thank H. Doyle for the initial identification of the *tor*HM phenotype and T. Schüpbach, J. Lengyel and H. Jäckle for providing flies and materials. We also thank A. González-Reyes, G. Struhl R. Wharton and L. Ambrosio for comments on the manuscript, our colleagues in the laboratory for many discussions and Nicolás Martín for his technical assistance. M.F. is supported by a fellowship from the Ministerio de Educacion y Ciencia and Marató de TV3. This work was supported by the DGICYT, CIRIT and the Fundación Ramón Areces.

REFERENCES


(Accepted 4 April 1996)