Negative spatial regulation of the lineage specific Cyllla actin gene in the sea urchin embryo

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Summary

The Cyllla - CAT fusion gene was injected into Strongylocentrotus purpuratus eggs, together with excess ligated competitor sequences representing subregions of the Cyllla regulatory domain. In this construct, the chloramphenicol acetyltransferase (CAT) reporter gene is placed under the control of the 2300 nucleotide upstream regulatory domain of the lineage-specific Cyllla cytoskeletal actin gene. CAT mRNA was detected by in situ hybridization in serial sections of pluteus stage embryos derived from the injected eggs. When carrier DNA lacking competitor Cyllla fragments was coinjected with Cyllla CAT, CAT mRNA was observed exclusively in aboral ectoderm cells, i.e. the territory in which the Cyllla gene itself is normally expressed (as also reported by us previously). The same result was obtained when five of seven different competitor subfragments bearing sites of DNA–protein interaction were coinjected. However, coinjection of excess quantities of either of two widely separated, nonhomologous fragments of the Cyllla regulatory domain produced a dramatic ectopic expression of CAT mRNA in the recipient embryos. CAT mRNA was observed in gut, mesenchyme cells and oral ectoderm in these embryos. We conclude that these fragments contain regulatory sites that negatively control spatial expression of the Cyllla gene.

Key words: sea urchin embryo, lineage specific, Cyllla actin gene, negative spatial regulation.

Introduction

The Cyllla cytoskeletal actin gene of the sea urchin Strongylocentrotus purpuratus is expressed during early embryogenesis only in the eleven cell lineages that constitute the aboral ectoderm of the pluteus (Cox et al. 1986; Cameron et al. 1989a; reviewed by Davidson, 1989). Control of Cyllla transcription depends on the interaction with endogenous factors of cis-regulatory sequences located within a 2300 nucleotide 5′ regulatory domain, as shown by gene transfer experiments carried out with a Cyllla • CAT fusion gene construct (Flytzanis et al. 1987; Hough-Evans et al. 1987). Detailed mapping studies have revealed about 20 sites within this domain where nuclear proteins bind with high specificity in vitro (Calzone et al. 1988; Thézé et al. 1990). These fall into 13 distinct sequence classes, suggesting that this number of different factors is required in vivo. As part of an effort to determine the biological significance of the individual elements of this complex regulatory system, we have determined the effect on Cyllla • CAT expression in vivo of competition for individual factors or sets of factors. Individual subfragments of the regulatory domain, each containing one or a few factor binding sites, were ligated together with carrier DNA, and coinjected in excess with respect to the Cyllla • CAT fusion into unfertilized eggs. In the accompanying paper, Franks et al. (1990) show that individual subfragments including the specific binding sites for the factors P7I, P5 or P4, each competitively depress Cyllla • CAT expression, as does a subfragment that includes sites for two different factors called P2I and P2II, and a subfragment that includes three other sites, for factors P8I, P8II and P8III. Interactions with these factors (or at least one of the P2 factors and at least one of the P8 factors) evidently are required for normal levels of Cyllla • CAT expression. Thus these interactions mediate positive regulatory functions. Of the remaining factors, interaction with P3B is necessary for embryonic viability (Franks et al. 1990), while no significant competitive depression of the level of CAT expression was observed for subfragments bearing the P7II, P3A, P1 or P6 binding sites.

In this paper, we describe the competitive effects of the Cyllla regulatory subfragments on the spatial rather than the quantitative expression of Cyllla • CAT. The cell types in which CAT mRNA is expressed in embryos bearing excess competitor fragments were determined by in situ hybridization, carried out on serial sections made at an advanced stage of embryonic development.
No qualitative effect on spatial expression was observed with any of the subfragments found by Franks et al. (1990) to compete for positively acting factors, viz. those listed above. However, coinjection of two wholly nonhomologous competitor subfragments, one containing binding sites for the factors P3B and P3A, and the other binding sites for factor P7II, resulted in a remarkable derangement of the spatial pattern of CyIIIa·CAT expression.

**Materials and methods**

**Eggs and embryos**

Gametes were collected and eggs injected as described previously (McMahon et al. 1985; Franks et al. 1990). The eggs were microinjected with approximately 2 pi of DNA solution, either before or after fertilization, in place in the Petri dish. Embryo samples were taken after hatching (which occurs at 18 h postfertilization) for CAT assays, and at 72 h for *in situ* hybridization.

**Microinjection solutions**

Solutions for injection contained 40% glycerol, 250–1500 molecules of a CyIIIa·CAT fusion gene per pl, and competitor and/or sea urchin carrier DNA, exactly as described in detail in the accompanying paper (Franks et al. 1990).

**CAT assays**

CAT enzyme content per embryo was estimated on samples of about 50 hatched blastulae, by a method derived from that of Gorman et al. (1982), as described by McMahon et al. (1984) and by Franks et al. (1990).

**Cytological preparation**

Preparation of embryo sections and microscope slides were as described previously (Hough-Evans et al. 1987, based on the method of Cox et al. 1984). Embryos that developed from eggs that had been microinjected with CyIIIa·CAT or with CyIIIa·CAT plus competitor subfragments were fixed at the desired stage (in most cases 72 h pluteus) in 1% glutaraldehyde (or in 2% paraformaldehyde, 0.5% glutaraldehyde) in buffer containing 2.5% NaCl, 25 mM phosphate buffer pH 7.5. Embryos enclosed in agarose boxes were embedded in Paraplast (Monojet) or Tissueprep 2 (Fisher Scientific) and sectioned at 5 μm, and serial sections were placed on polystyrene-coated slides.

In *situ* hybridization

The single-stranded antisense CAT RNA hybridization probes used here were transcribed as described previously (Hough-Evans et al. 1987) from a fragment of CAT coding sequence inserted into the polylinker of the pSP65 vector. Either 3H- or 35S-labeled nucleotides were incorporated, as indicated. *In situ* hybridization with tritiated probes was carried out as in earlier experiments by the procedures of Angerer and Angerer (1981) and Cox et al. (1984). These procedures were modified for 35S-labeled probes by the addition of 5 μm dithiothreitol and 1% β-mercaptoethanol to the hybridization solution, hybridization in an N2 atmosphere, and posthybridization washes that included 1% β-mercaptoethanol. The photographic emulsion (Kodak NTB-2) was diluted with three parts distilled water in 3H-probe experiments, and a 1:1 dilution was used in experiments carried out with 35S-labeled probe.

**Results**

Our object in these experiments was to identify regions of the CyIIIa regulatory domain that might be required in normal embryos to prevent expression of the CyIIIa gene (i.e. of CyIIIa·CAT), in any but the aboral ectoderm cell lineages. The consequence of effective competition for a regulatory factor that mediates negative control of spatial CyIIIa expression would be to induce ectopic expression in other lineages. Effective competition of course requires that the competitor sequences be present in sufficient quantity within the relevant nuclei to titrate out a biologically significant fraction of the respective factor molecules. Franks et al. (1990) showed that this condition can indeed be met for many different positively acting factors. In the experiments described here, embryos taken from the same competitor injection series as studied quantitatively for CAT enzyme expression by Franks et al. (1990) were allowed to develop to the 70–72 h pluteus stage, at which stage serially sectioned material provides an unequivocal orientation and identification of anatomical features and tissues.

An extensive series of control experiments confirmed that for the protocols, materials and procedures utilized in this work, CyIIIa·CAT expression is normally confined to cells of the aboral ectoderm. A quantitative summary of the results of all the available CyIIIa·CAT controls is given in Table 1. Using the criterion that label must be present in cells of two or more adjacent sections (to avoid artifacts of occasional random sticking of labeled particulates), we found that in this recent set of experiments (Table 1, expts 4–6), 81% of all serially sectioned embryos display cells containing significant detectable CAT mRNA. All of these displayed CAT mRNA in aboral ectoderm, furthermore. Three embryos, representing 2.5% of those studied in the

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<th>Table 1. Expression of CyIIIa·CAT in pluteus-stage embryos developed from injected eggs</th>
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<td>Experiment no.</td>
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<td>1</td>
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<tr>
<td>2</td>
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<td>3</td>
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<tr>
<td>4</td>
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<tr>
<td>5</td>
</tr>
<tr>
<td>6</td>
</tr>
<tr>
<td>Total</td>
</tr>
</tbody>
</table>

Embryos labeled in aboral ectoderm/Σ labeled=159/159=100%.
Embryos labeled ectopically/Σ labeled=3/159=2%.

Notes:

* Only embryos represented by 9 or more sections were scored. Embryos were scored as labeled only if labeled cells appeared in two or more adjacent sections. In later experiments (experiments 1 and 2 are from Hough-Evans et al. 1987) a larger proportion of injected embryos were labeled, probably due to improved injection and hybridization procedures.
† Embryos were scored as being ectopically labeled if labeled cells were seen in tissue other than aboral ectoderm, in more than one section.
recent experiments (Table 1), also displayed CAT mRNA in a few cells of other types. Examples of control embryo sections, in which significant fractions of the visible aboral ectoderm can be seen to contain CAT mRNA, are shown in Fig. 1. Gut, mesenchyme and oral ectoderm are unlabeled in these in situ hybridizations. The single injection gene transfer methodology used in these experiments results in mosaic DNA incorporation patterns. Hough-Evans et al. (1988) deduced from direct observations made by DNA in situ hybridization to the exogenous sequences, and other prior evidence, that most probably, in about three-fourths of recipient embryos, a single concatenate of the injected DNA is stably incorporated in a single blastomere nucleus after 1st, 2nd, 3rd or 4th cleavage. However, exogenous DNA incorporation is random with respect to cell type and cell lineage (Sucov et al. 1988; Franks et al. 1988a,b; Livant et al. 1988). In some cases, the labeling patterns shown in Fig. 1 of this paper permit us to identify those blastomeres of the early cleavage embryo that in fact incorporated the exogenous DNA, given knowledge of the regional cell lineage of the aboral ectoderm (Cameron et al. 1987; 1989a,b). For example, perusal of other serial sections (not shown) of the embryo illustrated in Fig. 1a, upper right, indicate that the incorporation appears to have occurred in one of the two first cleavage blastomeres, viz., that giving rise to the 3rd cleavage blastomeres VA, VL and the overlying Na and NL blastomeres, while in the Fig. 1a lower embryo, incorporation appears to have been confined to the single 3rd cleavage VA blastomere. This evidence is important in a specific way for our present concerns, since the VA progeny that give rise to aboral ectoderm do not segregate from those giving rise to gut until 6th cleavage, and from those giving rise to skeletogenic mesenchyme until 4th cleavage (Cameron et al. 1987). Since all aboral ectoderm regions of the VA domain express CAT mRNA in this embryo, the exogenous DNA must also have been present in gut (and probably mesenchyme cells). In these locations, however, the CyIIIA·CAT gene is manifestly silent, an excellent demonstration of differential expression. Similar analyses of the lineage affiliations of labeled cells in other embryos shown are given in the legend to Fig. 1. These observations leave no doubt that, as reported earlier, CyIIIA·CAT expression is repressed in gut and mesenchyme, in the same embryos in which it is active in aboral ectoderm. Furthermore, embryos in which large NL aboral ectoderm domains are labeled, but the adjacent ciliary band regions of the oral ectoderm do not express CAT mRNA (e.g. Fig. 1e) show that CyIIIA·CAT is not expressed in the progeny of the 5th cleavage NL1u and NL2u blastomeres, while it is expressed in the progeny of their sister cells, NL11 and NL21 (Cameron et al. 1989a). However, this form of evidence cannot be applied to the lack of expression of CyIIIA·CAT in the main facial and stomodeal region of the oral ectoderm, as illustrated clearly in the embryos shown in Fig. 1a–b (lower), 1f, 1i, and 1j. These regions descend from the single 3rd cleavage blastomere No, which gives rise only to facial and stomodeal oral ectoderm progeny. Thus, were incorporation of any of the exogenous CyIIIA·CAT DNA to occur in the No blastomere (or its progeny), the resulting pluteus would be scored in these experiments as unlabeled. For all incorporations in the No domain at or after 3rd cleavage (i.e. the majority; Hough-Evans et al. 1988) the expectation would thus be that 12.5% of the successfully injected embryos would display no CAT mRNA, and perhaps this factor largely accounts for the observation that in Table 1 (expts 3–6) 19% of the embryos were scored as silent with respect to CAT mRNA expression.

In vivo competitions that do not affect spatial expression

Spatial expression of CyIIIA·CAT was assessed in those samples of embryos that contained the maximum amounts of competitor DNA in the quantitative competition studies of Franks et al. (1990). Table 2 shows that in most cases, whether or not CAT expression was depressed by the introduction of competitor fragments, the spatial pattern of CyIIA·CAT expression was not affected. That is, CAT mRNA was confined to aboral ectoderm just as in the control series summarized in Fig. 1 and Table 1. We conclude that there is no evidence from these experiments that the DNA–protein interactions mediated by the subfragments, which include the sites for factors P81, II and III; P4; P5; P2I or P2II, affect spatial expression of CyIIIA·CAT negatively, because no significant ectopic expression occurred. In each of these cases, we know that the in vivo competition was effective (Franks et al. 1990). Nor was spatial expression of CyIIIA·CAT affected in the P6 competition sample; however, 'competition' with this subfragment also failed to depress the level of CyIIIA·CAT expression in the experiments of Franks et al. (1990). Therefore, for this case we lack independent evidence that the competition was effective. A null control subfragment (designated '0'; Thézé et al. 1990) which contains no known sites of DNA–protein interaction, also failed to alter spatial expression when introduced in excess as competitor. Competition with the whole regulatory domain, while stoichiometrically depressing CAT expression (Livant et al. 1988; Franks et al. 1990), similarly left the spatial pattern of expression unchanged. An obvious interpretation is that titration onto competitor sequences has sequestered required positive regulatory factors, in

<table>
<thead>
<tr>
<th>Fragment</th>
<th>Total no.</th>
<th>Embryos labeled in aboral ectoderm*</th>
<th>No. of embryos with (possible) ectopic expression</th>
</tr>
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<tbody>
<tr>
<td>P2 (1+II)</td>
<td>59</td>
<td>20</td>
<td>0</td>
</tr>
<tr>
<td>P4</td>
<td>48</td>
<td>11</td>
<td>1</td>
</tr>
<tr>
<td>P5</td>
<td>113</td>
<td>60</td>
<td>0</td>
</tr>
<tr>
<td>P6</td>
<td>70</td>
<td>57</td>
<td>0</td>
</tr>
<tr>
<td>P8 (1+II+III)</td>
<td>36</td>
<td>25</td>
<td>1</td>
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* As in Table 1; see note (*).
Fig. 1. Correct lineage-specific expression of the fusion gene CyIIIa • CAT in pluteus embryos that developed from injected eggs. In situ hybridization to 5 μm thick embryo sections was carried out using a single-stranded antisense RNA copy of the CAT gene. The probe was labeled with 35S-UTP in panels a, b, and c–j, and with 3H-UTP in panels c and d. Embryo sections are shown under phase-contrast and dark-field illumination. (a and b) Adjacent sections of three embryos that expressed CAT mRNA in many cells of the aboral ectoderm. The upper and lower right embryos are cut approximately in sagittal section; stomach, intestine and esophagus are visible, and the oral 'face' is toward the right. Analysis of serial sections of the upper right embryo establishes that label is found in cells deriving from 8-cell blastomeres Na, VA, NLr, and VLr (Cameron et al. 1987, 1989a). Both the VA and VL blastomeres also contribute cells to the gut, here completely unlabeled. The lower right embryo appears to be labeled only at the apex, whose cells are clonal descendants of the VA blastomere. The remaining embryo (upper left) is cut so that the only tissue seen is aboral ectoderm, except for two small groups of ciliated band cells. (c) Embryo cut lengthwise through stomach and intestine. Oral ectoderm is to the right. The remaining ectoderm, including the only labeled portion, is aboral. The labeling pattern in this embryo indicates that the Na blastomere incorporated the exogenous CyIIIa • CAT gene. (d) Section through aboral ectoderm, intestine and part of the stomach, on the left side of the embryo. This side of the ectoderm (derived from blastomeres NLr and VLr) is extensively labeled. VLr also contributes to the gut, which is not labeled. Both mouth (and oral ectoderm) and anus are several sections away on the slide. (e) This embryo is cut in cross-section through the esophagus and coelomic pouches. A small amount of oral ectoderm is present, adjacent to the esophagus, toward the upper right. The only labeled cells are in the patch of aboral ectoderm on the lower right. (f) Approximately longitudinal cut through the open mouth and esophagus (oral face, left). The aboral ectoderm is almost completely labeled on one side, in cells derived from NLr. (g) Two embryos cut in cross section. The sections illustrated are toward but not in the oral face, and all the ectoderm seen is aboral. In each embryo one side of the ectoderm is labeled rather extensively, probably in derivatives of an NL daughter cell of the 16-cell stage. (h) Two embryos in which only a few cells of the aboral ectoderm are labeled. The embryo on the left is cut in longitudinal section through the intestine. Some NLr and NLl (lateral ectoderm) descendants are labeled. The oral face of each embryo is toward the upper right of the figure. (i and j) Approximately mid-sagittal sections of an embryo that had expressed CyIIIa • CAT in a majority of cells of its aboral ectoderm (as observed in other serial sections not shown). This implies that Na, VA, NLr, VLr, NLl, and VLl cells all contain the injected gene. Oral face, left. Note that the labeling stops at the ciliated band (thickened cells at the upper and lower edges of the oral face). The sections shown are 5 μm apart. Particular regions of the embryo sections shown are indicated as follows: A, apex; B, ciliated band; C, coelomic pouch; E, esophagus; I, intestine; M, mouth; m, mesenchyme cell; O, oral ectoderm; S, stomach. Oral ectoderm lies between the two lines labeled 'O'; all the ectoderm not labeled as oral is aboral ectoderm.

Table 3. Ectopic expression of CyIIIa • CAT when competing P3 or P7II DNA fragments are injected in molar excess

<table>
<thead>
<tr>
<th>Fragment (expt)</th>
<th>Total no. embryos*</th>
<th>Total labeled†</th>
<th>Embryos with ectopic label‡</th>
<th>Ectopic as % of labeled embryos</th>
</tr>
</thead>
<tbody>
<tr>
<td>P3 (1)</td>
<td>47</td>
<td>39</td>
<td>20</td>
<td>51</td>
</tr>
<tr>
<td>P3 (2)</td>
<td>12</td>
<td>9</td>
<td>2</td>
<td>22</td>
</tr>
<tr>
<td>P3 (3)</td>
<td>13</td>
<td>11</td>
<td>6</td>
<td>55</td>
</tr>
<tr>
<td>P3 (4)</td>
<td>42</td>
<td>35</td>
<td>8</td>
<td>23</td>
</tr>
<tr>
<td>ΣP3</td>
<td>114</td>
<td>94 (82%)</td>
<td>36</td>
<td>38</td>
</tr>
<tr>
<td>P7II (1)</td>
<td>36</td>
<td>35</td>
<td>20</td>
<td>57</td>
</tr>
<tr>
<td>P7II (2)</td>
<td>46</td>
<td>43</td>
<td>31</td>
<td>72</td>
</tr>
<tr>
<td>P7II (3)</td>
<td>114</td>
<td>110</td>
<td>40</td>
<td>36</td>
</tr>
<tr>
<td>ΣP7II</td>
<td>194</td>
<td>188 (97%)</td>
<td>91</td>
<td>48</td>
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</table>

CyIIIa • CAT alan§(4) 9 9 0 0

* Complete embryos and embryos of which 9 or more serial sections were scored.
† Embryos labeled in two or more sections.
‡ Embryos with ectopic labeling in two or more sections.
§ These results also listed in Table 1, as expts 4, 5 and 6 of that Table. Expts 5, 6 of this series were carried out at the same time and on the same batch of eggs as P3 (4) and P7II (3); and expt 4 similarly served as the internal control for expts P3 (3) and P7II (1).

including any that might have promoted ectopic expression had they been present.

Ectopic spatial expression of CyIIIa • CAT caused by competition for P3A and P7II factors

The key result shown in this paper is illustrated in Figs 2 and 3, and summarized in Table 3. This is that in vivo competition with two subfragments of the CyIIIa regulatory domain results in a striking ectopic spatial expression of CyIIIa • CAT. CAT mRNA in these samples is detected in lineages that normally never express the CyIIIa gene itself, and in which the CyIIIa • CAT construct remains silent in the absence of competitor (except for 2.5 % or less of possible aberrant cases). One of these subfragments, here referred to as the P3 subfragment, contains two known sites for high specificity DNA-binding proteins, viz. the P3A and the P3B sites (Calzone et al. 1988; Thézé et al. 1990). The P3B site is an octamer protein binding site, and since competitive titration with this site results in embryonic lethality (Franks et al. 1990), the endogenous octamer protein is obviously a necessary factor. The site responsible for the specific spatial control function that is perturbed in the P3 competition experiment is most probably the P3A site. Neither a subfragment containing only this site nor the P7II site causes significant competitive decrease in CyIIIa • CAT expression even when present in what should be sufficient excess (Franks et al. 1990), and thus by this test neither functions positively in vivo. The in situ hybridization results obtained with the P3 and P7II competitions
indicate that in fact both interactions must function negatively in normal undisturbed embryos, presumably preventing Cyllla expression in other than the aboral ectoderm cell lineages. When excess molar quantities of either of these binding sites are introduced into the embryos, the result is a failure of these normal repressive interactions, as the factors become sequestered on the competitor fragments. Table 3 shows that from 22% to 55% of embryos in the P3 competition series, and 36% to 72% in the P7II competition series, have at least some cells that display illegitimate expression of CAT mRNA.

The effects of competition with the P3 and P7II subfragments are subtly different. Fig. 2 shows representative examples of ectopic expression with the P3 subfragment. In most cases the ectopic expression is confined to mesenchyme cells, and in some examples a significant fraction of the mesenchyme cells present in the section display CAT mRNA (e.g. Fig. 2d and h). Unfortunately we cannot clearly distinguish skeletogenic mesenchyme from secondary mesenchyme, since the mineral elements of the skeleton are dissolved during preparation. From their positions, however, both would seem to be expressing CATmRNA: thus for example the active mesenchyme cell along the aboral wall of the embryo shown in Fig. 2h is likely to be skeletogenic, while those applied to the wall of the gut as in Fig. 2c, d, f and g are more probably secondary, but these assignments are certainly not secure. Fig. 2 also includes some very clear examples of labeling in the facial oral ectoderm, which descends entirely from the progeny of the 3rd cleavage No blastomere (e.g. in Fig. 2a, b and e). We did not see any convincing cases among the P3 competition embryos of labeling in the wall of the gut, however. Possible labeling in either stomach or intestine was confined to occasional single cells that could not be verified or supported by labeling in the adjacent sections. Expression occurred in the aboral ectoderm in almost all the P3 competition embryos, whether or not they displayed ectopic CAT mRNA as well, as can be seen, for example in the sections shown in Fig. 2d, e and h. We conclude that the P3 subfragment contains a regulatory element the function of which is required to repress Cyllla expression in mesenchyme cells and oral ectoderm.

The effects of competition with the P7II fragment, as shown in Fig. 3, are even more dramatic. The central No domain of the oral ectoderm is strongly labeled in Fig. 3a and b (the same embryo seen in adjacent sections), and in Fig. 3c–f; and one side of the ciliary band, which derives from an NL blastomere (Cameron et al. 1989a) is strongly labeled in the embryos shown in Fig. 3h and j. Many of the mesenchyme cells to be seen, for example, in the embryo shown in Fig. 3g, are also labeled. Intense labeling of cells in the wall of the gut can be seen in the embryos shown in Fig. 3c, d and i. Again, almost all of the labeled embryos included in the P7II experiments of Table 3 display aboral ectoderm labeling as well, as can be seen in Fig. 3a–h. We conclude that the P7II interaction is required to repress Cyllla·CAT expression (and thus presumably Cyllla expression) in all major embryonic lineages except aboral ectoderm. Competitive interference with this interaction produces a catastrophic spatial derangement of expression, in which expression in other lineage element(s) wherein the exogenous DNA resides is added to the normal pattern of aboral ectoderm expression.

Discussion

Negative spatial regulatory functions appear to be confined to the P3A and P7II sites of the Cyllla gene

Franks et al. (1990), in the accompanying study, failed to detect any competitive decrease in expression of CAT mRNA from the Cyllla·CAT fusion when the P3A or P7II subfragments were coinjected in molar excess. From the quantities of these factors estimated in the embryo nuclei in vivo (Calzone et al. 1988), it appeared unlikely that this negative result could be due to insufficient excess of the competitor sequence. The results reported here (Table 3 and Figs 2 and 3), demonstrating a frequent, and often extensive ectopic spatial expression of CAT mRNA in the P3 and P7II competition samples, prove that the quantities of stably incorporated competitor sequence indeed sufficed to titrate out the respective factors, at least in some cells of many embryos. It follows that by the competition test these interactions cannot function positively in regulating Cyllla·CAT expression. Present evidence suggests that the sole function of these interactions is indeed negative, viz., repression of Cyllla expression except in the embryonic territory composed of the eleven aboral ectoderm cell lineages.

We have in this work and that reported by Franks et al. (1990) examined subfragments of the Cyllla regulatory domain that include all of the known sites of high-specificity DNA–protein interaction detected in vitro (Calzone et al. 1988; Thézé et al. 1990). Only one subfragment, that including the two sites bound by the factor P6, failed to result either in ectopic spatial expression or decrease in CAT expression when co-injected in molar excess with the Cyllla·CAT fusion. We did not examine the effect of P1 site competition on spatial expression in this work, and it is not excluded that this interaction might also exercise negative spatial control. However, this seems unlikely since, as Franks et al. (1990) found, P1 acts as a weak positive regulator of Cyllla·CAT expression.

Spatial regulation of lineage-specific Cyllla gene expression

Both of the sites that according to these results would mediate negative spatial regulation of the Cyllla gene are located close to one or more positively acting sites. This is particularly clear in the case of the P7II site, which is only about 100 nucleotides to the 3' side of the P7I site, that was demonstrated in the accompanying paper to function positively. This is less than the amount of DNA bound by a single nucleosome. Thus as in other systems in which negative regulatory interac-
Negative spatial regulation in the sea urchin embryo

Fig. 2. In situ hybridization showing ectopic CAT expression in embryos from eggs injected with P3 DNA fragments in competition with the CyIIIa·CAT fusion gene. All the panels except h show hybridization with tritium-labeled CAT probes; in h the probe was labeled with 35S-UTP. Embryos shown were collected in three completely independent competition injection experiments: (1) a–d; (2) e and h; (3) f and g. Embryo regions shown: A, apex; B, ciliated band; C, coelomic pouch, E, esophagus; I, intestine; M, mouth; m, mesenchyme cell; O, oral ectoderm; S, stomach. (a) Midsagittal section of an embryo labeled in oral ectoderm (near the open mouth) as well as aboral ectoderm (labeling seen in one cell just aboral (left) of the upper ciliated band; in other sections more of the aboral ectoderm was labeled). Esophagus and stomach are visible in this section. (b) Same embryo as shown in panel a, second section further along in the series. The oral ectoderm is labeled in several contiguous sections of this pluteus. (c) Longitudinal section through intestine, oral (upper) ectoderm, and aboral ectoderm. The only labeling is in a mesenchyme cell attached to the gut. (d) Mesenchyme cell labeling in an embryo cut in cross section. The intestine is cut tangentially; all the ectoderm in this section is aboral ectoderm. Two labeled mesenchyme cells are shown. In addition, this embryo is labeled in some cells of the aboral ectoderm. (e) Tangential section through the right side of an embryo in which the ciliary band bordering the oral face is shown on the left, heavily labeled. The remaining tissue in this section is aboral ectoderm. (f) This embryo was sectioned through the stomach and esophagus. A single labeled mesenchyme cell is shown. (g) Longitudinal section (oral face to the left) through esophagus and the wall of one coelomic pouch. A mesenchyme cell above the esophagus is labeled. (h) Embryo similar to that shown in d. Some of the mesenchyme cells seen in the phase photograph are labeled, while others are not. All of the ectoderm in this cross section is aboral. A tangential section of part of the esophagus is completely unlabeled.

tions play an important role, a likely mechanism would be that the negative function operates by interfering with or modifying a physically contiguous positive interaction. The P7I interaction might thus serve as the essential (positive) element of the repression submech-

anism mediated by the P7II factor. Similarly, the P3A binding site is but 13 nucleotides distant from the P3B octamer site on the 3′ side, and only 90 nucleotides
distant from the potent, positively functioning P5 binding site (Calzone et al. 1988; Thézé et al. 1990; Franks et al. 1990) on the 5' side.

We cannot state on the basis of this or other extant data whether there are positive as well as negative lineage-specific controls on spatial expression of these
aboral ectoderm-specific genes. Were such to exist, competitive titration in vivo (or deletion, or in vitro mutations) would merely have decreased or abolished the signal observed, as in the cases recorded in Table 2, without altering the spatial pattern of expression. However, that same result would be expected from competition for factors that have no spatial regulatory functions whatsoever, but serve as enhancers or positive temporal regulators, etc. Even if further experiments reveal that there are indeed lineage-specific, positively acting factors, the negative functions displayed in this study are a dominant regulatory feature, so that loss of these functions ruins the lineage specificity. This is also seen in the interspecific gene transfer experiment (Franks et al. 1988b). The heavily ecstatic pattern of CyIIa·CAT expression observed in *Lytechinus variegatus* embryos in that study strongly resembles that produced in the P7II competition series of Fig. 3 of this paper, in that expression occurs in all major lineage elements. The direct prediction follows that in *L. variegatus* nuclei the P7II factor is either missing or is evolutionarily divergent, so that it can no longer function on the P7II site of the *S. purpuratus* CyIIa gene. It appears unlikely that failure of the P3A interaction alone to occur would suffice to explain the phenotype of CyIIa·CAT expression in *L. variegatus* embryos since competitive titration of P3A in *S. purpuratus* does not generate ectopic expression in the gut (Fig. 2). The fact that competitive interference with the P7II interaction alone derepresses CyIIa·CAT expression in all major lineages suggests that the regulatory system logic is of the form that repression in oral ectoderm and mesenchyme requires both the P3A and P7II interactions, while repression in gut requires only the P7II interaction. Alternatively, these two interactions could have similar functions, but there could be such large concentrations of P3A factor in gut cells in particular that the incorporated competitor sequences were quantitatively insufficient to titrate them out.

In summary, the major result of this work is the discovery of lineage-specific, negative regulatory interactions in the sea urchin embryo. These interactions are an essential feature of the mechanism by which is achieved the initial differential spatial expression of a structural gene, that in normal development is transcribed exclusively in the aboral ectoderm lineages of the early embryo.

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References


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