Loss of the extraproteasomal ubiquitin receptor Rings lost impairs ring canal growth in *Drosophila* oogenesis

Tobias Morawe, Mona Honemann-Capito, Walter von Stein, and Andreas Wodarz

Abteilung Stammzellbiologie, Forschungszentrum der Deutschen Forschungsgemeinschaft für Molekularphysiologie des Gehirns, Georg-August-Universität Göttingen, 37077 Göttingen, Germany

In *Drosophila melanogaster* oogenesis, there are 16 germline cells that form a cyst and stay connected to each other by ring canals. Ring canals allow the cytoplasmic transport of proteins, messenger ribonucleic acids, and yolk components from the nurse cells into the oocyte. In this paper, we describe the protein Rings lost (Rngo) and show that it is required for ring canal growth in germline cysts. *rngo* is an essential gene, and germline clones of a *rngo*-null allele show defects in ovary development, including mislocalization of ring canal proteins and fusion of germline cells. Rngo appears to be a ubiquitin receptor that possesses a ubiquitin-like domain, a ubiquitin-associated domain, and a retroviral-like aspartate protease (RVP) domain. Rngo binds to ubiquitin and to the 26S proteasome and colocalizes with both in germline cells, and its RVP domain is required for dimerization of Rngo and for its function in vivo. Our results thus show, for the first time, a function for a ubiquitin receptor in *Drosophila* development.

Introduction

Germline cells of many species ranging from insects to mammals develop as syncytia (Matova and Cooley, 2001). This is also the case in *Drosophila melanogaster* oogenesis, in which germline cells stay connected by intercellular bridges, so-called ring canals. In the germarium of the *Drosophila* ovary, a germline stem cell divides asymmetrically to produce a daughter stem cell and a daughter cystoblast. The cystoblast undergoes four rounds of mitosis with incomplete cytokinesis, generating a 16-cell cyst with 15 nurse cells and one oocyte (Ong and Tan, 2010). The polyploid nurse cells contribute mRNAs, proteins, and organelles to the oocyte. Actin filaments are recruited to the ring canals together with several actin-binding proteins and proteins phosphorylated at tyrosine residues (phosphotyrosine [PY]). Hu-li tai shao–ring canal (Hts-RC) and Filamin also localize to the ring canals in a strictly controlled manner. Later, ring canals are further stabilized by the actin-bundling protein Kelch (Kel; Xue and Cooley, 1993; Kelso et al., 2002). Kel interacts with the ubiquitin E3 ligase Cullin-3, and both are essential for the growth of ring canals (Hudson and Cooley, 2010).

During the growth and expansion of the ring canals, proteins involved in ring canal assembly and maturation are subject to rapid turnover. One way to increase the turnover of proteins is by their degradation by the ubiquitin–proteasome system. Ubiquitinated proteins can be directly recognized by subunits of the 26S proteasome or by so-called ubiquitin receptors, which shuttle the ubiquitinated proteins to the proteasome. Ubiquitin receptors bind to ubiquitin via their ubiquitin-associated (UBA) domain and to the proteasome via their ubiquitin-like (UBQ) domain (Schauber et al., 1998; Bertolaet et al., 2001; Grabbe and Dikic, 2009).

In this paper, we present a molecular and phenotypic analysis of the *Drosophila* ubiquitin receptor CG4420, which we have named Rings lost (Rngo) according to its mutant phenotype in oogenesis. Like Ddi1/Vsm1, its homologue in yeast (Liu and Xiao, 1997; Lustgarten and Gerst, 1999), Rngo possesses

Correspondence to Andreas Wodarz: awodarz@gwdg.de

W. von Stein's present address is Miacom Diagnostics GmbH, 40225 Düsseldorf, Germany.

T. Morawe's present address is University Medical Center, Johannes-Gutenberg University, Institute for Pathobiochemistry, 55099 Mainz, Germany.

Abbreviations used in this paper: Cher, Cheerio; FL, full length; Hts-RC, Hu-li tai shao–ring canal; IP, immunoprecipitation; Kel, Kelch; MBP, maltose-binding protein; PY, phosphotyrosine; Rngo, Rings lost; RVP, retroviral-like aspartate protease; UAS, upstream activating sequence; UBA, ubiquitin associated; UBQ, ubiquitin-like.

The Rockefeller University Press $30.00
J. Cell Biol. Vol. 193 No. 1 71–80
www.jcb.org/cgi/doi/10.1083/jcb.201009142

an N-terminal UBQ and a C-terminal UBA domain, which flank a central retroviral-like aspartate protease (RVP) domain (Krylov and Koonin, 2001). Ddi1/Vsm1 regulates the proteasomal degradation of a variety of proteins, including cell cycle regulators, homothallism endonuclease, and a member of the Skp–Cullin–F-box complex (Kaplun et al., 2005; Díaz-Martínez et al., 2006; Ivantsiv et al., 2006; Gabriely et al., 2008). In addition, Ddi1/Vsm1 controls SNARE-mediated membrane fusion events (Lustgarten and Gerst, 1999; Marash and Gerst, 2003). Ddi1/Vsm1 and its homologues are the only members of the ubiquitin receptor family that possess an RVP domain (Elsasser and Finley, 2005; Gabriely et al., 2008). The catalytic center of aspartate proteases is formed by two aspartate residues and an activated water molecule, which is needed for hydrolysis (Sirkis et al., 2006). Retroviral aspartate proteases only possess one catalytic aspartate, so the proteins have to form homodimers to build a catalytic center.

We show that Rngo forms homodimers and binds to ubiquitin and to the proteasome. *rngo* is an essential gene, and the loss of *rngo* function in female germline cells affects the growth of ring canals and leads to cell fusion. Both the lethality and the oogenesis defects of *rngo* mutant animals can be fully rescued by transgenes encoding full-length (FL) Rngo-GFP and versions of Rngo lacking either the UBQ or the UBA domain. In contrast, the catalytic function of the RVP domain is essential for the function of Rngo. To our knowledge, this study is the first to demonstrate a specific function for a ubiquitin receptor in *Drosophila* development.

Results and discussion

CG4420 is the *Drosophila* homologue of yeast Ddi1/Vsm1 and vertebrate Ddi1/Ddi2

The *Drosophila* genome contains a single homologue of Ddi1/Vsm1 encoded by the *CG4420* transcription unit on the X chromosome (Fig. 1 a). Because of its mutant phenotype (see following paragraphs), we named this gene *rings lost*. *rngo* encodes an acidic protein (isoelectric point = 4.78) of 458 amino acids and a calculated molecular mass of 50,500 D. Rngo possesses an N-terminal UBQ, a central RVP, and a C-terminal UBA domain (Fig. 1 b). An alignment of the RVP domains of several eukaryotic Ddi1/Vsm1 homologues with the sequence of Rngo suggested that aspartate 257 most likely is the catalytic center of the *Drosophila* protein (Fig. 1, b and c).

Rngo is a ubiquitously expressed nuclear and cytoplasmic protein that colocalizes with ubiquitin and the proteasome in the female germline

To study the expression pattern and subcellular localization of Rngo, we raised an antibody against an FL GST-tagged Rngo protein. Rngo was ubiquitously expressed during embryogenesis and in larval and adult tissues (Fig. S2 f and not depicted). Because germline clones of the $rngo^{GE3956}$-null allele (see following paragraphs) showed severe defects during oogenesis, we focused our analysis on the subcellular localization of Rngo in ovaries. Rngo was ubiquitously expressed both in the somatic follicle cells and in the germline at all stages of development (Fig. 2, a–d; and Fig. S1). Rngo was uniformly localized in the cytoplasm, whereas in the nucleus, it was enriched in subnuclear structures. This was particularly obvious in the polyploid nurse cell nuclei and in the oocyte nucleus (Fig. 2, a and b). Because Rngo is a predicted proteasomal shuttle factor, we tested whether Rngo colocalized with ubiquitin and with the proteasome by performing double stainings against Rngo and ubiquitin (Fig. 2 c) and the proteasome (Fig. 2 d). These stainings showed that Rngo colocalized with ubiquitin and with the proteasome in female germline cells.

The specificity of the anti-Rngo antibody was tested in stainings of ovaries containing germline clones of the $rngo^{GE3956}$ allele (see following paragraphs; Fig. 2 e). The specificity of the anti-Rngo antibody was also tested in Western blots using protein extracts of $rngo^{GE3956}$ mutant L3 larvae in comparison with L3 larvae possessing the wild-type *rngo* allele (Fig. 2 f). In both stainings and Western blots, the signal obtained with the anti-Rngo antibody was completely abolished in tissues or protein extracts of $rngo^{GE3956}$ mutant animals, demonstrating that this antibody is highly specific for Rngo.

Rngo binds to ubiquitin and to Rpn10, a regulatory subunit of the 26S proteasome

Next, we asked whether Rngo physically associates with ubiquitin and with the proteasome. To test the binding to ubiquitin, we generated a series of FL and partially deleted Rngo fusion proteins N-terminally tagged with the maltose-binding protein (MBP) for expression in *Escherichia coli* (Fig. 3 a). The Rngo fusion proteins were incubated with agarose beads covalently attached to ubiquitin. Only variants of Rngo that possessed the UBA domain bound to ubiquitin (Fig. 3 b) as expected.

Because Ddi1/Vsm1 binds to Rpn10, a regulatory subunit of the 26S proteasome (Saeki et al., 2002), we tested whether Rngo can also bind to Rpn10. To that aim, we incubated GST–FL Rngo together with MBP-Rpn10 and performed a pull-down with glutathione agarose beads. We detected MBP-Rpn10 in the precipitate with GST–FL Rngo but not in the control (Fig. 3 c), demonstrating that Rngo forms a complex with Rpn10 in vitro. The binding of Rngo to ubiquitin and to Rpn10 was also confirmed in vivo by coimmunoprecipitation (IP; co-IP; Fig. 3 d).

Rngo homodimerization is mediated by the RVP domain and does not require the catalytic residue D257

It was previously found that proteins containing an RVP domain can form homodimers to establish a catalytic center around two conserved aspartate residues (Miller et al., 1989). This is also true for Ddi1/Vsm1 (Sirkis et al., 2006; Gabriely et al., 2008). Thus, we used a series of Rngo constructs (Fig. 3 a) to determine the structural requirements for homodimerization by co-IP. We coexpressed FL Rngo tagged at the C terminus with GFP and either FL Rngo or one of the mutated versions, RngoΔUBA, RngoΔUBQ, RngoΔRVP, or RngoD257A, tagged at the C terminus with the HA epitope in S2 cells and performed co-IP with an anti-GFP antibody. We found that only RngoΔRVP, which lacks the RVP domain, is unable to bind FL Rngo-GFP

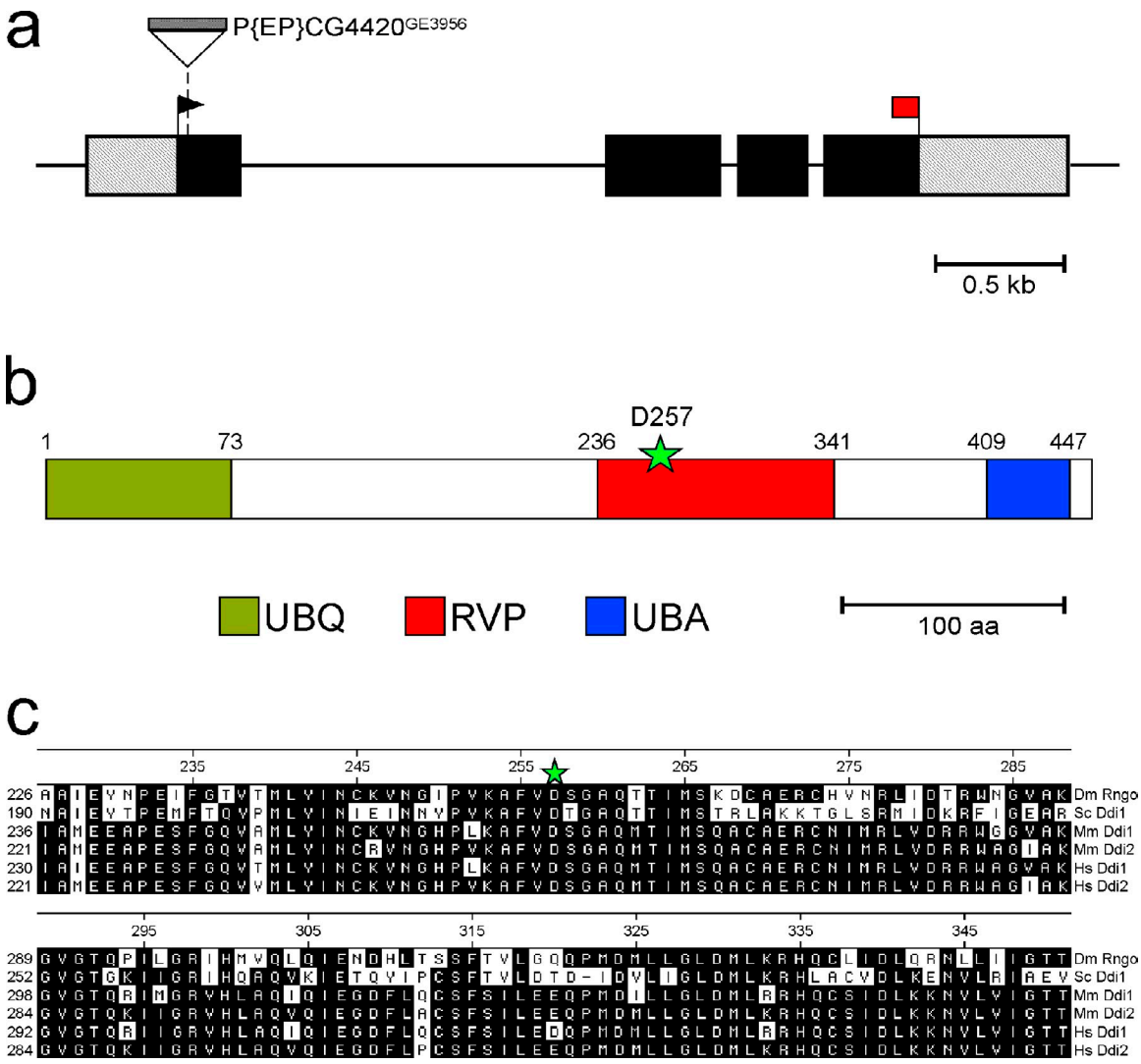

Figure 1. **Genomic organization of *rngo* and structure of the Rngo protein.** (a) The transcription start of *rngo* is marked by a black flag, and the stop is marked with a red flag. The position of the *P* element insertion representing a null allele of *rngo* is indicated. (b) Predicted structure of the Rngo protein. (c) Alignment of the RVP domain of Rngo with the corresponding region of its yeast (*Sc, Saccharomyces cerevisiae*), mouse (*Mm, Mus musculus*), and human (*Hs, Homo sapiens*) homologues. Residues identical to the consensus sequence are boxed in black. *Dm, Drosophila.*

(Fig. 3 e). The D257A substitution, which is predicted to abolish the catalytic activity of the RVP domain, did not interfere with dimerization (Fig. 3 e).

rngo is an essential gene

To analyze the function of *rngo* in development, we used the transposon insertion line $rngo^{GE3956}$, in which the *EP* element (Rørth, 1996) is inserted 203 bp downstream of the ATG start codon in the first exon of *rngo* (Fig. 1 a). The transposon insertion in $rngo^{GE3956}$ is predicted to result in the premature termination of translation, and according to our immunohistochemical and Western blot data, it represents a null allele of *rngo* (Fig. 2, e and f). Animals homo- or hemizygous for $rngo^{GE3956}$ were lethal at pupal stages. This late lethality is probably caused by maternal *rngo* expression that rescues an earlier requirement for Rngo because we detected Rngo in $rngo^{GE3956}$ mutant embryos (not depicted) but not in L3 larvae of the same genotype (Fig. 2 f). The lethality of $rngo^{GE3956}$ mutant animals and the ovarian phenotype of $rngo^{GE3956}$ germline clones (see following paragraphs) were fully rescued by ubiquitous expression of FL Rngo-GFP (Fig. S2, a and d).

Rngo is required for proper growth of ring canals in germline cells

To investigate the requirement for *rngo* during female germline development, we generated germline clones of the mutant $rngo^{GE3956}$ allele using the Flipase–Flipase recombination target technique (Harrison and Perrimon, 1993). Although control clones showed the wild-type staining pattern of Rngo, clones mutant for $rngo^{GE3956}$ completely lacked Rngo staining in the germline (Fig. 2 e and Fig. S1). We noted that egg chambers with $rngo^{GE3956}$ mutant germline cells did not develop beyond stages 8 and 9 of oogenesis because of degeneration and apoptosis of germline cells (Fig. S1 i). Closer analysis of the development of mutant egg chambers revealed severe abnormalities with respect to the localization of ring canal–associated proteins

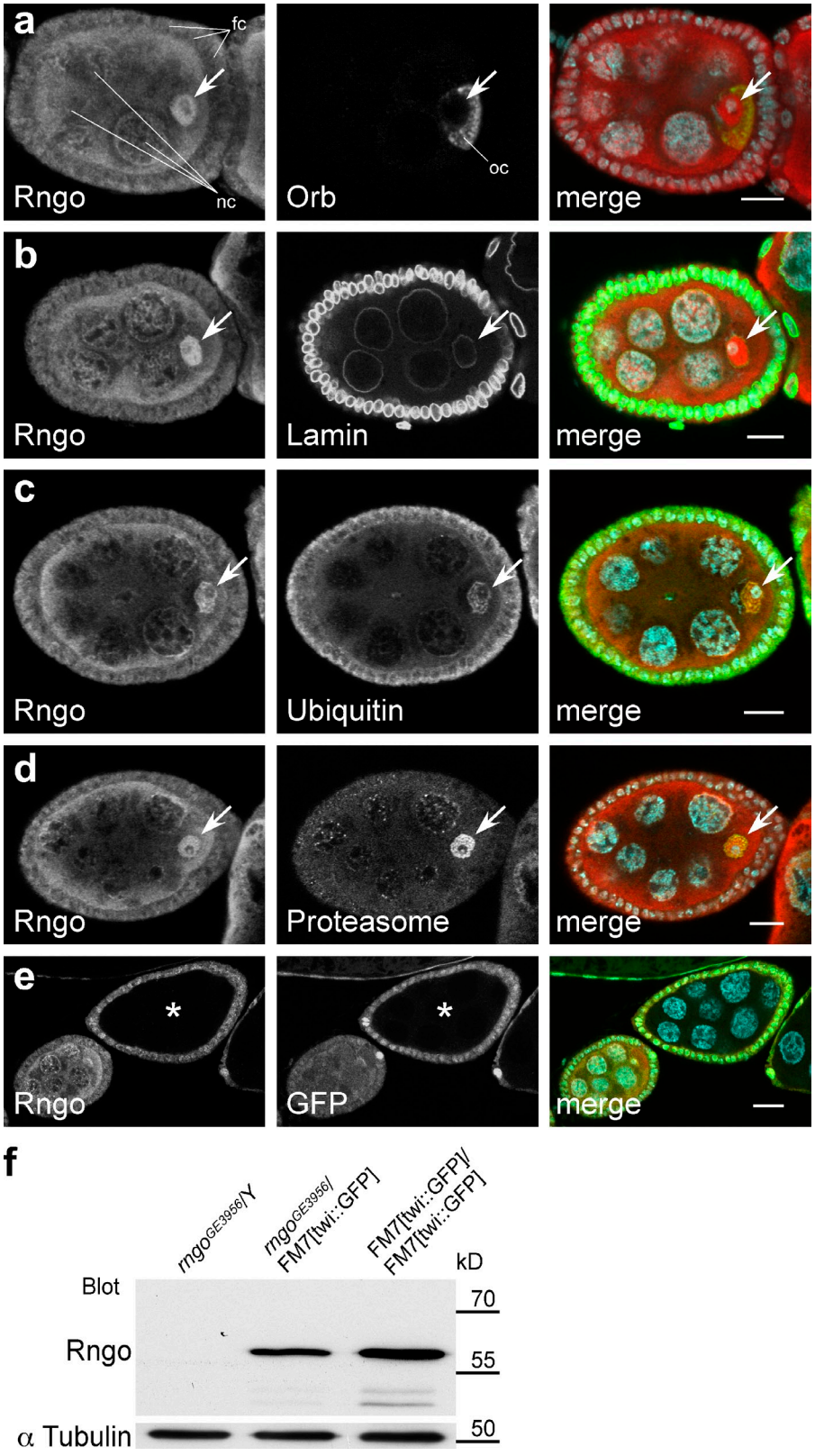

Figure 2. **Subcellular localization of Rngo during oogenesis.** (a) Rngo (red) is expressed in somatic cells and germline cells of egg chambers. It localizes to the cytoplasm and to the nuclei. The strongest staining can be seen in the nucleus of the oocyte (arrows), marked by the expression of Orb (green). (b–d) Costaining of Rngo with lamin (b, green), ubiquitin (c, green), and with the proteasome (d, green). (e) Germline cells homozygously mutant for *rngo*^{GE3956} (asterisk) completely lack Rngo staining. Clones are marked by loss of GFP expression (green). (f) L3 larval protein extracts were analyzed by Western blotting. In larvae possessing the wild-type *rngo* gene (right lanes), a band of 60 kD corresponding to FL Rngo is detectable, which is absent in the extract of *rngo*^{GE3956} mutant animals (left lane). α-Tubulin was used as a loading control. In a–e, DNA was stained with DAPI (turquoise, only shown in the merged images). Egg chambers are at stages 6 and 7. Anterior is to the left. fc, follicle cell; nc, nurse cell; oc, oocyte. Bars: (a–d) 10 µm; (e) 20 µm.

and the shape of the germline cells. In wild-type egg chambers, Hts-RC, Kel, Cheerio (Cher; *Drosophila* Filamin), and PY epitopes exclusively localized to the ring canals in the germline (Fig. 4, a, d, and f; Video 1; and Video 3). In contrast, Hts-RC, Cher, and PY epitopes spread over the whole plasma membrane of the germline cells in *rngo*^{GE3956} mutant germline clones (Fig. 4, b, c, e, and g; Video 2; and Video 3). Kel still localized to remnants of ring canals and to the plasma membrane of germline cells but was also found in the cytoplasm (Fig. 4 e). The defects in ring canal morphogenesis ranged from an almost complete

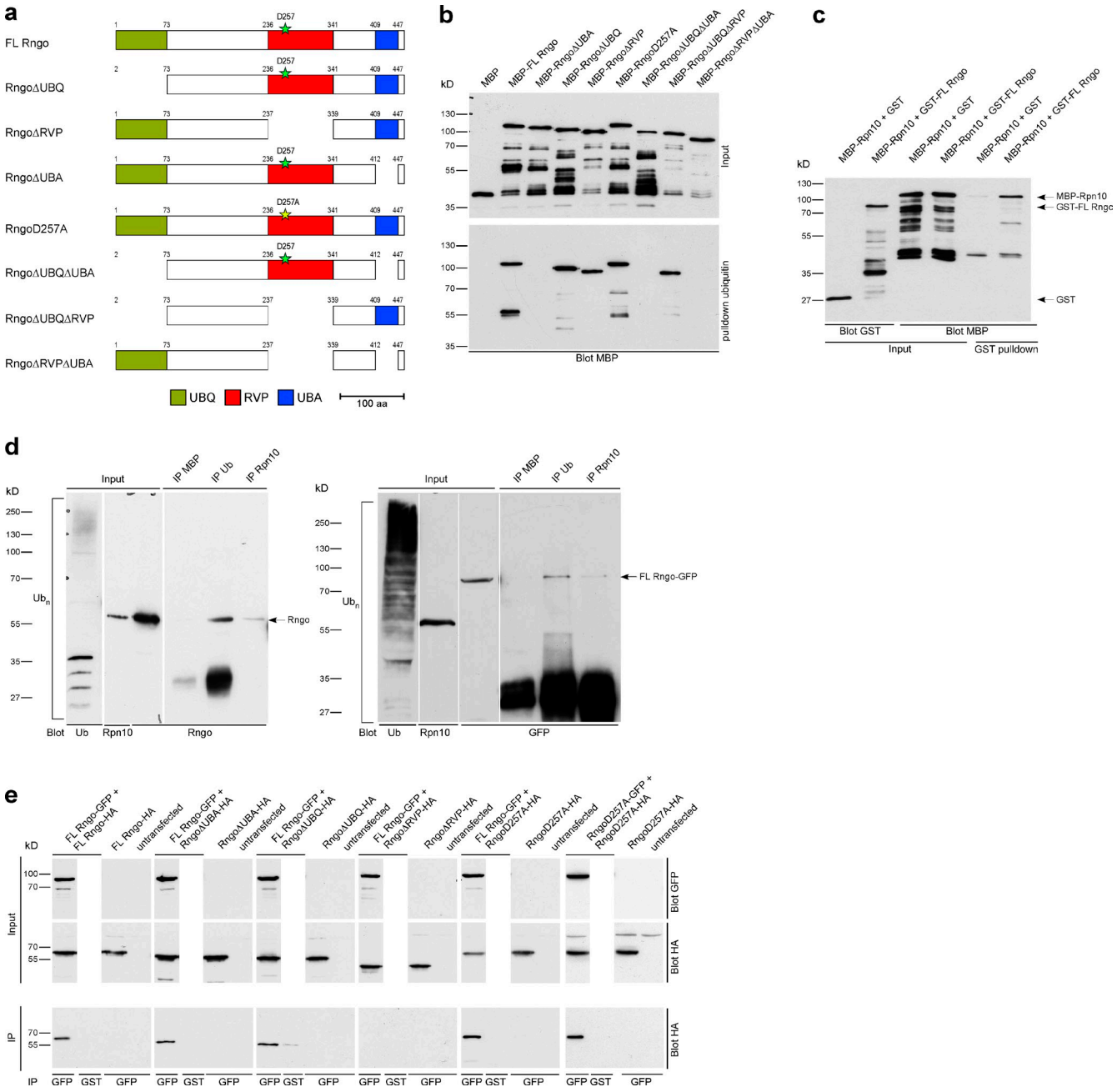

Figure 3. **Rngo binds to ubiquitin and to the proteasome and forms homodimers.** (a) A schematic diagram of Rngo fusion proteins used in this study. Numbers corresponding to amino acid residues indicate domain boundaries and the extent of the introduced deletions. (b) The UBA domain of Rngo is required for binding to ubiquitin. Ubiquitin-conjugated agarose beads were used to pull down the MBP-Rngo fusion proteins indicated above each lane. MBP was used as a negative control. (c) Direct binding of Rngo to the proteasomal subunit Rpn10. FL MBP-Rpn10 was pulled down by GST–FL Rngo but not by GST alone. (d) Rngo binds to ubiquitin (Ub) and Rpn10 in vivo. Extracts of wild-type ovaries (left) and ovaries expressing Rngo-GFP (right) were used for co-IP experiments with the indicated antibodies. The anti-MBP antibody was used as a negative control. (e) Rngo forms homodimers via its RVP domain. S2 cells were cotransfected with FL Rngo-GFP and either FL or mutated versions of Rngo tagged with the HA epitope. Cell extracts were used for IP with an anti-GFP antibody. IP with an anti-GST antibody was used as a negative control. Untransfected cells and cells transfected only with the respective HA-tagged version of Rngo were used as additional negative controls. White lines indicate that intervening lanes have been spliced out.

loss of ring canals (Fig. 4 c) to the formation of small, rudimentary ring canals connecting two nurse cells (Fig. 4, e and g) to the formation of unusually large ring canals connecting a nurse cell with the oocyte (Fig. 4 b). The quantification of these defects revealed that the growth of ring canals connecting two nurse cells was arrested at stage 5 in *rngo*^{GE3956} germline clones (Fig. 4 h), whereas ring canals connecting a nurse cell with the oocyte were always larger than their wild-type counterparts and continued to grow until stage 8 (Fig. 4 i). To our knowledge, *rngo* is the first mutation that differentially affects the growth of ring canals between nurse cells and between nurse cells and the oocyte. Ring canal defects and the mislocalization of ring canal–associated proteins were already detectable at early stages of oogenesis (Fig. S1), demonstrating that Rngo function is required throughout oogenesis.

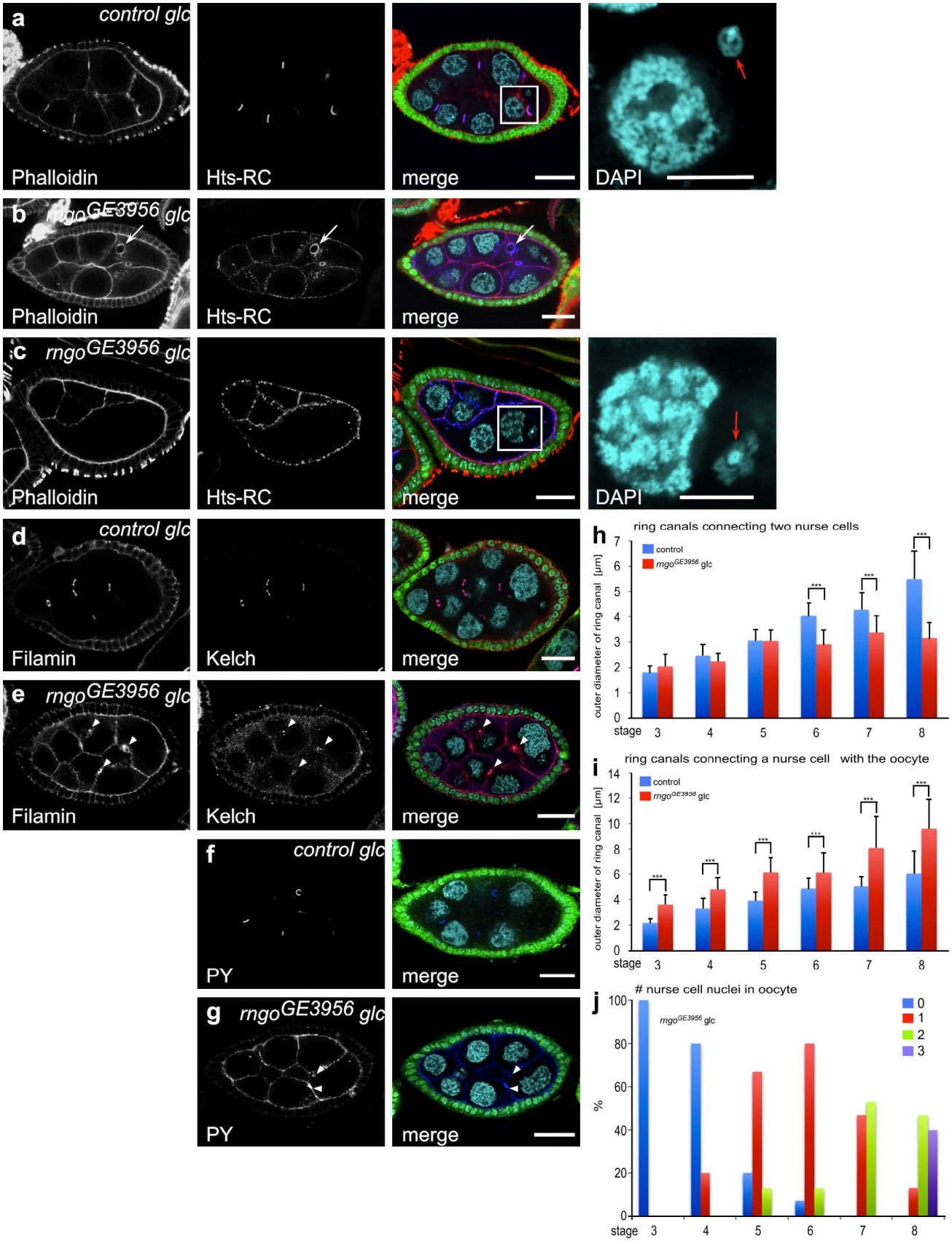

Figure 4. **Rngo is required for ring canal growth and plasma membrane integrity in the female germline.** (a–c) A control germline clone (glc, a) and *rngo*^{GE3956} germline clones (b and c) stained for F-actin (red) and Hts-RC (blue). Note the abnormally large ring canal (b, arrows) and the fusion of at least two nurse cells with the oocyte (c). Insets to the right of a and c show higher magnifications of the oocyte nucleus (red arrows) and an adjacent nurse cell

We wondered whether the mislocalization of ring canal–associated proteins in *rngo*^{GE3956} germline clones was accompanied by a change in their expression levels. To address this question, we performed Western blotting of ovaries dissected from wild-type females and from females with egg chambers carrying *rngo*^{GE3956} germline clones. Concomitant with a reduction in Rngo protein level, the levels of Hts-RC, Kel, Cher, and PY epitopes were significantly reduced, in contrast to the tubulin control (Fig. 5 a). This finding was confirmed by confocal analysis of control and *rngo*^{GE3956} germline clone egg chambers that were positioned next to each other in the same ovariole. Although the levels of Hts-RC, Kel, Cher, and PY epitopes were similar in adjacent wild-type and control germline clone egg chambers (Fig. 5, b, d, and f), they were strongly reduced in *rngo*^{GE3956} germline clone egg chambers (Fig. 5, c, e, and g).

In addition to defects in ring canal morphogenesis, we found that the oocyte nucleus frequently was misshapen in *rngo*^{GE3956} mutant germline clones. Instead of being round and compact as in wild type (Fig. 4 a, inset), the nucleus in *rngo*^{GE3956} mutant oocytes was enlarged and elongated (Fig. 4 c, inset), pointing to abnormal packing of the chromatin. This phenotype was fully penetrant after stage 7 of oogenesis.

Compared with wild-type controls, *rngo*^{GE3956} mutant egg chambers showed an abnormal organization of cortical F-actin. Although wild-type egg chambers always contained 15 nurse cells and one oocyte that were separated from each other by plasma membranes with an associated cortical actin filament network, egg chambers with *rngo*^{GE3956} germline clones frequently had <16 germline cells based on the counting of cell outlines (Fig. 4 c), whereas the number of nuclei was unaffected. Consequently, germline cells with more than one nucleus were frequently observed in *rngo*^{GE3956} germline clones. This was particularly obvious for the oocyte, which in addition to the oocyte nucleus, always contained one or more nurse cell nuclei at later stages of oogenesis (Fig. 4, c and j). This phenotype most likely results from the fusion of germline cells, which may be caused by decreased stability of the cortical actin cytoskeleton. Loss of *rngo* function in the follicle epithelium did not cause any obvious abnormalities in actin organization (Fig. S2 e), pointing to a germline-specific function of *rngo* in oogenesis.

The proteolytic activity of the RVP domain is essential for the function of Rngo

To test which domains of Rngo are required for its function in vivo, we performed rescue experiments using the upstream activating sequence (UAS)–GAL4 system (Brand and Perrimon, 1993). To that aim, we ubiquitously expressed FL Rngo-GFP and different GFP-tagged mutant versions of Rngo in animals mutant for *rngo*^{GE3956}. Although RngoΔUBQ-GFP and RngoΔUBA-GFP (Fig. 3 a) rescued both the lethality and the oogenesis defects of *rngo*^{GE3956} mutant animals to the same extent as FL Rngo-GFP (Fig. S2, a–d), neither RngoΔRVP-GFP (Fig. 3 a) nor RngoD257A-GFP, a point mutation that is predicted to destroy the catalytic activity of the RVP domain, showed any rescue. These results demonstrate that binding to ubiquitin and binding to the Rpn10 subunit of the proteasome are dispensable for the function of Rngo in our rescue assay, whereas the catalytic activity of the RVP domain is essential.

Conclusions

In this study, we characterize Rngo, the *Drosophila* homologue of the ubiquitin receptor Ddi1/Vsm1 from yeast. Rngo shares many features with Ddi1/Vsm1, including the binding to ubiquitin and to the proteasome and its ability to form homodimers (Bertolaet et al., 2001; Sirkis et al., 2006; Gabriely et al., 2008). In contrast to Ddi1/Vsm1, which is dispensable for the growth and survival of yeast (Lustgarten and Gerst, 1999; Clarke et al., 2001), *rngo* is an essential gene and is required for proper development of female germline cells. The defects observed in *rngo* mutants were less severe than those of *hts* mutations but were stronger than mutations in *kel* and *cher* (Yue and Spradling, 1992; Robinson et al., 1994; Li et al., 1999; Sokol and Cooley, 1999; Hudson and Cooley, 2010). Egg chambers with *rngo* germline clones showed mislocalization of Hts-RC, Cher, Kel, and PY epitopes and, unlike the aforementioned mutations, never developed beyond stage 9 of oogenesis and showed fusion of germline cells. These phenotypic differences between *rngo* and other genes involved in ring canal morphogenesis point to additional functions of Rngo, possibly in membrane trafficking.

How could these phenotypes relate to the biochemical functions assigned to Rngo? The predicted function of Rngo as a ubiquitin receptor implies that it binds to ubiquitinated proteins and either shuttles them to the proteasome or prevents their proteasomal degradation by interfering with the recognition of the ubiquitin modification by a proteasomal ubiquitin receptor. This may be important for the proper assembly of ring canals because their growth requires the dynamic remodeling of the actin cytoskeleton and a high turnover of actin-binding proteins. Evidence supporting this hypothesis comes from a recent study that demonstrated a function for Kel as a component of an E3 ubiquitin ligase complex together with Cullin-3 (Hudson and Cooley, 2010). This study proposed that Kel is required as an adapter protein to ubiquitinate various ring canal–associated proteins, which need to be degraded to disassemble the actin

nucleus in the boxed regions. Note the elongated shape of the oocyte nucleus in c. (d and e) A control germline clone (d) and *rngo*^{GE3956} germline clone (e) stained for Filamin (red) and Kel (blue). Note the rudimentary ring canals (arrowheads) and the diffuse cytosolic localization of Kel in e. (f and g) A control germline clone (f) and *rngo*^{GE3956} germline clone (g) stained for PY epitopes (blue). Rudimentary ring canals in g are marked by arrowheads. DNA was stained with DAPI (turquoise). Germline clones are marked by an absence of GFP (green) expression. Note that for imaging of Hts-RC, Kel, Filamin, and PY in *rngo*^{GE3956} germline clones, a much higher gain of the photomultiplier was used than in the respective wild-type controls. Egg chambers are at stages 7 and 8. Anterior is to the left. (h and i) Quantification of outer ring canal diameter of ring canals connecting nurse cells (h) and a nurse cell with the oocyte (i). (j) Quantification of the fusion between nurse cells and the oocyte. In h, $n = 40$ for stages 3–7, and $n = 19$ for stage 8. In i, $n = 16$ for stages 3–7, and $n = 6$ for stage 8. The statistical significance of the differences was calculated with the Student's *t* test; ***, $P < 0.01$. In j, $n = 15$ for all stages. Error bars represent SDs from three independent experiments. Bars: 20 µm; (insets) 10 µm.

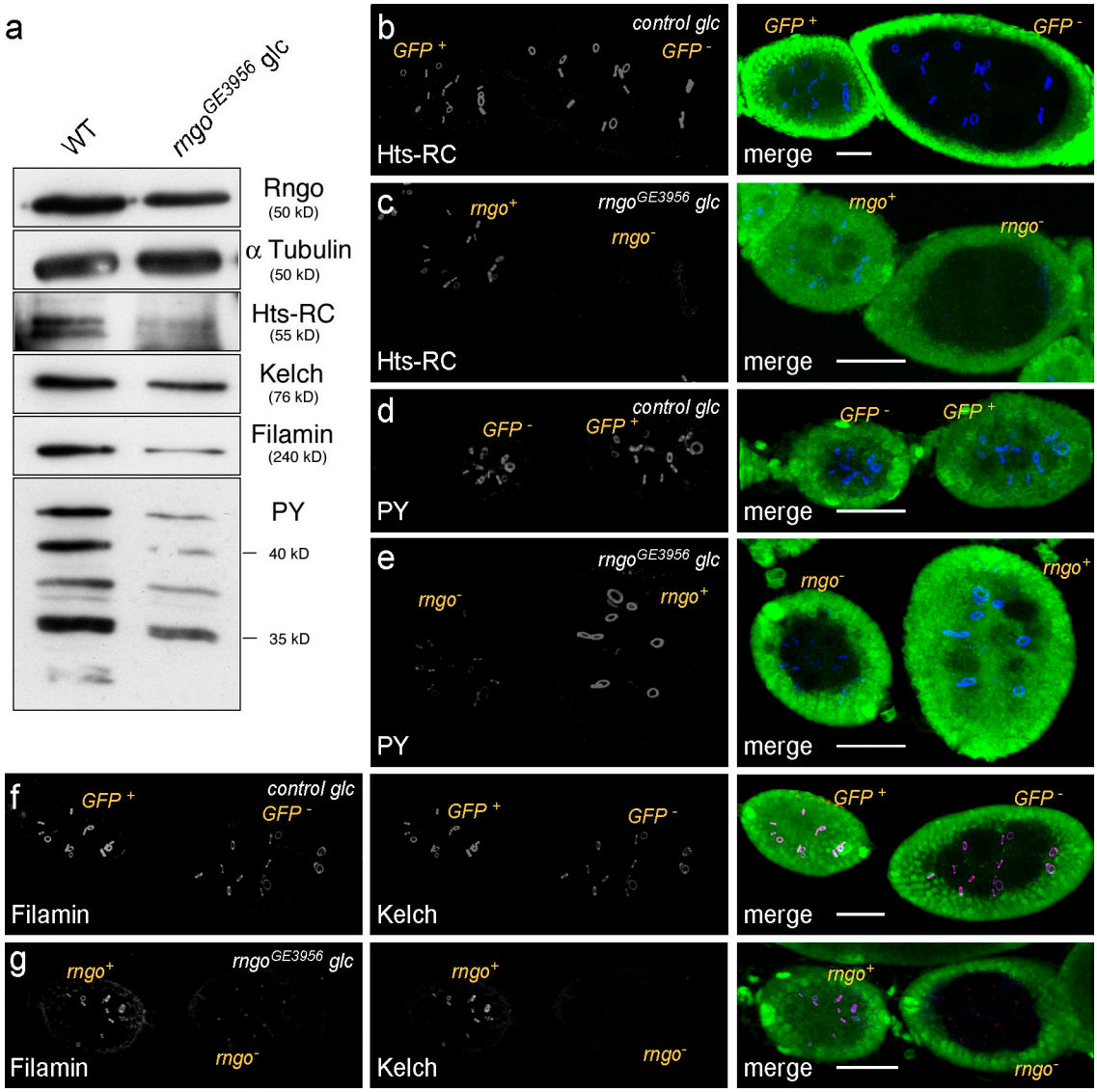

Figure 5. **The levels of ring canal–associated proteins are reduced in *rngo*^{GE3956} germline clones.** (a) Western blot of extracts from wild-type ovaries (left) and ovaries with *rngo*^{GE3956} germline clones (glc, right). α-Tubulin was used as a loading control. (b and c) A control germline clone lacking GFP shows the same level of Hts-RC (blue) as the adjacent wild-type egg chamber (b), whereas Hts-RC levels are strongly reduced in an *rngo*^{GE3956} germline clone egg chamber (c). (d–g) The same is true for PY epitopes (d and e, blue), Filamin (f and g, red), and Kel (f and g, blue). Germline clones are marked by the absence of GFP (green). Images are projections of z stacks. Egg chambers are at stages 5–7. Anterior is to the left. Bars, 20 µm.

cytoskeleton of the growing ring canal. Indeed, the staining intensity for F-actin, Cher, and Hts-RC was strongly increased in *kel* mutant egg chambers (Hudson and Cooley, 2010). We have now shown that the levels of Kel, Cher, and Hts-RC are strongly reduced in *rngo* mutant egg chambers. Thus, Rngo may antagonize the activity of the Kel–Cullin-3 E3 ligase complex. Our genetic rescue experiments demonstrated that the catalytic activity of the RVP domain of Rngo is essential for its function, in contrast to the UBA and UBQ domains. It is therefore tempting to speculate that the protease activity of the RVP domain may be directly involved in the deubiquitination of specific ring canal proteins, thus protecting them from degradation in the proteasome. To test this hypothesis, it will be important to identify the protease targets of Rngo and to elucidate whether these are indeed ubiquitinated by the Kel–Cullin-3 E3 ligase complex.

Materials and methods

Fly stocks and genetics

The following stocks were used in this study: P{EP}CG4420^{GE3956}/FM7, renamed *rngo*^{GE3956} in this study (GenExel), y^{1}arm^{4} w*/FM7c, ovo[D2] P{FRT(w^{hs})}9-2/Y; P{hsFLP} (stock no. 1,843), p{ftz/lacZ}YH1 (stock no. 616), P{FRT(w^{hs})}9-2 (stock no. 5,749), P{Ubi-GFP.nls}P{FRT(w^{hs})}9-2 (stock no. 5,832), P{FRT(w^{hs})}9-2; P{hsFLP}38 (stock no. 1,843), *daughterless*-GAL4 (stock no. 5,460), and y^{1} w* N^{1}/FM7c, P{GAL4-twi.G}108.4, P{UAS-2xEGFP}AX (stock no. 6,873; Bloomington *Drosophila* stock center). Expression of UASP-Rngo-GFP, UASP-RngoΔUBA-GFP, UASP-RngoΔUBQ-GFP, UASP-RngoΔRVP-GFP, and UASP-RngoD257A-GFP in transgenic flies was performed with the UAS-GAL4 system (Brand and Perrimon, 1993). Germline clones and follicle cell clones for *rngo*^{GE3956} were generated as previously described using a heat shock promoter-driven flipase on the second chromosome (Chou and Perrimon, 1996). To obtain hemizygous *rngo*^{GE3956} mutant L3 larvae, living embryos lacking GFP fluorescence derived from the FM7[twi::GFP] balancer chromosome were separated from their GFP-positive siblings under a fluorescent stereo microscope and raised in separate vials. To rescue the lethality and phenotype of hemi- or homozygous *rngo*^{GE3956} mutant flies, *rngo*^{GE3956}/FM7 females were

crossed to males that were homozygous for one of the UASP-Rngo-GFP constructs recombined with the *daughterless*-GAL4 driver on the third chromosome and carried the FM7 balancer. Rescued hemizygous males carrying the $rngo^{GE3956}$ allele and the GFP construct were crossed to $rngo^{GE3956}$/FM7 females also carrying the GFP construct to establish a viable and fertile stock homozygous for the mutant $rngo^{GE3956}$ allele.

Antibodies and immunohistochemistry

An antibody against Rngo was generated by immunizing a rabbit with a GST fusion protein containing the FL Rngo protein (Eurogentec). Final bleed serum was affinity purified and used for immunohistochemistry. For immunohistochemical stainings of ovaries the following antibodies were used: rabbit anti-Rngo, affinity purified at 1:1,000, mouse anti-26S proteasome (Rpn10) at 1:400 (Santa Cruz Biotechnology, Inc.), mouse anti-PY at 1:1,000 (Sigma-Aldrich), rabbit anti-GFP at 1:1,000 (Invitrogen), mouse antiubiquitin at 1:6,000 (FK2; Enzo Life Sciences), rat anti–N-filamin at 1:3,000 (Sokol and Cooley, 1999), provided by L. Cooley, Yale University, New Haven, CT, mouse anti–Hts-RC at 1:20 (Hts-RC; Developmental Studies Hybridoma Bank), mouse anti-Kel at 1:1 (kel1B; Developmental Studies Hybridoma Bank), and mouse anti-Orb at 1:20 (4H8; Developmental Studies Hybridoma Bank). Secondary antibodies conjugated to Cy2, Cy3 (Jackson Immunoresearch Laboratories, Inc.), and Alexa Fluor 647 (Invitrogen) were used at 1:200. To visualize F-actin, ovaries were incubated with 2 U rhodamine-conjugated phalloidin in PBS with 0.1% Triton X-100. DNA was stained with DAPI. Ovaries were fixed in 4% formaldehyde/PBS and stained according to standard procedures. Images were taken on a confocal microscope (LSM 510 Meta; Carl Zeiss) using 25× Plan-Neofluar, NA 0.8, and 63× Plan-Apochromat, NA 1.40, objectives and processed using Photoshop (Adobe).

Western blots and co-IP

Lysates of L3 larvae, ovaries, and S2 cells were prepared in TNT buffer (150 mM NaCl, 50 mM Tris-HCl, pH 8.0, and 1% Triton X-100) supplemented with protease inhibitors (Roche). Western blotting and co-IPs were performed as previously described (Wodarz, 2008). In brief, for Western blotting, cell lysates were subjected to SDS-PAGE, blotted onto nitrocellulose membranes, and blocked in 3% dry milk and 1% BSA in TBS with Tween (TBS-T). The following primary antibodies were incubated with the nitrocellulose filters in blocking buffer: rabbit anti-Rngo, affinity purified at 1:2,000, mouse anti–α-tubulin at 1:25 (12G10; Developmental Studies Hybridoma Bank), mouse anti-HA at 1:1,000 (12C25; Roche), mouse anti-GFP at 1:1,000 (Roche), mouse anti-MBP at 1:10,000 (New England Biolabs, Inc.), rabbit anti-GST at 1:10,000 (Sigma-Aldrich), mouse anti-PY at 1:1,000, mouse antiubiquitin at 1:1,000, mouse anti-26S proteasome at 1:500, rat anti–N-filamin at 1:1,000 (Sokol and Cooley, 1999), mouse anti–Hts-RC at 1:5, and mouse anti-Kel at 1:2. After repeated washing in TBS-T, blots were incubated with HRP-conjugated secondary antibodies in blocking buffer and washed again with TBS-T. Protein bands were visualized with BM chemiluminescence blotting substrate peroxidase (Roche). For co-IP, rabbit anti-GFP, mouse anti-26S proteasome, and mouse antiubiquitin antibodies were incubated with cell lysates followed by pull-down of the antibody–protein complexes with protein A/G–agarose beads. Rabbit anti-GST and mouse anti-MBP antibodies were used as negative controls. Washed beads were boiled in sample buffer and subjected to SDS-PAGE and Western blotting.

GST and ubiquitin pull-down

For GST pull-down the FL *rngo* sequence was subcloned into pGEX-4T-1 (GE Healthcare), and the FL sequence of Rpn10 was subcloned into pMGWA (*Drosophila* Genomics Resource Center). Each GST or MBP fusion protein expressed in *E. coli* was purified with glutathione Sepharose (GE Healthcare) or amylose resin (New England Biolabs, Inc.), respectively. GST and GST-Rngo were bound to 15 µl glutathione Sepharose resin in binding buffer (100 mM NaCl, 50 mM Tris-HCl, pH 7.5, and 0.5% Triton X-100 supplemented with protease inhibitors). The beads were subsequently incubated with 200 µl binding buffer plus MBP-Rpn10 for 2 h at 4°C and were then washed with binding buffer and eluted by adding 15 µl of 2× SDS sample buffer and boiling for 10 min at 96°C. The supernatants were separated by SDS-PAGE and analyzed by Western blotting.

For ubiquitin pull-down, the FL *rngo* sequence and the sequences of RngoΔUBA, RngoΔUBQ, RngoΔRVP, RngoD257A, RngoΔUBAΔUBQ, RngoΔUBAΔRVP, and RngoΔUBQΔRVP were subcloned into pMGWA. MBP fusion proteins expressed in *E. coli* were purified with amylose resin. MBP fusion proteins were diluted in 500 µl binding buffer (100 mM NaCl, 50 mM Tris-HCl, pH 7.5, and 0.5% Triton X-100), added to 15 µl ubiquitin–agarose (Enzo Life Sciences) and incubated for 2 h at 4°C. The beads were then washed with binding buffer and eluted by adding 15 µl of 2× SDS sample buffer and boiling for 10 min at 96°C. The supernatants were separated by SDS-PAGE and analyzed by Western blotting.

Online supplemental material

Fig. S1 is related to Fig. 2 and Fig. 4 and shows the requirement for Rngo already at the earliest stages of oogenesis and also the degeneration of *rngo* mutant egg chambers after stages 8 and 9 of oogenesis. Fig. S2 is related to Fig. 4 and shows stainings and Western blots of *rngo* mutant animals rescued by different Rngo-GFP transgenes. Video 1 is related to Fig. 4 and shows the 3D reconstruction of the wild-type staining pattern of Hts-RC in an egg chamber at stage 8. Video 2 is related to Fig. 4 and shows the 3D reconstruction of the staining pattern of Hts-RC in an *rngo* mutant egg chamber at stage 8. Video 3 is related to Fig. 4 and shows the 3D reconstruction of the staining pattern of Hts-RC in two adjacent egg chambers, one at stage 6 that is wild type for *rngo* and the other one at stage 8 that is mutant for *rngo*. Online supplemental material is available at http://www.jcb.org/cgi/content/full/jcb.201009142/DC1.

We thank Lynn Cooley, the Bloomington *Drosophila* stock center at the University of Indiana, and the Developmental Studies Hybridoma Bank at the University of Iowa for sending fly stocks and antibodies. We also thank Katja Brechtel-Curth for technical assistance and Ernst A. Wimmer and members of the Wodarz laboratory for discussions.

This work was supported by grants from the Deutsche Forschungsgemeinschaft to A. Wodarz (Sonderforschungsbereich 523, Teilprojekt B15, and Forschungszentrum für Molekularphysiologie des Gehirns).

Submitted: 30 September 2010
Accepted: 7 March 2011

References

Bertolaet, B.L., D.J. Clarke, M. Wolff, M.H. Watson, M. Henze, G. Divita, and S.I. Reed. 2001. UBA domains of DNA damage-inducible proteins interact with ubiquitin. *Nat. Struct. Biol.* 8:417–422. doi:10.1038/87575

Brand, A.H., and N. Perrimon. 1993. Targeted gene expression as a means of altering cell fates and generating dominant phenotypes. *Development*. 118:401–415.

Chou, T.B., and N. Perrimon. 1996. The autosomal FLP-DFS technique for generating germline mosaics in *Drosophila melanogaster*. *Genetics*. 144:1673–1679.

Clarke, D.J., G. Mondesert, M. Segal, B.L. Bertolaet, S. Jensen, M. Wolff, M. Henze, and S.I. Reed. 2001. Dosage suppressors of pds1 implicate ubiquitin-associated domains in checkpoint control. *Mol. Cell. Biol.* 21:1997–2007. doi:10.1128/MCB.21.6.1997-2007.2001

Díaz-Martínez, L.A., Y. Kang, K.J. Walters, and D.J. Clarke. 2006. Yeast UBL-UBA proteins have partially redundant functions in cell cycle control. *Cell Div.* 1:28. doi:10.1186/1747-1028-1-28

Elsasser, S., and D. Finley. 2005. Delivery of ubiquitinated substrates to protein-unfolding machines. *Nat. Cell Biol.* 7:742–749. doi:10.1038/ncb0805-742

Gabriely, G., R. Kama, R. Gelin-Licht, and J.E. Gerst. 2008. Different domains of the UBL-UBA ubiquitin receptor, Ddi1/Vsm1, are involved in its multiple cellular roles. *Mol. Biol. Cell*. 19:3625–3637. doi:10.1091/mbc.E07-05-0462

Grabbe, C., and I. Dikic. 2009. Functional roles of ubiquitin-like domain (ULD) and ubiquitin-binding domain (UBD) containing proteins. *Chem. Rev.* 109:1481–1494. doi:10.1021/cr800413p

Harrison, D.A., and N. Perrimon. 1993. Simple and efficient generation of marked clones in *Drosophila*. *Curr. Biol.* 3:424–433. doi:10.1016/0960-9822(93)90349-S

Hudson, A.M., and L. Cooley. 2010. *Drosophila* Kelch functions with Cullin-3 to organize the ring canal actin cytoskeleton. *J. Cell Biol.* 188:29–37. doi:10.1083/jcb.200909017

Ivantsiv, Y., L. Kaplun, R. Tzirkin-Goldin, N. Shabek, and D. Raveh. 2006. Unique role for the UbL-UbA protein Ddi1 in turnover of SCFUfo1 complexes. *Mol. Cell. Biol.* 26:1579–1588. doi:10.1128/MCB.26.5.1579-1588.2006

Kaplun, L., R. Tzirkin, A. Bakhrat, N. Shabek, Y. Ivantsiv, and D. Raveh. 2005. The DNA damage-inducible UbL-UbA protein Ddi1 participates in Mec1-mediated degradation of Ho endonuclease. *Mol. Cell. Biol.* 25:5355–5362. doi:10.1128/MCB.25.13.5355-5362.2005

Kelso, R.J., A.M. Hudson, and L. Cooley. 2002. *Drosophila* Kelch regulates actin organization via Src64-dependent tyrosine phosphorylation. *J. Cell Biol.* 156:703–713. doi:10.1083/jcb.200110063

Krylov, D.M., and E.V. Koonin. 2001. A novel family of predicted retroviral-like aspartyl proteases with a possible key role in eukaryotic cell cycle control. *Curr. Biol.* 11:R584–R587. doi:10.1016/S0960-9822(01)00357-8

Li, M.G., M. Serr, K. Edwards, S. Ludmann, D. Yamamoto, L.G. Tilney, C.M. Field, and T.S. Hays. 1999. Filamin is required for ring canal assembly and actin organization during *Drosophila* oogenesis. *J. Cell Biol.* 146:1061–1074. doi:10.1083/jcb.146.5.1061

Liu, Y., and W. Xiao. 1997. Bidirectional regulation of two DNA-damage-inducible genes, MAG1 and DDI1, from *Saccharomyces cerevisiae*. *Mol. Microbiol.* 23:777–789. doi:10.1046/j.1365-2958.1997.2701631.x

Lustgarten, V., and J.E. Gerst. 1999. Yeast VSM1 encodes a v-SNARE binding protein that may act as a negative regulator of constitutive exocytosis. *Mol. Cell. Biol.* 19:4480–4494.

Marash, M., and J.E. Gerst. 2003. Phosphorylation of the autoinhibitory domain of the Sso t-SNAREs promotes binding of the Vsm1 SNARE regulator in yeast. *Mol. Biol. Cell*. 14:3114–3125. doi:10.1091/mbc.E02-12-0804

Matova, N., and L. Cooley. 2001. Comparative aspects of animal oogenesis. *Dev. Biol.* 231:291–320. doi:10.1006/dbio.2000.0120

Miller, M., M. Jaskólski, J.K. Rao, J. Leis, and A. Wlodawer. 1989. Crystal structure of a retroviral protease proves relationship to aspartic protease family. *Nature*. 337:576–579. doi:10.1038/337576a0

Ong, S., and C. Tan. 2010. Germline cyst formation and incomplete cytokinesis during *Drosophila melanogaster* oogenesis. *Dev. Biol.* 337:84–98. doi:10.1016/j.ydbio.2009.10.018

Robinson, D.N., K. Cant, and L. Cooley. 1994. Morphogenesis of *Drosophila* ovarian ring canals. *Development*. 120:2015–2025.

Rørth, P. 1996. A modular misexpression screen in *Drosophila* detecting tissue-specific phenotypes. *Proc. Natl. Acad. Sci. USA*. 93:12418–12422. doi:10.1073/pnas.93.22.12418

Saeki, Y., A. Saitoh, A. Toh-e, and H. Yokosawa. 2002. Ubiquitin-like proteins and Rpn10 play cooperative roles in ubiquitin-dependent proteolysis. *Biochem. Biophys. Res. Commun.* 293:986–992. doi:10.1016/S0006-291X(02)00340-6

Schauber, C., L. Chen, P. Tongaonkar, I. Vega, D. Lambertson, W. Potts, and K. Madura. 1998. Rad23 links DNA repair to the ubiquitin/proteasome pathway. *Nature*. 391:715–718. doi:10.1038/35661

Sirkis, R., J.E. Gerst, and D. Fass. 2006. Ddi1, a eukaryotic protein with the retroviral protease fold. *J. Mol. Biol.* 364:376–387. doi:10.1016/j.jmb.2006.08.086

Sokol, N.S., and L. Cooley. 1999. *Drosophila* filamin encoded by the cheerio locus is a component of ovarian ring canals. *Curr. Biol.* 9:1221–1230. doi:10.1016/S0960-9822(99)80502-8

Wodarz, A. 2008. Extraction and immunoblotting of proteins from embryos. *Methods Mol. Biol.* 420:335–345. doi:10.1007/978-1-59745-583-1_21

Xue, F., and L. Cooley. 1993. kelch encodes a component of intercellular bridges in *Drosophila* egg chambers. *Cell*. 72:681–693. doi:10.1016/0092-8674(93)90397-9

Yue, L., and A.C. Spradling. 1992. hu-li tai shao, a gene required for ring canal formation during *Drosophila* oogenesis, encodes a homolog of adducin. *Genes Dev.* 6:2443–2454. doi:10.1101/gad.6.12b.2443