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The *Drosophila* RGS protein Loco is required for dorsal/ventral axis formation of the egg and embryo, and nurse cell dumping

Stephen Pathirana\(^a\), Debiao Zhao\(^b\), Mary Bownes\(^a\,*\)

\(^a\)Institute of Cell and Molecular Biology, University of Edinburgh, Edinburgh EH9 3JR, UK

\(^b\)Roslin Institute, Roslin, Midlothian EH10 4AN, UK

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**Abstract**

The *loco* gene encodes members of a family of RGS proteins responsible for the negative regulation of G-protein signalling. At least two transcripts of *loco* are expressed in oogenesis, *loco-c2* is observed in the anterior-dorsal follicle cells and is downstream of the epidermal growth factor receptor signalling pathway, initiated in the oocyte. *loco-c3* is a new transcript of *loco*, which is expressed in the nurse cells from stage 6 onwards. Analysis of newly generated mutants and antisense technology enabled us to establish that disrupting *loco* in follicle cells results in ventralized eggs, while disrupting *loco* in nurse cells results in short eggs, due to defective dumping of the nurse cell cytoplasm into the oocyte. © 2001 Elsevier Science Ireland Ltd. All rights reserved.

**Keywords**: Oogenesis; Follicle cells; Epidermal Growth Factor Receptor signalling; G-protein signalling; Polarity

1. Introduction

A fertilised egg has the ability to give rise to a complete organism, with all its different cell types arranged into tissues, organs and systems. To achieve this, the oocyte has to be highly organised, and may contain localised maternal products that, in some organisms, direct early events and cell divisions in the embryo. Without these molecules positioned correctly, an embryo is unable to develop normally. The highly organised patterning of the *Drosophila* oocyte is established during oogenesis and is dependent on cooperation between the oocyte, other germ-line cells and associated somatic cells.

The mechanisms underlying the determination of anterior–posterior (AP) and dorsal–ventral (DV) polarity have been intensively researched in recent years (e.g. Nusslein-Volhard, 1991; Roth and Schüpbach, 1994; Gonzalez-Reyes et al., 1995; Roth et al., 1995). Despite our increased knowledge there are still gaps in our understanding. For example, many components interacting with the *gurken-torpedo* signalling pathway including *rhomboid, kekkon, argos, pointed* and *Broad-complex* have been described (Ruohola-Baker et al., 1993; Neuman-Silberberg and Schüpbach, 1994; Roth and Schüpbach, 1994; Deng and Bownes, 1997; Wasserman and Freeman, 1998; Ghiglione et al., 1999; Zhao and Bownes, 1999), but we still have not established how all these components fit together and cooperate to establish DV polarity and dorsal-anterior egg structures.

In egg chambers at stage 8 of oogenesis *gurken* (*grk*) mRNA localises at the posterior of the oocyte, where it is translated. Grk protein signals to the adjacent follicle cells, which adopt a posterior fate as opposed to a default, anterior fate (Gonzalez-Reyes et al., 1995). These posterior follicle cells signal back to the oocyte resulting in the repolarisation of microtubules within the oocyte (Gonzalez-Reyes et al., 1995). It is the correct polarisation of the oocyte cytoskeleton that is responsible for establishing the AP axis of the embryo (Pokrywka, 1995). The maternal mRNAs *bicoid* and *nanos* are positioned at the poles of the egg and are responsible for initiating AP patterning within the embryo (Nusslein-Volhard et al., 1987; Berleth et al., 1988; Nusslein-Volhard, 1991). The AP axis of the egg is identified by anterior structures such as the micropyle and operculum, while the posterior is more rounded and the chorion is smooth.

After repolarisation of the microtubules the nucleus migrates anteriorly during stages seven to eight (Gonzalez-Reyes and St Johnston, 1994). *grk* mRNA localises at the nucleus and protein produced locally signals to adjacent follicle cells again. Torpedo (*TOP*, the Epidermal Growth Factor Receptor Signalling Pathway) initiated in the oocyte. © 2001 Elsevier Science Ireland Ltd. All rights reserved.

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* Corresponding author. Tel.: +44-131-650-5369; fax: +44-131-650-8650.

E-mail address: mary.bownes@ed.ac.uk (M. Bownes).
Factor Receptor (EGFR) homologue (Schüpbach, 1987; Clifford and Schüpbach, 1989; Roth et al., 1995; Sapir et al., 1998) is activated in this subset of follicle cells and they adopt a dorsal fate. Thus, the DV axis is established perpendicularly to the primary AP axis and by the same signalling mechanism (Gonzales-Reyes et al., 1995).

The establishment of DV polarity of the egg is manifest in the overall shape of the egg, the dorsal surface is flatter than the ventral surface and the dorsal appendages, the respiratory structures of the egg, are located dorso-laterally and anteriorly. The formation of these dorsal-anterior structures is dependent on an interaction between the dorsal signal, grk, and the anterior signal decapentaplegic (dpp) (Peri and Roth, 2000). The embryonic DV axis is determined by information built into the perivitelline space (Stein et al., 1999; Grosshans et al., 1994; DeLotto and DeLotto, 1998; Misra et al., 1998). The establishment of polarity in both the embryo and the eggshell relies on a common initial signal from the oocyte received by the anterior-dorsal follicle cells (Neuman-Silberberg and Schüpbach, 1993). This signal is responsible for activating different genetic pathways, which result in morphological differentiation in the egg and embryo.

The induction of a subset of follicle cells to adopt a dorsal fate is dependent on the correct localisation of the grk mRNA in the oocyte. However, we do not know in detail how the follicle cells respond once the grk signal is received to pattern the eggshell. Nor do we know exactly how this leads to the ventral follicle cells establishing the ventral signal in the perivitelline space, which is needed to establish the embryonic D/V axis. Towards this goal we have identified a number of genes expressed in specific subsets of follicle cells using the GAL4/UAS enhancer trap system (Brand and Perrimon, 1993; Deng et al., 1997). This paper describes the analysis of one of the genes isolated from this screen.

The two cDNAs isolated from the library screen were fully sequenced. They represented different transcripts of the same gene and had sequence similarity to a newly identified family of RGS genes involved in G-protein regulation. Independently Grunderath et al. (1999) identified transcripts for the same gene, loco. cDNA 118a proved to be identical to

### 2. Results

#### 2.1. Isolation of the loco gene and determination of its expression pattern in oogenesis

One of the enhancer trap lines, C139 exhibited lacZ staining in the anterior-dorsal follicle cells. This line was plasmid rescued and 2.3 kb of genomic DNA flanking the P-element was recovered. This genomic fragment was used to screen a Drosophila λ fix genomic library. Two λ clones were isolated (λ652 and λ653), which contained DNA 5’ and 3’ of the P-element insert. These λ clones were used to screen a Drosophila ovarian cDNA library. Two cDNAs were isolated, 96a and 118a. Restriction enzyme digests of the two λ clones and Southern blotting, using the rescued fragment and the two cDNAs as probes, showed that the λ clones spanned a region of 20 kb. The positions of the P-element, the rescued fragment and the two cDNAs are shown in Fig. 1A.

#### 2.2. The cDNAs isolated represent transcripts of the RGS gene loco, including a novel transcript

The two cDNAs isolated from the library screen were fully sequenced. They represented different transcripts of the same gene and had sequence similarity to a newly identified family of RGS genes involved in G-protein regulation.
to the transcript loco-c2 which they described. The other transcript cDNA 96a contains the same core region as the two transcripts described in Granderath et al. (1999), including exons 2–4, but contains a completely different 5′ exon of 800 bp (Fig. 1C); this transcript was named loco-c3. Reverse transcriptase polymerase chain reaction (RT-PCR) performed on ovarian tissue confirmed that the cDNAs represent genuine ovarian transcripts. RT-PCR also confirmed the presence of loco-c1 in oogenesis. Mapping of the exon/intron boundaries was undertaken using a mixture of sequence alignment of cDNAs to genomic sequence in the NCBI database and PCR, using the two λ clones as templates, along with the corresponding genomic DNA. The full region spanning the gene has been added to the database from the Genome Project (AC 017222) and confirms our data. The new exon we identified in loco-c3 maps to a region 2.5 kb upstream of exon II-0; this means that the intron between exon III-1 and exon II-0 of loco-c3 is just over 15 kb (Fig. 1). The first exon, III-1, of loco-c3 is 800 bp, 120 bp of which are coding. The start codon is 120 nucleotides from the 3′ end of the exon, indicating that this exon is largely untranslated.

2.3. The two transcripts present in ovaries have different expression patterns

Having established that there are at least two loco transcripts present in oogenesis, in situ hybridisation to wild type ovaries was carried out with transcript specific RNA probes to investigate the spatial and temporal expression of the different transcripts. To detect loco-c2, we used a probe consisting of exon II-1. Expression is first seen in the germarium at stage 2, in the prefollicular mesoderm surrounding the cystocytes (Fig. 2A). The prefollicular mesoderm goes on to form the follicular epithelium (King, 1970; Fig. 2A). Expression is then observed in the follicle cells at stage 8 (Fig. 2B). From stage 10 onwards loco-c2 transcripts are present in the anterior-dorsal follicle cells and persist there until the follicle cells degenerate (Fig. 2C–E). There appears to be a higher level of expression in the dorsal midline follicle cells and at the margin between the oocyte and nurse cells, than there is laterally (Fig. 2D, F). Note that there is distinct difference in the level of transcript in adjacent cells rather than there being a gradient across this area.

In situ hybridisation to loco-c3 RNA, using exon III-1 as a probe, demonstrates that the expression pattern is initially similar to loco-c2, as we detect transcripts in the germarium (Fig. 2E). The transcript is then undetectable until stage 6 when loco-c3 transcripts are observed in the nurse cells. Levels increase dramatically at stage 10 (Fig. 2F) and transcripts persist until the nurse cells degenerate. Clearly the two loco transcripts detected in oogenesis are very differently regulated.

2.4. Expression of loco in follicle cells is downstream of the gurken-torpedo signalling pathway

Since loco-c2 transcripts were observed in the anterior-dorsal follicle cells, we investigated if their expression was regulated by the EGFR signalling pathway. In situ hybridisations to loco RNA (probe for all exons used) in ovaries from a gvrKc mutant were undertaken and no loco expression was observed in follicle cells, though the nurse cell expression remained unchanged (Fig. 3A). Similar results were obtained using torpedo mutant ovaries (Fig. 3B). In an fs(1)kJ10 mutant background (Haenlin et al., 1987), where gurken mRNA is not localised, we observed expression of loco extending further ventrally (Fig. 3C), and in a transgenic fly line that overexpresses gurken because it carries four copies of the gene (Neuman-Silberberg and Schüpbach, 1994), loco-c2 expression is seen in all the anterior follicle cells (Fig. 3D). These results indicate that expression of the loco-c2 transcript is downstream of the gurken-torpedo signalling pathway in follicle cells, and therefore the expression pattern is governed by the gurken signal from the oocyte to the overlying follicle cells.

2.5. Is the expression of loco regulated by default pointed in oogenesis?

As well as being isolated in our screen for genes involved in DV axis determination in the oocyte, loco was identified in a screen for genes downstream of pointed in specific subsets of cells in the central nervous system (CNS) (Granderath et al., 1999). pointed 1 and 2 are expressed in the anterior-dorsal follicle cells in oogenesis (Morimoto et al., 1996). The expression of pointed in oogenesis is dynamic, expression first being observed in the germarium, then later at stage 8, downstream of torpedo, in the posterior follicle cells and again at stage 10, also downstream of torpedo, in anterior-dorsal follicle cells (Morimoto et al., 1996). As pointed is expressed in anterior-dorsal follicle cells in a similar pattern to loco at stage 10, it is possible that loco is downstream of pointed at this particular stage of oogenesis. We therefore analysed the relationship between loco and pointed in these cells. Using a pointed 1/UAS sense fly line, we drove expression of pointed in all the follicle cells using a T155 GAL4 driver. Fig. 4A shows an in situ hybridisation to RNA in the GAL4/UAS-pointed ovaries, using a pointed probe, and clearly shows high levels of pointed expression in all the follicle cells that cover the oocyte at stage 10. We then followed the expression of loco-c2 in egg chambers where pointed was being ectopically expressed. We saw a normal spatial distribution in anterior-dorsal follicle cells at stage 10, though levels of expression were somewhat reduced (Fig. 4B). This reduction in expression is not uniform over the anterior-dorsal region, with the anterior-most follicle cells maintaining their normal level of expression. At later stages the expression pattern is slightly different to wild type as there is a
patch of cells expressing loco in the dorsal position, which has not migrated as far anteriorly as would be expected at this stage. This is due to overexpression of pointed in oogenesis resulting in failure to make dorsal appendages. This suggests that cells normally expressing loco do not migrate as far as in wild type egg chambers (Fig. 4C). This experiment shows that there is not a simple relationship between loco and pointed. Granderath et al. (2000) have shown clearly that pointed and gcm synergistically control loco in glial cell formation, so it is likely that there are other genes involved in regulating loco expression in the ovary. Ectopic pointed expression does disrupt the normal loco-c2 expression pattern at stage 10, with its level of expression dropping in the anterior-dorsal follicle cells, except in the anterior-most follicle cells. This indicates that loco-c2 is downstream of pointed, although not directly.
2.6. Generation and analysis of mutants

The P-element used to isolate the gene was mapped initially by Southern hybridisation of the rescued fragment to restricted λ clones. Sequencing of the rescued fragment places it 280 bp 5' of exon I-1 (Fig. 1). Interestingly, this is in a similar location to the P-element insertion obtained by Granderath et al. (1999).

P-element mutagenesis was carried out on fly line C139 selecting for potential aberrant excisions (white-eyed lines). One hundred and seven white-eyed lines were generated, of which nine were homozygous lethal. All lines were screened by Southern analysis, using genomic fragments as probes surrounding the P-element. Three lines showed band shifts relating to aberrations in the vicinity of the original P-element. S94ME371, a largely lethal line, which generates occasional homozygous females has a partial deletion and duplication of the P-element resulting in an 8 bp duplication of genomic DNA 5' of the P-element. Homozygous females from line S94ME371 lay eggs that exhibit a range of phenotypes that can be divided into two groups. The short egg phenotypes are a result of disrupted cytoplasmic dumping from the nurse cells into the oocyte and result in eggs ranging from slightly shorter than wild type to a quarter of the expected length (Fig. 5D). The other group of phenotypes include eggs where the D/V polarity is affected, resulting in eggs which have fused dorsal appendages to varying degrees. This ranges from eggs with dorsal appendages slightly closer together, eggs with appendages fused at the base, eggs with appendages fused along the

Fig. 3. (A–D) Egg chambers from different mutants. (A) A stage 10 egg chamber from a gurken (grk004) mutant line. Without gurken, Torpedo cannot be activated in the follicle cells. The dorsal-anterior expression of cDNA 96a is lost. (B) A stage 10 egg chamber from torpedo (top003) mutant fly line. Again no expression of the cDNA is observed in the follicle cells. (C) A stage 10 egg chamber from an fs(1)K10 mutant fly line. fs(1)K10 is essential for the correct localisation of gurken mRNA to the oocyte nucleus, we observe expression of loco mRNA in the follicle cells, although it is not confined to the anterior-dorsal follicle cells, but its expression extends ventrally correlating with distribution of gurken mRNA extending ventrally. (D) A stage 10 egg chamber from a fly line which overexpressed gurken, having four copies of the grk gene (Neuman-Silberberg and Schüpbach, 1994). loco mRNA is observed in more cells than in wild type. All the evidence indicates that loco lies downstream of grk and top and is positively regulated.

Fig. 4. The relationship between loco and pointed during oogenesis was investigated. (A) A stage 10 egg chamber from a UAS pnt sense line, in which pnt is being driven by C710 a GAL4 driver for all the follicle cells. In situ hybridisation with a pnt probe shows that pnt is expressed in all of the follicle cells. (B, C) loco-c2 expression in egg chambers with ectopic pnt expression. At stage 10 the expression pattern of loco-c2 is reduced in all anterior-dorsal follicle cells except for those at the margin between the anterior of the oocyte and the nurse cells (B; this is a dorsal view). (C) loco-c2 expression at stage 13, this is markedly different from wild type (compare with Fig. 3D).
entire length (one appendage), to eggs with no appendages (Fig. 5B, C). This can be interpreted as a reduction or loss of dorsal identity. The embryos that were lethal failed to develop cuticular structures and were generally degenerated. This is dealt with in the subsequent section.

loco\textsuperscript{D13}, a lethal loco mutant, and deficiencies Df(3R)15CE1 and Df(3R)17D1, deleting the cytological regions 93E/F-94C/D and 93E/F-94B/C, respectively, were used in complementation analysis with excision line S94ME371, now called loco\textsuperscript{371}, loco\textsuperscript{371} complements Df(3R)15CE1, Df(3R)17D1 and loco\textsuperscript{D13}. This was an unexpected result, as the molecular data for loco\textsuperscript{371} demonstrate that there is a disruption of the loco gene and loco has been mapped to 94B/C where the deficiencies lie. The organisation of loco and the positions of the Df lines are shown in Fig. 1B. loco\textsuperscript{D13} is a deficiency line with a deletion (12 kb) extending from exon I-1 3' of loco. Since loco is in the orientation 3'→5' with respect to the chromosome numbering system the defect in mutation in loco\textsuperscript{371} clearly maps outside this deletion and could therefore complement by virtue of producing some transcripts. The position of the 8 bp insertion is likely to disrupt the regulation of some loco transcripts rather than causing the transcripts to be absent. Similarly, the two Df lines include the loco complementation group and clearly delete loco core exons, but they complement our mutations in the 5' region of the loco gene. We propose that loco\textsuperscript{371} disrupts expression of loco in such a way that two copies of a regulatory mutation, as in the homozygotes, is worse developmentally than having one copy, as seen when crossed to loco deficiencies. This is entirely possible if loco\textsuperscript{371} is causing ectopic expression or abnormal expression of some isoforms.

2.7. Investigating the role of loco in oogenesis using antisense RNA

Antisense loco pCaSpeR-hs and pUAST constructs were made and used to generate heatshock and UAS fly lines. As loco-c2 is expressed in the anterior-dorsal follicle cells, disruption of loco here may result in either DV defects in egg patterning, DV defects in embryo patterning or both. The eggs laid by the GAL4/UAS antisense flies were observed and defects in the eggs described. Two lines exhibited a weak ventralised phenotype, 96UAS-ve6a laying some eggs with fused appendages and 118aUAS-ve laying some eggs with fused appendages and ventralised eggs. The weak phenotype observed probably results from low levels of antisense expression not removing all loco function. The lack of effect in several lines can be attributed to positional effects (Deng et al. 1999).

Analysis was carried out on all the pCaSpeR-hs lines. After heatshock, eggs were collected and observed to see if there were any abnormalities in the eggs laid. Of the 17 lines observed two were studied in detail as they exhibited the strongest phenotypes. Under the same heatshock regime no such egg abnormalities were observed with the wild type control (OrR). 96hs-ve5A produced eggs which either had fused appendages (14%) or appendages were completely absent and the egg was ventralised (4%). The heatshock data produced corresponded with GAL4/UAS data given above in that abnormal phenotypes included a range of dorsal defects, from eggs with slightly fused appendages to eggs which are completely ventralised (Fig. 6D, F, H).

The other line analysed in detail was 96hs-ve2A where 9% of eggs laid were shorter than wild type. The short egg phenotype observed in these lines varied from slightly

Fig. 5. The phenotypes observed in the mutant lines. (A) A lateral view of a wild type egg chamber. (B–D) are the various phenotypes observed in the mutant line loco\textsuperscript{371}. (B) A fused appendage phenotype, (C) a ventralised egg with no dorsal appendages and (D) a short egg, the result of cytoplasmic dumping not occurring properly.

shorter than normal eggs to eggs that were approximately a quarter the length of wild type eggs (Fig. 6E). A short egg phenotype is often associated with failure of the nurse cells to dump their contents at the end of oogenesis (Cooley and Theurkauf, 1994). Since we observe expression of \textit{loco} in the nurse cells these phenotypes could result from disruption of \textit{loco} function in nurse cells.

The two different phenotypes resulting from two transgenic lines 5A and 2A required further investigation as both fly lines contained the same \textit{hs-antisense-loco} construct. This could indicate that the activation of the heatshock construct results in the misexpression of another transcript or creates a fusion product in one of the heatshock lines. The organisation of the vector makes the latter unlikely and the misexpression of a new transcript is also unlikely as two antisense lines with insertions in different chromosomal positions give the same short egg phenotype. Another possibility is that as the different heatshock lines are inserted into different chromosomal locations the heatshock induces antisense \textit{loco} in different cells at different developmental stages, and this could account for the observed differences.

To investigate this possibility further, in situ hybridisation to the antisense \textit{loco} RNA in the heatshock lines, following the heatshock regime used to generate this phenotype was undertaken. The heatshock lines did not express antisense-\textit{loco} ubiquitously, and the two lines generating the different egg phenotypes had different antisense-\textit{loco} expression patterns. 2A had germ-line specific expression in the ovaries (Fig. 6A), while 5A had expression in the follicle cells overlying the oocyte at stage 10 (Fig. 6B). This confirms that there are positional effects, due to the insertion site of the heatshock construct. This differential expression proves very useful as the individual heatshock lines are effectively interfering with the somatic and germ-line transcripts of \textit{loco} separately. Line 5A drives follicle cell expression and generates the same phenotype as the \textit{GAL4/UAS} cross that also drives antisense \textit{loco} in the follicle cells. This disrupts \textit{loco-c2} in the anterior-dorsal follicle cells and results in eggs with dorsal-anterior defects. Disruption of \textit{loco-c3} in the nurse cells as seen in line 2A, however, results in a dumpless phenotype. The results observed are therefore consistent with antisense-\textit{loco} interfering with \textit{loco} function in the two sites of antisense expression.

As heatshock induces antisense RNA for a short period of time in either the germ-line or follicle cells in 2A or 5A, respectively, we used this system to investigate at which stage in oogenesis the two functions of \textit{loco} are required. The time elapsed between heatshock and eggs with abnormal phenotypes being laid was determined. For line 2A short eggs were observed 15–20 h after heatshock at a frequency of 9% (Fig. 6I). This correlates with the oocytes that form these abnormal eggs receiving the heatshock at stage 10 of oogenesis. This would disrupt \textit{loco} when it is present in both follicle cells and nurse cells. Using line 5A the fused appendage phenotype is first observed in deposited eggs approximately 19 h after heatshock, followed by the ventralised phenotype at 23 h (Fig. 6J). This suggests that egg chambers that receive the heatshock at or before stage 10 go on to be fully ventralised, while the egg chambers that receive the heatshock after stage 10 only have fused appendages. Control experiments subjecting wild type flies to the same heatshock regime did not generate these phenotypes. All these observations confirm that the phenotypes observed are a product of antisense disrupting native transcript as opposed to an artefact of the heatshock regime. We have also generated antisense \textit{fringe} transgenic heatshock lines that exhibit different phenotypes after heatshock to those we observe in the \textit{loco} antisense heatshock transgenic lines (Zhao et al., 2000). These \textit{fringe} lines also have different spatial antisense expression consistent with our observations in the \textit{loco} heatshock lines. These observations show the specificity of the antisense technology.

2.8. Is \textit{loco} involved in DV patterning of the embryo as well as the egg?

The egg phenotypes we observe with both the mutant lines and the heatshock line showed loss of dorsal regions of the eggshell and range from fused appendages to eggs that completely lack dorsal appendages. In the eggs that entirely lacked dorsal appendages there was a distinct difference in the overall shape of the egg, which appeared symmetrical, with the operculum missing. The majority of the eggs with fused appendages hatched into healthy larvae but the ventralised eggs failed to hatch. The embryos inside these eggs arrested early in development, and had little morphological structure. This suggested that maternal \textit{loco} is essential for embryonic development. To ascertain if the embryos that failed to develop were also ventralised we investigated the expression of \textit{twist}. \textit{twist} transcripts can be used as a marker for ventral embryonic cells, and is activated very early in embryogenesis, as soon as the epithelium is formed (Fig. 7B). It persists in the ventral cells until late in development. \textit{twist} in situ hybridisation on 0–4 h, blastoderm stage OrR embryos shows a band of staining in the ventral cells (Fig. 7A). This band reaches a maximum width of 18–20 cells (Fig. 7B). Amongst the abnormal embryos laid by fly line \textit{loco}143, some have an increased width of \textit{twist} expression with the band being in excess of 24 cells (Fig. 7C,D). Blastoderm embryos were also observed in which the \textit{twist} expression was disrupted; in some \textit{twist} expression was patchy and expanded at the anterior and posterior poles (Fig. 7E), in some expression was completely absent in the posterior half of the embryo (Fig. 7F). The results showed that normal \textit{twist} expression is disrupted in embryos laid by mutant \textit{loco} mothers, confirming that \textit{loco} is not only involved in the establishment of the axis of the egg, but also required to establish the axis of the embryo.

2.9. Development of embryos laid by \textit{loco} mothers

Since the embryos that die have little morphology at the
time they should hatch we collected eggs from homozygous loco mothers in 4 h batches and observed their development. Nuclear multiplication occurred and the blastoderm began to cellularise. In some instances, cellularisation was not even across the entire surface and some eggs produced abnormal blastoderms (Fig. 8A2), a common defect was a failure of correct invagination of the gut. Invagination began too far towards the posterior and large ‘holes’ appeared in the central yolk region (Fig. 8B3–4). These embryos gradually became more abnormal as development proceeded and eventually degenerated without secreting cuticle.

Other abnormalities were observed, where midgut inva-

Fig. 6. (A) A stage 10 egg chamber from fly line 96hs-ve2a (an antisense loco heatshock fly line) after it had been exposed to a heatshock (HS) regime. RNA in situ hybridisation with a probe against the antisense strand of loco shows that this line only drives antisense loco expression in the germ-line. In (B) a similar experiment was carried out using 96hs-ve5a (another antisense loco line carrying the same construct as in (A)). In this line HS only drives antisense loco expression in the follicle cells. As both lines contain the same construct, the difference in expression patterns must be due to position effects. (C) The ovarian phenotype observed in line 96hs-ve2a after the HS regime. This is a dumpless phenotype, and results in small eggs being laid (E). Note (G) shows a wild type egg and is not of the same scale as (E). (I) The numbers of short eggs laid by line 96hs-ve2a following the HS regime. It illustrates that the phenotype was observed 15–20 h after HS. Phenotypes (D), (F) and (H) are laid by in 96hs-ve5a females following HS treatment. (D) is the weakest phenotype observed with the dorsal appendages fused at the base. In (F) there is a single fused appendage in the middle, both (D) and (F) are representative of a reduced dorsal area in the eggshell. (H) shows the most severe phenotype, which is a complete loss of dorsal appendage. There is also a change in the shape of the egg, which is longer and thinner. (J) The numbers of eggs laid with fused appendages and with ventralised eggs following HS of line 96hs-ve5a. It illustrates that the fused egg phenotype was first observed 19 h after HS followed by the ventralised phenotype 23 h after HS. The fused appendage phenotype was more abundant than the ventralised phenotype, presumably reflecting a smaller developmental window when the HS can affect DV axis determination compared to affecting appendage determination and differentiation.

Fig. 7. (A) A wild type embryo, which had been hybridised to a twist RNA probe. twist expression can clearly be seen along the ventral surface of the embryo. (B) A ventral view of a similar embryo, showing width of the staining (18–20 cells). (C–F) are embryos laid by homozygous loco371 mutant mothers. (C) A lateral view of an embryo from loco371, this shows a broader band of expression than observed in any of the wild type embryos. (D) Part of (C) at higher magnification, showing expression spanning at least 24 cells. In (E) the expression of twist is more patchy and extends further dorsally at the poles. In (F) twist expression is lost in much of the blastoderm and is limited to the anterior.
gination did not occur properly (Fig. 8B2). Embryos were also observed with abnormal head regions that failed to show any signs of head invagination (Fig. 8C2).

3. Discussion

The data in this paper demonstrate that the RGS gene loco is expressed in Drosophila oogenesis. There are at least two different transcripts present, which are expressed in different subsets of cells at different stages of oogenesis and are involved in different developmental processes. Analysis of UAS and heatshock induced antisense expression and loco mutants, along with molecular studies, enabled us to match transcripts with specific developmental mechanisms.

The egg phenotypes observed laid by loco371 homozygous females suggest a role for loco in DV axis formation of the egg. This data was corroborated by heatshock induced antisense-loco experiments. However, the mutant analysis was not straightforward. Although our molecular studies clearly show that we have generated mutants in the loco gene and there are no other P-elements in the stocks, the complementation analysis did not show a more severe phenotype when our newly generated mutants were crossed to the existing deficiencies in the region. We know that loco is a large gene with several differently spliced forms, which would suggest a complex mechanism of gene regulation. Preliminary analysis with antibodies has also shown there are different isoforms of the protein present at distinct developmental stages suggesting different roles for different protein isoforms. As a negative regulator of G-protein levels, the types of protein expressed would be critical in maintaining equilibrium in signalling systems. All these factors could contribute to observed behaviour of loco371 which has a small insertion and retains rearranged parts of the P-element in the loco gene. This would be likely to interfere with expression of some transcripts but not others. This misregulation would lead to unusual complementation analysis, as having two copies of a gene which is expressed in the wrong cells or at the wrong time, or as the wrong isoform is likely to be more developmentally disruptive than a single copy. This would explain why homozygotes are mostly lethal and hemizygotes are not.

The heatshock antisense results were crucial for interpreting how the different mutant phenotypes were generated and which transcript and cell type they depended on. The different heatshock lines generate transcripts in different cell types. This allowed us to disrupt loco separately in the germ-line and follicle cells. loco-c3 is expressed in the nurse cells and, when disrupted, results in a dumpless phenotype resulting in smaller than normal eggs being laid. When loco-c2 is disrupted in the anterior-dorsal follicle cells, this results in a range of dorsal defects in the eggs. The anterior-dorsal egg defects vary from dorsal appendages, which are fused at the base, to appendages fused along the whole length, to completely absent appendages.

Our results suggest a role for G-protein signalling in DV pattern formation in oogenesis. Granderath et al. (1999) have carried out a two hybrid screen with loco and illustrated that Gia interacts with loco. This is direct evidence for a conserved role between loco and mammalian RGS genes.

In recent years, the study of the EGFR signalling pathway has highlighted how complex the DV patterning of the eggshell is. In oogenesis the proper formation of dorsal structures of the egg rely on this tight regulation. Romboid (Ruohola-Baker et al., 1993) is known to upregulate the initial activation of the EGFR signal by Gurken. Romboid is thought to act by cleaving Spitz, releasing activated Spitz (Schweitzer et al., 1995; Golembo et al., 1996; Wasserman and Freeman, 1998) which binds to Torpedo (EGFR) upregulating it. Another ligand of EGFR, Vein, is also thought to be involved in this process (Wasserman and Freeman, 1998). In this way, the initial paracrine signal from gurken...
in the oocyte becomes an autocrine signal within the follicle cells.

The secreted protein Argos is produced following high levels of EGFR activation (Wasserman and Freeman, 1998; Zhao and Bownes, 1999). This secreted protein represses the EGFR signal, possibly by interacting with the external domain of EGFR preventing any further ligands from binding. Because Argos is a secreted protein it has been suggested that it diffuses from the region where it is made, resulting in gradient around the dorsal midline follicle cells. It is postulated Argos separates the single EGFR signal into two peaks resulting in two dorsal appendages (Wasserman and Freeman, 1998). The regulation of the EGFR signal does not stop here as Kekkon I, which is a transmembrane protein, is thought to associate with the G-protein signalling. Granderath et al. (1999) have shown that the operculum is patterned independently and its size can be affected by the genes dpp and bunched (Dobens et al., 2000). In addition an interaction is needed between dpp at the anterior and gurken, the dorsal signal, to form dorsal appendages (Peri and Roth, 2000). It superficially appears that loco affects operculum formation when observing the most severely ventralised eggs. However, the micropyle and a ridge of the operculum similar to that seen normally on the ventral anterior of the egg are visible on a loco ventralised egg. This indicates that the ability to form the operculum is still present, and loco is affecting DV axis determination.

Why is there such an elaborate process to specify cell fates along this axis and how does loco fit into the existing pathway? loco is downstream of torpedo in the follicle cells and appears to be activated both at high and moderate levels of torpedo activation. The levels of expression are higher in the dorsal midline follicle cells and the follicle cells lying at the nurse cell/follicle cell junction. This suggests that loco expression is controlled by other genes expressed in the anterior-dorsal follicle cells as well as the Grk signal.

We know that the role of RGS proteins is to negatively regulate G-protein signalling. Granderath et al. (1999) have shown with a two hybrid screen that loco binds Gia. Wolfgang et al. (1991) showed Gia is present in the anterior-dorsal follicle cells. Thus it seems likely that G-protein signalling has a role in DV axis formation. In the absence of loco there is a loss of DV polarity in the egg and embryo. This phenotype is similar to the one induced by Gurken mutants and suggests that in the absence of loco repression EGFR signalling occurs. Since RGS genes negatively regulate G-protein signalling one can assume that in wild type ovaries G-protein signalling inhibits EGFR signalling but the presence of loco prevents this inhibition in anterior-dorsal follicle cells. This adds to the complexity of regulation of the EGFR pathway and suggests that the tight regulation or modulation of EGFR is critical for the correct sequence of morphological events to occur in the specification of follicle cell fates along the DV axis with time. This helps explain the range of loco phenotypes observed in the egg as the resulting phenotype will depend on the time and extent to which loco is affected. It also helps explain the weak phenotypes observed as there are several feedback loops occurring that presumably compensate to varying degrees for disruption of loco activity, trying to maintain correct EGFR signalling.

Granderath et al. (2000) showed that the relationship between pointed and loco-c1 transcript is dependent on the gene gem, and that pointed and gem act synergistically to activate loco-c1. In the follicle cells it is loco-c2 that is present. Our evidence suggests that pointed is involved in regulation of loco-c2 in ovarian follicle cells, however, in a manner similar to the regulation of loco-c1 in glial cells, other genes are probably involved in the regulation of loco.

Several different pathways are essential for the anterior-dorsal patterning of the egg. It has recently been illustrated that the operculum is patterned independently and its size can be affected by the genes dpp and bunched (Dobens et al., 2000). In addition an interaction is needed between dpp at the anterior and gurken, the dorsal signal, to form dorsal appendages (Peri and Roth, 2000). It superficially appears that loco affects operculum formation when observing the most severely ventralised eggs. However, the micropyle and a ridge of the operculum similar to that seen normally on the ventral anterior of the egg are visible on a loco ventralised egg. This indicates that the ability to form the operculum is still present, and loco is affecting DV axis determination.

The DV defects in twist expression observed in the embryos of eggs laid by fly line loco371, help clarify the role of loco in oogenesis, showing that disruption of maternal loco in oogenesis results in the disruption of native twist expression, a marker for ventral cell fate, and clear DV defects are observed in the embryos that fail to hatch, as many fail to form normal guts. The range of patterning defects observed are related to the disruption of native twist expression. This suggests maternally expressed loco is required for normal embryonic development. We cannot distinguish if the failure of embryos to develop properly and the observed defects in twist expression in the early embryo result from the mutant follicle cells affecting the developing egg chamber and oocyte or the maternal contribution of loco from the nurse cells deposited in the egg being needed for zygotic development of the D/V axis. However, the twist expression observed only in the activation of the embryo does suggest that disruption of loco in anterior-dorsal follicle cells may affect embryonic patterning. Dorsal follicle cell identity is determined as the follicle cells migrate posteriorly over the egg chamber, coming into contact with the localised gurken signal over the oocyte nucleus. If the EGFR signalling was disrupted in follicle cells during the course of this migration, it would result in an embryo that only had abnormal D/V patterning along part of its AP axis.

3.1. The role of loco in nurse cell cytoplasmic dumping

The small egg phenotype observed in both the mutant lines and heatshock antisense lines indicates that loco is required for cytoplasmic dumping from the nurse cells to the oocyte. Several mutants have been identified that are involved in this process (Mahajan-Miklos and Cooley, 1994), and the phenotypes can be attributed to two defective processes. The first is the failure of the ring canals to grow, restricting the flow of cytoplasm from the nurse cells to the oocyte (Cooley, 1998). The second is a change in the actin
cytoskeleton, with the nurse cells failing to centralise the nurse cell nuclei (Guild et al., 1997). When this happens the nuclei block the ring canals preventing dumping. Which process requires loco during nurse cell dumping remains to be determined.

In this paper, we have identified two roles for the loco gene in oogenesis; cytoplasmic dumping and DV axis formation. Gao mRNA is present in oocyte and nurse cells and Gs protein in follicle cells; Gao mRNA is present in nurse cells and the oocyte, with Gia protein present in stage 10 anterior-dorsal follicle cells and the oocyte (Wolfgang et al., 1991). The expression patterns of the different Gα subunits correlate with the expression patterns of the loco isoforms, further suggesting a role for G-protein signalling in nurse cell dumping and a link between G-protein signalling and the EGFR pathway in follicle cells.

In mammals there are several different Gα subunits, these Gα subunits are also present in Drosophila. In mammals the different Gα subunits are regulated by different RGS proteins. With the Drosophila Genome Project complete we have searched for additional Drosophila RGS genes, but none were found. As different Drosophila G-protein α subunits are likely to need regulation, it may be that the different transcripts of loco regulate different Gα subunits.

4. Experimental procedures

4.1. Stocks

Wild type flies were Or.R. The grkHK and grkWG were provided by Nüsslein-Volhard (Schüpbach, 1987), fsl(Kl10 (Wieschaus et al., 1978) and topl (one allele of EGFR, Schüpbach, 1987). pmtP1UAS, pmtP2UAS were obtained from the Bloomington Stock Center. Df[3R]17D1, Df[3R]15C5E1 and locoP13 were obtained from Christian Klamt. The GAL4 drivers T155 and CU1 and the fly line containing four copies of gurken transgene were obtained from T. Schupbach (Queenan et al., 1997). Neuman-Silberberg and Schüpbach, 1987). All flies were raised on standard cornmeal–yeast–agar medium at 25°C.

4.2. Library screening

Genomic rescued DNA, 2.3 kb, was obtained from fly line C139. This genomic rescued fragment was used to screen a Drosophila CantonS λFix genomic library (Stratagene). Two λ clones were obtained, λ652 and λ653. These were both used to screen an ovarian ZAPII cDNA library (a gift from Y.N. Jan, UCSF, San Francisco, CA, USA). Two cDNAs were obtained, cDNA 96a and 118a, which are 1.7 and 0.8 kb, respectively. Both cDNAs were incomplete and lacked their 3’ end. An expressed sequence tag (EST) database search was carried out with both cDNAs and one EST was identified, LD27000 (Accession No. AA941661). This was sequenced and contained the missing 3’ sequence. RT-PCR was carried out on ovarian tissue to establish the structure of the cDNAs.

4.3. Whole mount in situ hybridisation of ovaries

The whole mount in situ hybridisation was conducted as described by Zhao and Bownes (1999).

4.4. DNA sequencing

The dideoxy chain determination method was used initially in the form of a Sequenase 2.0 kit (US Biochemicals), followed by automated sequencing on Perkin-Elmer ABI 373A and 377A machines using dye labelled primers, then dye labelled terminator reactions. Sequenced fragments were assembled using GCG and GENE-JOCKEY software. Sequence analysis was done with GCG GAP, MAP, FASTA, TFASTA and PILEUP software.

4.5. RT-PCR

RT-PCR was carried out as described by Deng et al. (1999).

4.6. Constructs and P-element mediated germ-line transformation

The complete cDNA 96a was cloned into both pCaSpeR-UAS and pCaSpeRHS in the antisense orientation. P-element mediated germ-line transformation was conducted as described by Deng et al. (1999).

4.7. Antisense analysis

Antisense constructs were made containing antisense core exons 2 and 3 in pCaSpeRhs, (Thummel and Pirrotta, 1991) under heatshock control and in pUAST under UAS control (Phelps and Brand, 1998). Several transgenic fly lines were generated.

The pUAST lines were crossed to the GAL4 follicle cell drivers Cu1 and T155; both these fly lines exhibit GAL4 expression in all follicle cells after stage 8 (Queenan et al., 1997). The GAL4/UAS progeny from the crosses were transferred into a cage on apple juice plates. The eggs on each plate were collected and observed.

For the CaSpeR HS lines, 50–100 flies were raised in each milk bottle at 25°C for 3 days and then transferred into a fresh bottle with yeast paste smeared on top of the cornmeal food and kept at 25°C for 32 h. The flies were then transferred into a cage on apple juice plates, the flies were heat-shocked at 38°C for 40 min. The flies were moved back to 25°C and the apple juice plates changed at 4 h intervals. The eggs on each plate were collected and observed.

4.8. Antibody production

A GST-loco gene-fusion was used to produce protein containing 175 aa of Loco core region (Pharmcia Biotech
gene fusion system. The antibody was raised in sheep at the Scottish Antibody Production Unit.

4.9. Western analysis.

OrR embryos were collected over 24 h periods and were stored at −20°C. loco mutant embryos were collected by selecting unhatched embryos at 26 h. Western blotting and ECL detection were carried out as described in Deng et al. (1999).

4.10. Observation of living embryos

Living mutant and wild type embryos were observed in KELF oil, which allows development to be followed with the chorion intact. This approach was taken as mutant embryos tended to degenerate by the time they should have hatched, making it difficult to determine the primary developmental defects. No defects were observed in wild type embryos.

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