Hrb27C, Sqd and Otu cooperatively regulate gurken RNA localization and mediate nurse cell chromosome dispersion in Drosophila oogenesis

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Summary

Heterogeneous nuclear ribonucleoproteins, hnRNPs, are RNA-binding proteins that play crucial roles in controlling gene expression. In Drosophila oogenesis, the hnRNP Squid (Sqd) functions in the localization and translational regulation of gurken (grk) mRNA. We show that Sqd interacts with Hrb27C, an hnRNP previously implicated in splicing. Like sqd, hrb27C mutants lay eggs with dorsoventral defects and Hrb27C can directly bind to grk RNA. Our data demonstrate a novel role for Hrb27C in promoting grk localization. We also observe a direct physical interaction between Hrb27C and Ovarian tumor (Otu), a cytoplasmic protein implicated in RNA localization. We find that some otu alleles produce dorsalized eggs and it appears that Otu cooperates with Hrb27C and Sqd in the oocyte to mediate proper grk localization. All three mutants share another phenotype, persistent polytene nurse cell chromosomes. Our analyses support dual cooperative roles for Sqd, Hrb27C and Otu during Drosophila oogenesis.

Key words: Drosophila, Oogenesis, hnRNP, Gurken, mRNA localization, Nurse cell nuclear morphology, Hrp48

Introduction

Heterogeneous nuclear ribonucleoproteins (hnRNPs) are RNA-binding proteins that function in a variety of cellular processes such as transcription, splicing, nuclear transport, localization, translation and protein stability (for a review, see Dreyfuss et al., 1993; Krecic and Swanson, 1999; Dreyfuss et al., 2002). HnRNP association is highly dynamic and can change with every step of RNA processing, as required by the specific RNA in the complex. Each mRNA is presumably bound by a unique combination of hnRNPs that ultimately specify its fate by influencing the structure of the RNA and modulating its interactions with trans-acting factors (Dreyfuss et al., 1993; Dreyfuss et al., 2002). Thus, hnRNPs play a crucial role in controlling gene expression.

Squid (sqd), also known as Drosophila hrp40 (Matunis et al., 1992a; Matunis et al., 1992b; Matunis et al., 1994), encodes an hnRNP that has been characterized mainly for its role in dorsoventral (DV) axis formation during oogenesis where it plays an important role in gurken (grk) mRNA localization and protein accumulation (Kelley, 1993; Norvell et al., 1999). All Drosophila hnRNPs identified so far have structural similarities to human hnRNP A/B proteins (Dreyfuss et al., 1993). Sqd contains the common hnRNP structural features (Krecic and Swanson, 1999; Dreyfuss et al., 2002): two RNA-binding domains, auxiliary glycine-rich and M9-like domains, and existence in multiple protein isoforms.

Grk is a TGFα-like ligand that is produced in the oocyte and signals to the EGFR (Epidermal Growth Factor Receptor) expressed in all follicle cells that comprise the epithelium surrounding the germline cells. During mid-oogenesis, establishment of the DV axis of the egg and embryo depends on the precise spatial restriction of grk RNA and protein to the dorsal anterior region of the oocyte to produce localized activation of EGFR (Neuman-Silberberg and Schüpbach, 1993; Neuman-Silberberg and Schüpbach, 1994). In sqd mutants, grk RNA is mislocalized and translated around the entire anterior of the oocyte producing ectopic EGFR activation and induction of excess dorsal cell fates, which results in an expansion of dorsal appendage material around the anterior circumference of the egg (Kelley, 1993). The three Sqd isoforms (A, B and S) are generated by alternative splicing and differ only in their extreme C-terminal regions. They have different subcellular localization patterns and distinct roles in the regulated nuclear export and localization of grk mRNA, as well as in Grk protein accumulation (Norvell et al., 1999). A working model for the role of Sqd in the regulation of Grk expression as proposed by Norvell et al. (Norvell et al., 1999) suggests that SqdS associates with grk RNA in the oocyte nucleus to facilitate regulated nuclear export and RNA localization within the cytoplasm, where SqdA then associates with the grk transcript to facilitate translational regulation. SqdB does not appear to play a role in DV patterning.

To identify proteins that interact with Sqd to function in the regulation of Grk expression, we performed a yeast two-hybrid screen with Sqd and isolated the hnRNP, Hrb27C. We found that hrb27C mutants have DV defects as a result of mislocalized grk RNA. Thus, it appears that Hrb27C and Sqd function together to regulate Grk expression. We have also identified a physical interaction between Hrb27C and Ovarian tumor (Otus). Examination of otu mutants reveals that otu also
plays a role in regulating grk mRNA localization. sqd, hrb27C and otu mutants also share a nurse cell chromosome organization defect, indicating that these proteins function together in other processes during oogenesis. mRNA biogenesis is a multi-step process, presumably involving many trans-acting factors. We report the identification of several proteins that interact with each other and regulate both grk RNA localization and nurse cell chromosome dynamics during oogenesis.

Materials and methods

Yeast two-hybrid screen

The two-hybrid screen was performed using the Matchmaker LexA System (Clontech). The LexA-Sqda bait was constructed by PCR amplification of a fragment from pSCL.3 (Kelley, 1993). The 5′ primer CCC CCC ATG GAA GCC GGA GAA CCA GAT G was used to add an NcoI site 5′ to the third exon, and the 3′ primer was T7. The resulting PCR product was cut using NcoI and XhoI to generate a 566 bp fragment that was cloned into the pLexA vector (Clontech) to create a N-terminal fusion of LexA with amino acids 214-321 of Sqda. The ovarian cDNA prey library, ovo1b, was provided by J. Großhans. The ovarian cDNA prey library, ovo1b, was provided by J. Großhans (Großhans et al., 1999) and 9.7x10^6 colonies were screened. 183 positive colonies were identified and four of these were Hrb27C.

Generation of Sqda antibodies, immunoprecipitations and western analysis

The full-length Sqda-GST fusion described in Norvell et al. (Norvell et al., 1999) was purified and used for mouse monoclonal antibody production. Immunoprecipitations were performed according to Van Buskirk et al. (Van Buskirk et al., 2000) with the following modifications: a complete mini protease inhibitor cocktail tablet (Roche) was used in lieu of other protease inhibitors in the lysis buffer, 1U/µl RNase inhibitor (Roche) was added to the lysis buffer, lysates were not pre-cleared with pre-immune serum coated beads, and lysates were rotated with the antibody coated beads for 60 minutes at 4°C. The following antibodies were used: monoclonal anti-Sqda serum (8F3; 3:10 dilution); monoclonal anti-Tubulin (1:250 in TBST + 5% milk; Sigma T-9026). HRP-anti guinea pig or HRP anti-mouse (1:500 in TBST + 5% milk) or monoclonal anti-Tubulin (1:250 in TBST + 5% milk; Sigma T-9026). HRP-anti guinea pig or HRP anti-mouse (Jackson ImmunoResearch) was used at 1:2000 in TBST.

Fly stocks

The following hrb27C alleles were generously provided by Don Rio and the Bloomington Stock Center: hrb27C [10280, rF680, k16303, k10413, 02647, k02814]. The following alleles are lethal P-element insertions at various distances from the coding region: hrb27C[90280] (1.5 kb), hrb27C[rF680] (1.8 kb), hrb27C[k16303] (2.2 kb), hrb27C[k10413] (2.2 kb) and hrb27C[02647] (3.3 kb) (Hammond et al., 1997). There are no molecular data on hrb27C[90280], hrb27C[k16303] is an EMS allele produced by Mary Lilly, hrb27C FRT alleles (FRT40A-377, rF680, -02647, -10280, -k02814) alleles were generously provided by Mary Lilly. The FLP-DFS (yeast flipase recombination target-site specific recombinase-dominant female sterile) system described by Chou and Perrimon (Chou and Perrimon, 1992; Chou and Perrimon, 1996) was used to generate germline clones of hrb27C. Progeny from yw hsFLP; ovd FRT40A/CyO × FRT40A-Hrb27C (x – one of the alleles listed above) were heat shocked at 37°C for 2 hours a day for 3 days during the second and third larval instar. The sqd allele is a P-element insertion that specifically disrupts germline expression during mid-oogenesis (Kelley, 1993; Matunis et al., 1994). The isofom specific transgenes of sqd in a sqd mutant background were described in Norvell et al. (Norvell et al., 1999). The otu alleles and Df(1)R42/FM7t, which uncovers otu, were obtained from the Bloomington Stock Center. hp6 (Van Buskirk and Schüpbach, 2002) was the allele used for Df-PCR and western analysis. Otu104 flies that carry a transgene expressing only the 104 kDa isoform of Otu under the control of the otu promoter (Sasu et al., 1995) were provided by Lillie Searles.

In situ hybridization

Ovaries were dissected in PBS and fixed for 20 minutes in 4% paraformaldehyde in PBS with Heptane and DMSO. Subsequent steps were performed as previously described (Tautz and Pfeifle, 1989) using a grk RNA probe.

Immunohistochemistry

Ovaries were fixed for 20 minutes in 4% paraformaldehyde in PBS plus Heptane. After several rinses in PBST (PBS + 0.3% Triton), ovaries were blocked for 1 hour in 1% BSA + 1% Triton. After a 1 hour incubation in a 1:10 dilution of monoclonal anti-Grk sera (ID12) (Queenan et al., 1999) in PBST, the ovaries were washed in PBST overnight at 4°C. AlexaFluor 568-conjugated anti-mouse secondary (Molecular Probes) was used at 1:1000 in PBST. During secondary incubation, DNA was stained with 1:10,000 Hoechst (Molecular Probes). For DNA stain alone, ovaries were dissected and fixed as described above, incubated in 1:10,000 Hoechst for 1 hour, washed and mounted. Only stage 6 and older egg chambers were counted to assay the nurse cell phenotype.

UV cross-linking analysis

Fresh ovarian lysate was prepared according to Norvell et al. (Norvell et al., 1999) with the addition of a complete mini protease inhibitor tablet (Roche) to the lysis buffer. Radiolabeled RNA probes were made according to Norvell et al. (Norvell et al., 1999) using 1 µg of linearized (HindIII for grk and osk, XbaI for nos) DNA template. The templates for transcription include the 158 bp HincII-HindIII fragment from grk genomic DNA cloned into pBS, the 126 bp EcoRI-DraI fragment from osk genomic DNA cloned into pBS, and the nos-6 construct (Gavis et al., 1996). Unlabelled competitor RNAs were synthesized using Ampliscribe in vitro transcription system (Epicenter) and the final product was purified by phenol extraction and ethanol precipitation. For the binding reaction, lysate equivalent to approximately three ovaries was incubated with 1.5 µl of 10× binding buffer [500 mM Tris-HCl (pH 8.3), 750 mM KCl, 30 mM MgCl2], probe (5x10^5 to 1x10^7 cpm), and water to a final volume of 15 µl. The reactions were incubated for 15 minutes on ice, crosslinked on ice at 999 m in a Stratamax UV croslinker. The probe was digested for 15 minutes at 37°C with 7 units of RNase ONE (Promega) and 1 unit of RNase H (Roche). The immunoprecipitations were performed after RNase digestion, by incubation of the entire reaction with antibody-coated [anti-Hrp48 or anti-Cy5E (Santa
consistent with dorsalization. For two of the stronger alleles, the different classes of abnormal eggshell phenotypes are completely dorsalized eggs in the stronger alleles (Fig. 2A–D). Ranging from wild-type morphology in the weaker alleles to disrupted in their germline display a variety of phenotypes, Perrimon, 1996). Eggs laid by females that have Hrb27C, the FLP-DFS system (Chou and Perrimon, 1992; Chou and Hammond et al., 1997), we made germline clones using sqd1 mutations during oogenesis, To assess the effects of hrb27C mutants affect DV axis formation

hhrb27C mutants affect DV axis formation

To assess the effects of hrb27C mutations during oogenesis, we analyzed seven alleles of hrb27C. As hrb27C is an essential gene (Hammond et al., 1997), we made germline clones using the FLP-DFS system (Chou and Perrimon, 1992; Chou and Perrimon, 1996). Eggs laid by females that have Hrb27C disrupted in their germline display a variety of phenotypes, ranging from wild-type morphology in the weaker alleles to completely dorsalized eggs in the stronger alleles (Fig. 2A–D). The different classes of abnormal eggshell phenotypes are consistent with dorsalization. For two of the stronger alleles, hrb27C602814 and hrb27C166509, the observed DV defects range from being slightly dorsalized, with an expansion of the operculum (Fig. 2B), to a crown of appendage material (Fig. 2D), similar to eggs laid by strong sqd mutants (sqd1) (Kelley, 1993). We also observed intermediate phenotypes with a broad/fused appendage that spans at least the width of the eggshell occupied by wild-type appendages (Fig. 2C). As observed in sqd1 mutants, most of the eggs were short, which is probably because of a failure to transfer all the nurse cell cytoplasmic contents to the oocyte prior to egg deposition.

To determine whether the observed dorsalized eggshell phenotypes of hrb27C are a result of defects in grk expression, we analyzed grk mRNA localization by in situ hybridization in ovaries from females whose germline was mutant for hrb27C. In wild-type stage 9 egg chambers, grk mRNA is localized to the region overlying the oocyte nucleus. Grk protein is also restricted to this same region and dorsal cell fates are induced by a local activation of EGFR in the overlying follicle cells (Neuman-Silberberg and Schüpbach, 1993; Neuman-Silberberg and Schüpbach, 1994) (Fig. 2E,G). In hrb27C mutants, we observed defects in grk RNA localization that varied depending on the strength of the allele. In the weaker mutants, all of the RNA was properly localized at stage 9, while in two of the stronger mutants, hrb27C166509 and hrb27C277, 26% (n=23) and 12% (n=67), respectively, of stage 9 egg chambers showed grk mRNA mislocalized in an anterior ring (Fig. 2F). Thus, it seems that Hrb27C is involved in the proper localization of grk mRNA to the dorsal anterior region of the oocyte.

As Sqd plays a role in both RNA localization and translational control, our findings raise the possibility that the splicing of grk is directly linked to localization, or, the model we favor, that Hrb27C has functions in oogenesis other than splicing.

**Fig. 1.** Sqd and Hrb27C interact. (A) A schematic of the SqdA protein [321 amino acids (aa)] containing two RNA-binding domains (RRMs) (striped boxes), an M9-like nuclear transport motif (black box) and a glycine rich C-terminal region (hatched box). The underlined region represents the region used as bait in the yeast two-hybrid screen. The Hrb27C protein (422 aa) also contains two RNA-binding motifs (striped boxes). We isolated four different clones of Hrb27C: two contain all but the first 11 amino acids, one contains all but the first 28 amino acids and one is truncated to exclude the first 109 amino acids (underlined). (B) The Hrb27C-activation domain (AD) fusion interacts with the LexA-SqdA fusion but not with LexA alone or a LexA-p53 fusion. The AD alone does not interact with any LexA fusion proteins. (C) Western blot probed for Hrb27C and Sqd after immuno precipitation (IP) from ovarian lysate with either Sqd or SpnF antibody in the absence (−) or presence (+) of RNase A. Hrb27C co-purifies in an RNA-dependent manner with Sqd but not SpnF. WCL, whole cell lysate (one-tenth volume).
regulation of grk RNA (Norvell et al., 1999), we wanted to know if the same was true for Hrb27C. To determine if the mislocalized RNA in hrb27C mutants is translated, we analyzed Grk protein expression by whole-mount antibody staining. We did observe egg chambers where Grk was mislocalized throughout the oocyte cytoplasm and in a ring around the entire anterior of the oocyte (Fig. 2I), indicating that at least in some cases, mislocalized grk RNA is translated in the absence of Hrb27C. In many egg chambers, Grk was diffuse throughout the oocyte with an enrichment in the dorsal anterior region, but we also observed some egg chambers where Grk protein was localized normally (Fig. 2G,H). However, the occasional observation of Grk protein on the anterior region, but we also observed some egg chambers where Grk protein was localized normally (Fig. 2G,H). The genetic and physical interactions of Sqd and Hrb27C

Hrb27C binds to grk RNA

The genetic and physical interactions of Sqd and Hrb27C suggest that these two proteins function together to regulate grk mRNA localization. As Sqd can bind to grk RNA (Norvell et al., 1999) and Hrb27C interacts with Sqd, we wanted to determine whether Hrb27C is able to bind to grk RNA. By performing UV crosslinking analysis in ovarian lysate using a small proportion of the grk 3′UTR (Fig. 3A) as a probe, we observed an interacting protein with a molecular weight (approximately 48 kDa) that is consistent with that of Hrb27C. We confirmed the identity of this protein by specifically immunoprecipitating it with Hrb27C antibodies and not with control antibodies (Fig. 3B). As a positive control, we performed the same experiments with the AB region of the osk 3′UTR (Fig. 3A) (Kim-Ha et al., 1995) which has previously been shown by Gunkel et al. (Gunkel et al., 1998) to bind p50, recently identified as Hrb27C (T. Yano, S. Lopez de Quinto, A. Shevenchenko, A. Shevenchenko, T. Matsui and A. Ephrussi, personal communication). Furthermore, Hrb27C

Table 1. hrb27C enhances the dorsoized phenotype of sqd mutants

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<th>Genotype</th>
<th>% Eggshell phenotype</th>
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<td>Wild type</td>
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<tr>
<td>sqd/sqd&lt;sup&gt;12&lt;/sup&gt;</td>
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<tr>
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<td>97.7</td>
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<td>97.6</td>
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<td>hrb27C&lt;sup&gt;10413&lt;/sup&gt;/hrb27C&lt;sup&gt;16203&lt;/sup&gt;, sqd&lt;sup&gt;1&lt;/sup&gt;/sqd&lt;sup&gt;12&lt;/sup&gt;</td>
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<td>hrb27C&lt;sup&gt;10413&lt;/sup&gt;/hrb27C&lt;sup&gt;20647&lt;/sup&gt;, sqd&lt;sup&gt;1&lt;/sup&gt;/sqd&lt;sup&gt;12&lt;/sup&gt;</td>
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The percentage of dorsoized eggshell phenotypes observed from females transheterozygous for sqd, transheterozygous for hrb27C or transheterozygous for both.
does not interact with the 3' UTR of nanos (nos) and no proteins are precipitated by the Hrb27C antibody after crosslinking with nos probe (Fig. 3B). Purified GST-Hrb27C can be crosslinked to the same region of the 3' UTR of grk, while other GST fusions are not able to bind to grk RNA (data not shown). Finally, to demonstrate the specificity of the Hrb27C interaction with grk RNA and to confirm that the same protein binds to both grk and osk UTRs, we performed UV crosslinking in the presence of cold competitor RNAs. For these experiments, the 3' UTR regions of grk and osk that were previously used as probes were added as unlabeled competitors prior to addition of the labeled osk 3' UTR probe. Hrb27C is completely competed away from osk RNA by addition of 200-fold excess grk 3' UTR but not by the nos 3' UTR (Fig. 3C). The same results were obtained using grk as the probe and osk as the competitor (data not shown). Together, these data indicate that Hrb27C can specifically bind to grk RNA and suggest that a complex containing Sqd and Hrb27C binds to grk RNA to promote RNA localization and translational regulation of Grk.

**Nurse cell chromosomes of sqd and hrb27C mutants fail to disperse**

We have also detected a phenotype earlier in oogenesis that is shared by both sqd and hrb27C mutants, raising the possibility that the two proteins participate in multiple processes during oogenesis. In wild-type oogenesis, the nurse cell chromosomes undergo several cycles of endoreplication that result in chromatids that are in tight association, otherwise known as polytene. Prior to their dispersal, the chromosomes take on a characteristic blob-like appearance and by stage 6, they are completely dispersed (King, 1970; Dej and Spradling, 1999) (Fig. 4A,B). In both sqd and hrb27C mutants, the nurse cell chromosomes fail to completely disperse and remain in the blob-like polytene conformation (Fig. 4C,D). Strong alleles of sqd (sqd1) and germline clones of a null allele, sqdK12, have nurse cell chromosomes that are arrested in the blob-like conformation, whereas the nurse cell chromosomes of the hypomorphic allele, sqdK12, disperse properly. Germline clones of all lethal hrb27C alleles and some of the viable transheterozygous allele combinations display some degree of polytene chromosome morphology (Fig. 4D). The sqd1/sqdK12 allele combination and other viable transheterozygous hrb27C allele combinations (hrb27C10280/hrb27C410413, hrb27C10280/hrb27C416303) have nurse cell chromosomes that disperse properly. Interestingly, when sqd1/sqdK12 is combined with the transheterozygous hrb27C allele combinations that disperse normally, the nurse cell chromosomes of the double mutants become arrested in the blob-like conformation and fail to disperse.

To determine the role of the Sqd isoforms in the dispersion of the nurse cell chromosomes, we assayed the ability of genomic cDNA transgenes that express one particular Sqd isoform (Norvell et al., 1999) to rescue the nurse cell phenotype of sqd1 mutants. Expressing either two copies of SqdA, SqdB or SqdS in a sqd1 background partially rescues the nuclear morphology from only 3% wild type to 14%, 54% or 61% wild type, respectively (Fig. 4E). These data suggest that each isoform is able to participate in regulating nurse cell chromosome morphology. Whereas SqdS and SqdA play the major roles in establishing the DV axis (Norvell et al., 1999), SqdS and SqdB, the two isoforms found in nuclei, have the largest effects in regulating nurse cell chromosome morphology. Consistent with the distinct yet overlapping function of the isoforms described by Norvell et al. (Norvell et al., 1999), expressing one copy of each of two different isoforms is able to rescue the nurse cell nuclear morphology better than expressing two copies of the same isoform. SqdA/SqdB rescues 96%, SqdB/SqdS rescues 96% and SqdS/SqdA rescues 92% of the nurse cell nuclear morphology to wild type (Fig. 4E).

**The ovarian tumor gene can rescue the nurse cell nuclear morphology of sqd mutants**

Nurse cell chromosomes that fail to disperse are also observed in certain alleles of ovarian tumor (otu) (King et al., 1981; King and Storto, 1988; Heino, 1989; Mal’ceva and Zhimulev, 1993; Heino, 1994; Mal’ceva et al., 1995). otu produces two protein isoforms, Otu98 and Otu104, by alternative splicing of a 126 bp exon. Genetic and molecular analyses reveal distinct requirements for each isoform during oogenesis (Storto and King, 1988; Steinhauer and Kalfayan, 1992; Sass et al., 1995; Tirronen et al., 1995). In particular, a mutant that specifically disrupts the Otu104 product has persistent polytene nurse cell chromosomes, suggesting that the 98 kDa Otu isoform is not capable of mediating wild-type chromosome dispersion (Steinhauer and Kalfayan, 1992). This phenotype was also described for mutants in half pint (hfp; pU668 – FlyBase). Hfp encodes a polyU-binding factor and plays an important role in the alternative splicing of otu.

![Fig. 3. Hrb27C can bind to the 3' UTR of grk. (A) Schematics of the entire 3' UTR of grk, osk and nos with the regions used as probes or competitors underlined. (B) UV crosslinking analysis of ovarian proteins that can interact with grk, osk or nos. The banding profiles reveal that the same proteins bind to grk and osk RNAs, but these proteins do not bind to nos RNA. The identity of the protein that binds to grk and osk is Hrb27C because it can be immunoprecipitated with Hrb27C antibodies, but not with CycE antibodies. (C) UV crosslinking analysis of osk (labeled probe) in the presence of grk, osk (positive control) or nos (negative control) as unlabelled competitor. A 200-fold excess grk or osk is able to compete binding of Hrb27C (arrow) from osk, while excess nos is not.](image-url)
In hfp mutants, there is a dramatic decrease in the levels of the Otu104-encoding transcript as seen by RT-PCR analysis of germarial RNA, and Otu104 is not detectable on a western blot. The nurse cell phenotype of hfp mutants can be rescued by a transgene that expresses the 104 kDa Otu isoform under the control of the otu promoter (Van Buskirk and Schüpbach, 2002). To determine whether defects in Otu104 cause the polytene phenotype of sqd mutants, we assayed the ability of the Otu104 transgene to rescue this defect in sqd mutants. In sqd mutants, 98% of the egg chambers from sqd1 mutants and from sqd2 mutants carrying transgenes expressing the specified Sqd isoforms (A, B or S) (n>400 for each genotype) (E). The percentage of polytene nurse cell nuclei in stage 6 and later egg chambers from sqd1 mutants and from sqd2 mutants carrying one (n=339) or two copies (n=818) of the Otu104 transgene. (G) RT-PCR analysis of otu transcripts in previtellarial egg chambers. Although the larger otu transcript is absent from hfp mutants, it is present in sqd mutants. (H) Western analysis using an Otu antibody of previtellarial egg chambers from wild type (WT), sqd1 and hfp mutants. sqd mutants show a reduction in the amount of the 104 kDa Otu isoform. Western analysis of the samples using a Tubulin antibody reveals equal loading of the sqd and wild-type samples.

As Otu104 can rescue the nurse cell phenotype of both hfp and sqd, we asked whether sqd affects the alternative splicing of otu, as is the case for hfp mutants. RT-PCR analysis of RNA isolated from sqd1 germaria reveals that otu is properly spliced in sqd mutants (Fig. 4G). To determine if Otu104 protein accumulates properly in sqd1 mutants, we performed a western blot on extracts prepared from germaria of wild-type and sqd1 mutant females. Western analysis reveals that although both Otu isoforms are present in sqd1; the level of the 104 kDa isoform appears reduced in sqd1 mutants compared with wild type (Fig. 4H). Though the decrease in the levels of Otu104 observed in sqd1 mutants is not as striking as that seen in hfp mutants, the decrease is consistent over many experiments. As a single copy of Otu104 can rescue the nurse cell phenotype of sqd mutants (Fig. 4F), and the polytene nurse cell phenotype is observed in females heterozygous for a deficiency that removes otu and even in females heterozygous for the Otu104-specific mutants, otu11 or otu13 (data not shown), it seems that the level of Otu104 is crucial for proper nurse cell chromosome dispersion.

Given that hrb27C mutants share the polytene nurse cell chromosome phenotype of sqd mutants, we assayed the
ability of two copies of Otu104 to rescue the phenotype of a viable transheterozygous combination of hrb27C (hrb27C377/hrb27C62647). While the Otu104 rescue of the hrb27C phenotype was not as complete as that of sqd1 mutants, we consistently observed a qualitatively improved (less blob-like) nuclear morphology. The Otu104-partial rescue of the nurse cell dispersion defect of hrb27C suggests that both Sqd and Hrb27C may act with or through Otu104 to regulate chromosome dispersal.

**Otu interacts with Hrb27C and affects DV patterning**

As **otu** mutants share a similar nurse cell nuclear morphology defect with **sqd** and **hrb27C**, we tested whether Otu physically interacts with these proteins. Although we have not been able to detect a physical interaction between Sqd and Otu, we do detect a physical interaction between Otu and Hrb27C by co-immunoprecipitation (Fig. 5A). This interaction is RNA independent as RNAse treatment of the lysate prior to immunoprecipitation does not disrupt it (data not shown). It is therefore possible that Otu could be part of the same complex with Sqd and Hrb27C through its interaction with Hrb27C. To evaluate a potential role for Otu in **grk** regulation, we analyzed the eggshell phenotype of eggs laid by **otu** and **otu** mutant females. Indeed, although only a few mature eggs are produced, some of these eggs are clearly dorsalized with a crown of dorsal appendage material (Fig. 5B). **otu** mutant eggs show a range of dorsalization similar to the phenotypes of **hrb27C** mutants (see Fig. 2). We also assessed **grk** RNA localization in **otu** mutants by in situ hybridization and found that **grk** RNA is mislocalized in 34% (n=92) of the stage 9 egg chambers (Fig. 5C). **grk** RNA is also mislocalized in egg chambers from **otu** mutant females. Additional support for the role of Otu cooperating with Sqd in regulating Grk expression derives from the fact that eggs laid by females expressing two to four additional copies of Otu104 in a **sqd** mutant background have extra appendage material, but not a complete crown (data not shown). These results suggest that Otu could be in a complex with Hrb27C and Sqd that regulates **grk** RNA localization and potentially translational regulation.

Collectively, the data presented here suggest that Otu, Hrb27C and Sqd function in two different cell types in at least two processes during oogenesis. Interestingly, there seem to be different requirements for Sqd and Otu depending on the cell type. In the nurse cells, Otu seems to be essential as expressing additional copies of Otu104 rescues the Otu104 reduction seen in **sqd** mutants (data not shown) and rescues the nurse cell chromosome morphology defect. In the oocyte, Sqd is essential for proper **grk** RNA localization. Here, extra copies of Otu104 only partially alleviate the DV defects of the **sqd** mutation. Thus, it seems that specific interacting factors make differential contributions to the coordinated function of these proteins in various cell types.

**Discussion**

The important roles of nuclear RNA-binding proteins in the regulation of gene expression (for a review, see Dreyfuss et al., 2002) are becoming increasingly evident as more protein complexes and their RNA targets are identified. Some hnRNPs can play multiple roles in the processing of a single RNA target; for example, in vertebrates, hnRNP A2 has been implicated in the nuclear export, cytoplasmic localization and translational regulation of myelin basic protein (for a review, see Carson et al., 2001). In Drosophila, the hnRNP Sqd has been shown to regulate one of its target RNAs, grk, at the level of localization as well as translational regulation (Norvell et al., 1999). Identification of the various partners that cooperate with Sqd should allow us to understand how one particular hnRNP can play such diverse roles in various cellular environments.

**Hrb27C and Sqd interact and regulate the localization of grk mRNA**

We have identified a physical and genetic interaction between Hrb27C and Sqd. The two proteins were previously biochemically purified as part of an hnRNP complex from Drosophila cells (Matunis et al., 1992a; Matunis et al., 1992b), but it was not known if they interact directly nor had their RNA targets been isolated. We originally identified the interaction in a two-hybrid screen and we have confirmed it biochemically by co-immunoprecipitation. In vivo, this interaction requires the presence of RNA; this result was unexpected because the yeast two-hybrid constructs that originally revealed the interaction did not contain the RRMs and presumably cannot bind RNA. The interaction may require the full-length proteins to be in unique conformations that are achieved only when they are bound to RNA. The truncated proteins used in the yeast two-hybrid screen may be folded in such a manner that the protein-protein interaction domains are exposed even in the absence of RNA binding, making it possible for the interaction to occur in yeast.

We also observed a striking genetic interaction between Sqd and Hrb27C; weak hrb27C mutants can strongly enhance the DV defects of weak sqd mutants. This suggests that the
physical interaction has in vivo significance. The phenotypes of sqd and hrb27C place both proteins in a pathway required for proper grk localization and suggest a previously undetected role for Hrb27C. hrb27C mutants lay variably dorsIALIZED eggs, and in situ hybridization analysis reveals that grk RNA is mislocalized. As the mislocalized RNA in hrb27C mutants is translated, causing a dorsализed egg phenotype, it is likely that Hrb27C also functions with Sqd in regulating Grk protein accumulation. A role in the regulation of RNA localization and translation is novel for Hrb27C/Hrp48; it has been previously described as functioning in the inhibition of IVS3 splicing of P-element encoded transposase (Siebel et al., 1994; Hammond et al., 1997). Hrb27C has nuclear functions and has been observed in the nucleus and cytoplasm of somatic and germline cells in embryos (Siebel et al., 1995). As Sqd is localized to the oocyte nucleus (Matunis et al., 1994) where it is thought to bind grk RNA (Norvell et al., 1999), we favor a model where Hrb27C and Sqd bind grk RNA together and are exported possibly as a complex into the cytoplasm.

Two unpublished studies have implicated Hrb27C in osk RNA localization (J. Huynh, T. Munro, K. Litière-Smith and D. St Johnston, personal communication) and translational regulation (T. Yano, S. Lopez de Quinto, A. Shevchenko, A. Shevchenko, T. Matsui and A. Ephrussi, personal communication). Translational repression of osk RNA until it is properly localized is essential to prevent disruptions in the posterior patterning of the embryo (Gavis and Lehmann, 1992; Gavis and Lehmann, 1994; Kim-Ha et al., 1995; Webster et al., 1997). An analogous mechanism of co-regulation of mRNA localization and translation appears to control Grk expression. Certain parallels between osk and grk regulation are very striking. Both RNAs are tightly localized and subject to complex translational regulation; they also share certain factors that mediate this regulation. In addition to Hrb27C, the translational repressor Bruno appears to be a part of the regulatory complexes that are required for the proper expression of both RNAs (Kim-Ha et al., 1995; Webster et al., 1997; Norvell et al., 1999; Filardo and Ephrussi, 2003). It will be interesting to determine if there are other shared partners that function in the regulation of both RNAs, as well as identity the factors that give each complex its localization specificity.

Otu plays a role in grk RNA localization and interacts with Hrb27C

Otu is also involved in the localization of grk mRNA and interacts physically with Hrb27C. Though a definitive role of Otu in regulating Grk expression has not been previously described, Van Buskirk et al. (Van Buskirk et al., 2002) found that four copies of Otu104 are able to rescue the grk mRNA mislocalization defect of hfp mutants. Our analysis of the hypomorphic alleles, otu1 and otu11, reveals a requirement for Otu in localizing grk RNA for proper DV patterning. Alternative splicing of the otu transcript produces two protein isoforms: a 98 kDa isoform and a 104 kDa isoform that differ by the inclusion of a 126 bp alternatively spliced exon (6a) in the 104 kDa isoform (Steinhauser and Kalfayan, 1992). This alternatively spliced exon encodes a tudor domain, a sequence element present in proteins with putative RNA-binding abilities (Ponting, 1997). Interestingly, the otu11 allele, which contains a missense mutation in exon 6a (Steinhauser and Kalfayan, 1992), shows the grk localization and dorsализation defect, strongly suggesting that the tudor domain of Otu plays an important function in grk localization. As otu mutants also show defects in osk localization (Tirronen et al., 1995), it appears that like several other factors, Otu is required for both grk and osk localization. Additionally, Otu has been isolated from cytoplasmic mRNP complexes (Glenn and Searles, 2001).

Hrb27C, Sqd and Otu function in nurse cell chromosome regulation

Surprisingly, we found an additional shared phenotype of hrb27C, sqd and otu mutants. During early oogenesis, the endoreplicated nurse cell chromosomes are polytene. As they begin to disperse, the chromosomes are visible as distinct masses of blob-like chromat in that completely disperse by stage 6 (King, 1970; Dej and Spradling, 1999). The formation of polytene nurse cell chromosomes is due to the endocycling that occurs during early oogenesis (Dej and Spradling, 1999) (for a review, see Edgar and Orr-Weaver, 2001). The mechanism of chromosome dispersal is hypothesized to involve the degradation of secu in the anaphase-promoting complex/cyclosome as a result of separase activity that cleaves cohesin (Kashevsky et al., 2002) (for a review, see Nasmyth et al., 2000). The significance of chromosome dispersion is not clear, but Dej and Spradling (Dej and Spradling, 1999) suggest that it could facilitate rapid ribosome synthesis. A defect in the dispersal of polytene chromosomes has been previously described for otu mutants (King et al., 1981; King and Storto, 1988), and we have found that both sqd and hrb27C mutants also have nurse cell chromosomes that fail to disperse. Weak double transheterozygous allele combinations of sqd and hrb27C produce the persistent polytene nurse cell chromosome phenotype that is not observed in either of the weak mutants alone. Thus, genetic and physical interactions between these gene products suggest that they function together in regulation of this process.

The failure to disperse nurse cell chromosomes has also been observed in mutants of hfp where the nurse cell nuclear morphology defect is due to improper splicing of Otu104 (Van Buskirk and Schüpbach, 2002). As was shown for hfp, expressing Otu104 in a sqd mutant background is able to rescue the polytene nurse cell chromosome phenotype. Although Hfp affects otu splicing, it is not clear how Sqn functions to mediate this phenotype, but evidence supports a role in Otu104 protein accumulation. The transcript that encodes Otu104 is clearly present in sqd mutants, as assayed by RT-PCR, but the level of Otu104 protein is decreased. Our results suggest that the level of Otu104 is crucial to maintaining proper nurse cell chromosome morphology as the polytene phenotype of sqd mutants can be rescued by expressing only one extra copy of Otu104 and the majority of egg chambers from females heterozygous for otu13, otu11, or a deficiency lacking otu, have nurse cell chromosomes that fail to disperse.

The reduced level of Otu104 in sqd mutants raises the possibility that Sqd could translationally regulate otu RNA and that the polytene nurse cell chromosome phenotype may be a result of the decreased level of Otu104. Alternatively, Sqd and Hrb27C could form a complex that recruits and stabilizes Otu104 protein, and this complex in turn functions directly or indirectly to regulate chromosome dispersal. An indirect role seems more likely, given that Otu has never been observed in the nucleus (Steinhauser and Kalfayan, 1992). As Otu104 can rescue the phenotype of sqd mutants and we can co-precipitate
Otu and Hrb27C, it seems plausible that Sqd and Hrb27C interact with Otu in the nurse cell cytoplasm to affect an RNA target that could then mediate chromosome dispersion.

**Model for a RNP complex containing Sqd, Hrb27C, and Otu**

Our genetic data support a model in which Sqd, Hrb27C, and Otu function together in a complex that affects at least two processes during oogenesis: DV patterning within the oocyte and mediation of nurse cell chromosome dispersion. Although our biochemical data are consistent with this model, it is also possible that Hrb27C and Sqd could form a complex that is distinct from a complex containing Hrb27C and Otu. However, the in vivo genetic interactions and mutant phenotypes reveal that all three proteins affect both processes and lead us to favor a model in which all three proteins function in one complex.

Our results allow us to expand upon the model proposed by Norvell et al. (Norvell et al., 1999) for the regulation of grk mRNA expression (Fig. 6). Sqd and Hrb27C associate with grk RNA in the oocyte nucleus. Hrb27C and Sqd remain associated with grk in the cytoplasm where Otu and possibly other unidentified proteins associate with the complex as necessary to properly localize, anchor and translationally regulate grk RNA. A likely candidate to be recruited to the complex is Bruno, which interacts with Sqd (Norvell et al., 1999).

Although we do not know the RNA target of Sqd, Hrb27C and Otu in the nurse cells, the proteins could form a complex composed of different accessory factors to regulate localization and/or translation of RNAs encoding proteins that affect chromosome morphology.

Although Hrb27C, Sqd and Otu function together to affect different processes in the oocyte and the nurse cells, they probably function to mediate the precise spatial and temporal regulation of a target RNA that is unique to each cell type where the presence of additional factors would provide specificity to each complex. The importance of the precise localization and translational regulation of grk is well defined, and we have now identified Hrb27C and Otu as additional proteins that facilitate these processes. The transition from polytene to dispersed chromosomes in the nurse cells is less well characterized, but most probably requires precise spatial and temporal regulation as well. A complex containing Sqd, Hrb27C and Otu could function to ensure that the target RNA is properly localized and functional in the nurse cells only at the proper stage of development to promote chromosome dispersal.

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