Introduction

Cells in a given tissue can respond differently to stress signals based on their balance between prosurvival and death-promoting factors (Bree et al., 2002). Homeostasis and repair of regenerative tissues such as hair, skin, and testis is often severely impeded by stress signals (e.g., irradiation) but can also regain function once the stress has been removed. Tissue regeneration is controlled by rare populations of residential adult stem cells that often reside in direct contact with microenvironment niche cells (Lin, 2002; Jones and Wagers, 2008). The regenerative potential of adult stem cells relies on their capability to yield two types of cells upon division: one that detaches from the niche, differentiates, and replaces lost cells within the tissue, and one that is kept within the niche as a stem cell for future use (Morrison and Spradling, 2008). Therefore, the niche serves as a control unit that regulates the rate of stem cell proliferation and protects the overall stem cell pool from depletion.

In this study, we used the model system of Drosophila melanogaster testis to identify the exact cells within a regenerative tissue that are most resistant to apoptotic signals and reveal the core that enables tissue recovery. Spermatogenesis is governed by germline stem cells (GSCs) that share the niche together with cyst stem cells (CySCs) and adhere around a sphere of somatic cells called the hub (Fig. 1A). The hub is a compact cluster of ∼12 cells that secret short-range signals and express adhesion molecules to maintain the surrounding stem cells (Kiger et al., 2001; Tulina and Matunis, 2001; Leatherman and Dinardo, 2010). One of the two daughter cells that are formed by a GSC division remains adherent to the hub for self-renewal, while the other is displaced and undergoes transit amplification divisions before becoming a terminally differentiated spermatocyte (Insco et al., 2009).

GSCs in male and female gonads as well as intestinal stem cells were shown to be more resistant to cell death compared with their differentiated progeny (Xing et al., 2015). However, because the niche is critical in maintaining the stem cells in their undifferentiated state, we postulated that the hub cells use an even more stringent mechanism to resist genotoxic signals. We also proposed that the protection of the niche from demise involves specific genetic programming that is tightly regulated by miRNAs. miRNAs are an established class of posttranscriptional RNA regulators that negatively regulate gene expression through translational inhibition and/or degradation of mRNA targets (Djurankovic et al., 2012). miRNAs identify their targets through base-pairing of six to eight seed elements with recognition sites located mainly in the 3′ UTR or within the ORF of the mRNA (Brodersen and Voinnet, 2009). All miRNAs are encoded in the genome itself, and their final processing into functional units occurs in the cytoplasm by a single enzyme, Dicer (Dcrl; Ghildiyal and Zamore, 2009; Saxe and Lin, 2011). Antia apoptotic miRNAs such as bantam were previously shown to promote tissue growth and prevent apoptosis during development (Brennecka et al., 2003; Ge et al., 2012). In this study, we show that the postmitotic hub cells are highly resistant to apoptosis...
induction. To identify the mRNAs and miRNAs that protect the niche from apoptosis, we used transcriptomics and miRNAomics, which revealed the identity of several miRNAs that antagonize apoptosis and create a durable niche that enables spermatogenesis under harmful conditions.

Results and discussion

Hub cells are resistant to cell death

To identify the cells that are most resistant to apoptosis within the regenerative Drosophila testis, we exposed young adult flies to high doses of damage-induced UVB (180 kg m⁻² s⁻¹) or x-ray irradiation (4,000 rads). We examined tissues after irradiation at multiple time points with TUNEL to in situ label DNA fragments characteristic of apoptotic cells (Arama and Steller, 2006). TUNEL staining 4 h after irradiation showed that although GSCs and spermatogonia germ cells underwent massive apoptosis, the hub cells were completely intact and did not show any detectable TUNEL signal (Fig. 1, A, B, and F). We also examined tissues after irradiation at multiple time points with TUNEL to in situ label DNA fragments characteristic of apoptotic cells (Arama and Steller, 2006). TUNEL staining 4 h after irradiation showed that although GSCs and spermatogonia germ cells underwent massive apoptosis, the hub cells were completely intact and did not show any detectable TUNEL signal (Fig. 1, A, B, and F).

Figure 1. The inability of x-ray, UV, and proapoptotic genes to induce hub cell death. (A) Side view schematic representation of the GSC niche. Hub cells (blue), cyst cells (gray), GSCs, and spermatogonia (green). (B–E) Testes of WT flies that were immunostained for Fas3 (hub; blue), Vasa (germ cells; green), and TUNEL (red) at the indicated time after x-ray (B, n = 45; C, n = 30, 4,000 rads) and UVB exposure (D, n = 37, 180 kg m⁻² s⁻¹). Arrows and arrowheads mark TUNEL-positive GSCs and spermatogonia, respectively. Note that tissue regeneration occurs 17 d after x-ray exposure (E, n = 26). (F) Shown are average number per testis of GSCs (gray) and hub cells (black) after irradiation along with 95% confidence intervals (error bars). Note that GSC average number decreases 24 h after irradiation and increases after 17 d, whereas hub cell number is not affected. Statistical significance was determined by one-way ANOVA, and post hoc analysis was performed with Tukey multicomparison test. *, P ≤ 0.05 GSC average number between 24 h x-ray/UV irradiated and nonirradiated. (G) mCherry overexpression (updTS::mCherry) is induced only in the hub after 1 d at the restrictive temperature (29°C), Fas3 (hub; blue), and mCherry (red). Dashed line marks the apical edge of the testis. (H–J) Overexpression of hid (H, updTS::hid, n = 39), rpr (I, updTS::rpr, n = 97), or grim (J, updTS::grim, n = 60) in the hub for 14 d at 29°C did not result in hub cell death. Fas3 (hub; blue), Vasa (germ cells; green), and TUNEL (red). (K) Eye of control (gmr-GAL4 outcrossed to w¹¹¹⁸). (L–N) Overexpression of hid (L, gmr::hid), rpr (M, gmr::rpr), or grim (N, gmr::grim) induces eye cell death. All images in all figures are single sections; scale bars are 10 µm.
the hub of adult males for 14 d at the restrictive temperature was unable to induce cell death (Fig. 1, H–J). A subsequent quantitative RT-PCR (qRT-PCR) analysis verified that these overexpressed transgenes are indeed transcribed in the hub (Fig. S1 B). To ascertain that our transgenes are able to cause apoptosis elsewhere, we ectopically expressed them by two alternative approaches: using the same driver during development (upd-GAL4) and in the Drosophila eye (gmr-GAL4). As expected, overexpression of these genes caused larvae lethality (not depicted) and eye loss (Fig. 1, K–N), respectively. Together, these data suggest that although the hid, rpr, and grim transgenes have the potential to confer apoptosis, their ability to do so in the hub is markedly attenuated.

miRNAs in the hub antagonize apoptosis
To find whether there are factors within the hub that antagonize the overexpression of hid and grim via sequences located in their 3′ UTR, we examined the expression pattern of GFP reporters that are attached to the 3′ UTR of either hid or grim (Brennecke et al., 2003). As depicted in Fig. 2 (A–C) compared with the control GFP reporter that expresses uniformly in the hub and germ cells, the presence of hid or grim 3′ UTR silenced GFP expression in the hub. These results suggest that miRNAs and/or other factors that inhibit translation via the 3′ UTRs of hid and grim are expressed in the hub.

The 3′ UTR of hid can be regulated by >20 miRNAs and includes five recognition sites for the bantam miRNA. Because bantam was previously shown to down-regulate the expression of hid (Brennecke et al., 2003), we tested whether hid-induced apoptosis is blocked by bantam in the hub. First, we attempted to generate UAS transgenic lines with insertion of four and five point mutations in the bantam recognition sites. However, despite our best efforts, these mutations were lethal and no transgenic flies were obtained, indicating that the leakiness of expression manifested by these constructs was sufficient to induce apoptosis. Therefore, we ectopically induced the expression of hid-3′UTRmut (updTS::hid-3′UTRmut,GAL80ts) that carries two point mutations at the bantam recognition sites and compared it with the transgene that contains the WT hid 3′ UTR (upd-GAL4;UAS-hid-3′UTRWT). After 14 d at the restrictive temperature (29°C), the average hub cell number of hid-3′UTRmut was reduced by 80%, and the remaining hub cells showed strong TUNEL staining (Fig. 2, D–G). Moreover, 18% of

Figure 2. miRNAs in the stem cell niche prevent hub cell death. (A–C′) Apical tip of control, hid, or grim GFP reporters (green) expressed under Tubulin promoter and immunostained for Fas3 (red and asterisks; hub). Control GFP reporter (A and A′), hid 3′ UTR GFP reporter (B and B′), and grim 3′ UTR GFP reporter (C and C′). Note reduced GFP expression in the hub. (D–G) Testes of flies raised for 14 d at 29°C immunostained for Fas3 (hub; blue), TUNEL (red and inset), and Vasa (germ cells; green). (D) Overexpression of hid-3′UTRWT in the hub (updTS::hid-3′UTRWT). (E and F) Overexpression in the hub of hid carrying two point mutations in bantam recognition sites (updTS::hid-3′UTRmut) results in hub (asterisk) cell death (E) or complete niche loss (F). Arrowhead marks spontaneous GCD and serves as TUNEL control. (G) Shown are average number of hub cells per testis along with 95% confidence intervals (error bars). Total number of testes scored: control (upd-GAL4;GAL80ts outcrossed to w1118), n = 29; updTS::hid-3′UTRWT, n = 39; and updTS::hid-3′UTRmut, n = 55. Statistical significance was determined as in Fig. 1 F; **, P ≤ 0.005 between hid-3′UTRmut and both hid-3′UTRWT and control. (H) qRT-PCR of hid transcript levels relative to rpl32 of RNA extracted from testes of control or hid-3′UTRWT or hid-3′UTRmut, levels are normalized to control. Error bars denote SD of three biological repeats each in triplicate measurements. *, P < 0.05 between hid-3′UTRmut and control. (I–K) Overexpression of hid-3′UTRWT together with bantam sponge for 4 d at 29°C resulted in hub cell loss. (K) Shown are average number of hub cells per testis along with 95% confidence intervals (error bars). The total number of testes scored: updTS::banSP, n = 38; updTS::hid-3′UTRWT, n = 37; and updTS::hid-3′UTRWT, banSP, n = 42. Statistical significance was determined as in Fig. 1 F; **, P ≤ 0.005 between hid-3′UTRWT, banSP and both banSP and hid-3′UTRWT.
the testes presented with complete niche loss (Fig. 2 F). Quantification of hid by qRT-PCR revealed that the mRNA levels of hid-3′UTRmut were significantly elevated (Fig. 2 H).

Surprisingly, complete removal or replacement of hid 3′ UTR was even less lethal than hid-3′UTRwt (unpublished data), indicating the existence of currently unknown stabilizing elements within the hid 3′ UTR that oppose the actions of miRNAs and enhance hid mRNA stability and/or translation. Next, we used a UAS-bantam sponge transgene that contains an artificial 3′ UTR region with 20 binding sites for bantam, allowing it to quench most bantam molecules, making them unavailable to regulate other targets (Herranz et al., 2012). As expected, expression of the bantam sponge by itself in the hub did not affect hub viability. However, as depicted in Fig. 2 (I–K) the sponge-induced reduction in bantam levels enabled hid-3′UTRwt to induce hub cell death. These results provide proof of the principle that the inability of hid to induce hub cell death is due at least in part to the action of antiapoptotic bantam miRNA.

RNAi-mediated knockdown of dcr1 in the hub leads to apoptosis

Following the proof of concept that the niche is protected from apoptosis by bantam, we tested whether additional miRNAs play a role in protecting the hub of adult males from apoptosis. We therefore disrupted the general process of miRNA production in the hub by RNAi-mediated knockdown of Dcr1, the final processor of all miRNA production. This was done using the TARGET system to drive UAS-dcr1RNAi only in the hub of the entire testis. Facilitation of dcr1 inhibition in this system is possible, since in flies the RNAi and the miRNA pathways use different Dcr enzymes and mutant clones cannot be obtained in postmitotic hub cells (Lee et al., 2004). Immunofluorescence staining of testes from dcr1RNAi flies with anti-Dcr1 antibody (Ab) verified that Dcr1 expression is indeed reduced only in the hub cells (Fig. S2, A and B). Because the time window to detect apoptotic events is narrow, we examined testes with TUNEL staining at multiple time points after shifting the conditional dcr1RNAi flies to the restrictive temperature (Fig. 3 A). Although many samples showed spontaneous germ cell death (GCD) that occurs often in the germline, no TUNEL signal was observed in the hub of control flies (Fig. 3 B; Yacobi-Sharon et al., 2013). Compared with control, after 6-d incubation of dcr1RNAi (upd-GAL4;GAL80°;UAS-dcr1RNAi) males at 29°C, the average hub cell number decreased by 30% (Fig. 3, C and G). Nevertheless, all testes contained a functional niche. However, after 8 d, the average hub cell number was reduced by 80% (Fig. 3 G). In these experiments, 70% of the testes showed positive TUNEL staining in hub cells, while the remaining 30% had already lost their niche (Fig. 3 D). Moreover, 100% of testes of dcr1RNAi males kept for 14 d at the restrictive temperature presented with a completely absent niche (Fig. 3, E and G). Some of the testes contained remnants of mature sperm, while others had completely empty tubes. Hub cells, CySCs, GSCs, and spermatagonia germ cells were lost, indicating that in the absence of miRNAs, hub cells undergo cell death, causing the neighboring stem cells to detach from the niche and differentiate.

To further confirm that apoptosis is indeed the underlying mechanism for hub death in the absence of miRNAs, we blocked apoptotic cell death by simultaneous expression of the baculovirus P35 caspase inhibitor (Hay et al., 1995) together with dcr1RNAi in the hub (upd-GAL4;UAS-P35;UAS-dcr1RNAi,GAL80°). In these experiments, the average hub cell number of the testes of flies raised at 29°C for 16 d increased to four hub cells, and 70% of the testes presented with functional niche (Fig. 3, F and G), indicating that P35 prevented dcr1RNAi-induced hub cell loss. To determine that the effect of hub cell death is not caused by off-targets of the dcr1RNAi line (24667; Vienna Drosophila Resource Center; VDRC), we tested an additional line (106041; VDRC) that also caused apoptosis of the hub cells. Moreover, RNAi-mediated knockdown of pasha, another processor of miRNA biogenesis, also induced hub cell death (Fig. S2, C–G). In contrast with the hub, introduction of dcr1RNAi into GSCs, CySCs, and spermatogonia (esg-GAL4,UAS-gfp;UAS-dcr1RNAi,GAL80°) did not cause any cell loss (Fig. S2, H and I), which is in agreement with previous findings showing that dcr1 mutant clones in GSCs exhibit a delayed cell cycle but the cells remain alive (Hatfield et al., 2005). Together, these results indicate that miRNAs have a distinct role in protecting the hub from demise.

Identification of the apoptotic genes that are regulated by miRNA in the hub

We next focused on identifying the specific set of genes that regulate hub apoptosis. For this, we performed a transcriptome analysis of cDNA libraries of four RNA samples each in two biological repeats obtained from testes of conditional dcr1RNAi males and age-matched controls at two time points: 6 d, before apoptosis is detected (Fig. 3, C, G, and H), and 8 d, immediately after apoptosis occurs (Fig. 3, D, G, and H). Using differential gene analyses, we focused on changes in genes that are known regulators of apoptosis (Fig. 3 H). Importantly, although dcr1RNAi was induced only in hub cells, we were able to detect a significant increase in the levels of nine previously reported apoptosis-associated genes in the 6-d dcr1RNAi group, seven of which were also significantly increased in 8-d dcr1RNAi. These genes include the transcription factors grainy head (grh) and lola (Cenci and Gould, 2005; Bass et al., 2007), the immune deficiency (imd) gene (Georgel et al., 2001), the phagocytic proteins croquemort (Franc et al., 1999), and scab (Nonaka et al., 2013), and the IAP antagonist hid (Fig. 3 H; Grether et al., 1998). In addition to the apoptosis-associated genes, we detected a significant decrease in 13 cell-survival genes in the 8-d dcr1RNAi, seven of which were already significantly decreased at 6-d dcr1RNAi. These genes include the antiapoptotic factor DEF related protein 3 (drep3; Park and Park, 2012), the telomere maintenance protein nbs (Oikemus et al., 2006), and two components of the cell survival EGF pathway, EGFR and Spitz (Fig. 3 H; Bergmann et al., 1998).

Consistent with these observations, qRT-PCR analysis of RNA extracted from testes of 6- or 8-d conditional dcr1RNAi showed a significant enrichment of four apoptosis-associated transcripts (grh, arrt, atg7, and hid) relative to age-matched controls (Fig. S3 A). qRT-PCR analysis also verified a significant decrease in two cell survival transcripts (debel and bim; Fig. S3 B). Moreover, immunostaining the testes of dcr1RNAi with anti-Hid Ab revealed induction of Hid in the hub cells, verifying transcriptome analysis and supporting apoptosis induction of hub cells without miRNAs (Fig. S3, C and D).
To determine whether induction of proapoptotic genes in dcr1RNAi is the main cause for hub cell apoptosis, we reduced both hid and dcr1 simultaneously in the hub for 8 d at 29°C (upd::UAS-dcr1RNAi,UAS-hidRNAi). These experiments showed that hid knockdown completely rescues the dcr1RNAi phenotype, indicating that antiapoptosis by miRNAs is a key pathway regulated in the niche to preserve its integrity (Fig. S3, E–H).

Identification of miRNAs that express in the hub

We performed a miRNAome analysis of testes from WT flies using NanoString Fly technology, and 100 miRNAs were identified and quantified (Table S1). We next hypothesized that the nine apoptosis-associated mRNAs that were found to be elevated before apoptosis in the 6-d dcr1RNAi sample are direct targets of miRNAs in the hub (D, 8 d) and niche depletion, and only mature sperms are detected (E, 14 d). P35 rescues dcr1RNAi (upd-GAL4;UAS-P35;UAS-dcr1RNAi,GAL80ts). Shown are average number of hub cells per testis along with 95% confidence intervals (error bars). The total number of testes from upd::dcr1RNAi scored: 6 d, n = 43; 8 d, n = 25; 14 d, n = 37; P35 rescues dcr1RNAi, n = 36. Statistical significance was determined as in Fig. 1F; *, P ≤ 0.05 between 6 d and control; **, P ≤ 0.005 between 8 d dcr1RNAi and control and P35 rescue. Note that for dcr1RNAi at 14 d, the GSC average number is zero. (H) Transcriptome analysis for apoptotic genes whose levels were changed in 6- or 8-d dcr1RNAi relative to age-matched controls.

miRNAs protect the hub from x-ray and UV irradiation

Removal of miRNAs from the hub by dcr1RNAi is a gradual process that ends 14 d after induction at the restrictive temperature and results in niche dissemination (Fig. 3 E). This was shown to occur in the hub, as the stem cell niche is protected from apoptosis.
Figure 4. Expression of antiapoptotic miRNAs in the hub. (A) Venn diagram of computationally predicted (green) and evolutionarily conserved miRNAs sites (yellow) for the nine apoptosis-associated genes increased in dcr-2RNAi compared with the miRNAs that are expressed in the testis according to the NanoString Fly miRNAome (red) revealed 17 potential antiapoptotic miRNAs. (B–F) Testis niches from GFP sensors (green) immunostained for Fas3 (red and asterisks; hub). Testes of control GFP sensor (B and B′), bantam sensor (C and C′), and miR-9a sensor (D and D′) expressed under the Tubulin promoter. Testes of control sensor (E and E′) and miR-277 sensor (F and F′) expressed under the Ubiquitin promoter. GFP of control and miR-9a sensors (B, D, and E) is expressed in the hub. GFP of bantam and miR-277 sensors is inhibited by endogenous levels of bantam and miR-277 in the hub (C and F).

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completely abolished. To find out whether miRNAs in the hub provide protection from external irradiation–induced apoptosis, we irradiated the flies of 6-d conditional dcr-2RNAi in the hub with x-ray (4,000 rads) or UV (180 kg·m²·s⁻²) radiation. As expected, irradiated control and nonirradiated conditional dcr-2RNAi showed similar average numbers of hub cells (Fig. 5, A, B, D, and G). However, 100% of the testes examined from irradiated conditional dcr-2RNAi did not survive apoptosis and showed either TUNEL-positive hub cells (Fig. 5 E) or complete regeneration arrest (Fig. 5 F). This result indicates that the inability of external stress to induce apoptosis can be modulated by a reduction in miRNA levels. In contrast, exposing flies expressing either bantam or miR-277 sponge (upd-GAL4;UAS-bantamSp or upd-GAL4;UAS-miR-277Sp) to the same irradiation protocol was insufficient to induce hub susceptibility to irradiation (not depicted). This suggests that the hub is protected from apoptosis by multiple miRNAs. Because each of the apoptosis-associated genes can be repressed by many miRNAs (e.g., hid 3’ UTR may be potentially regulated by >20 miRNAs), knocking down one miRNA is insufficient to affect hub resistance to irradiation.

Moreover, our transcriptome and qRT-PCR analyses showed that without miRNAs in the hub, the transcript levels of the transcription factor grh increases by 12-fold. We therefore hypothesized that overexpression of the Grh coding region, which lacks most of the 3’ UTR, and miRNA recognition sites (including 89/1,946 bp; Baumgardt et al., 2009), should also result in a sensitized hub for irradiation. As shown in Fig. 5 I, Grh overexpression indeed sensitized the hub to UV irradiation (180 kg·m²·s⁻²), and 58% of the testes showed strong TUNEL staining. These data suggest that under normal conditions, the expression of grh is repressed by miRNAs to prevent hub loss.

In summary, knockdown of miRNAs in the hub resulted in the induction of several apoptosis-associated genes including transcription factors and the IAP antagonist hid, indicating that miRNAs are incorporated into a large regulatory network that prevents hub apoptosis. The expression of the IAP antagonists rpr, hid, and grim is tightly repressed in living cells. However, they are rapidly up-regulated in response to an apoptotic signal and induce cell death by competitively binding and antagonizing Diap1, which leads to activation of the cell death program (Vasudevan and Ryoo, 2015). Antiapoptotic miRNAs that inhibit IAP antagonist translation act at the level of execution, which is practically downstream of all apoptotic events. In this study, we show that overexpression of IAP antagonists, which induces apoptosis in many cell types (Grether et al., 1995; Chen et al., 1996; White et al., 1996; Hétié et al., 2014), is unable to kill the hub cells. This implies that the hub contains a strong antiapoptotic mechanism. In contrast, removal of miRNA expression from the hub is in itself sufficient to induce hub cell death and as such may serve as a future strategy to induce death in tumors that are resistant to apoptosis by genotoxic signals.

The function of the hub is to keep the stem cells in an undifferentiated state, and spermatogenesis can be maintained even when only one hub cell remains alive (Resende et al., 2013). However, when all hub cells die, spermatogenesis cannot be regained and the testis degenerates. We show that several miRNAs that are expressed in the hub protect it from apoptosis. Nevertheless, knocking down one miRNA is insufficient to affect hub resistance to irradiation. These results are in line with previous findings, indicating that individual miRNAs are not essential for viability (Miska et al., 2007). Nonetheless, because the hub is resistant to a variety of harmful signals, additional protective mechanisms besides miRNAs are probably involved in preservation of hub integrity.

Contrary to other regenerative tissues where antiapoptotic miRNAs are found primarily in the stem cells themselves (Hatfield et al., 2005; Weng and Cohen, 2015; Xing et al., 2015), we found that in the Drosophila testis, they are expressed in
the postmitotic niche cells. We propose that because male spermatogonia germ cells have the unique ability to dedifferentiate and regain GSC identity (Brawley and Matunis, 2004), an antipoptotic propensity in them is dispensable. Rather, the ability to protect the reproductive system from apoptosis must be maintained by the postmitotic niche cells that nonautonomously enable recovery of the stem cell population after irradiation.

Materials and methods

Generation of DNA constructs

pUASTattB-hid FL, pUASTattB-hid-3′UTRMut, pUASTattB-rpr, and pUASTattB-grim were generated in our laboratory by cloning the genes with their 3′ UTR into pUASTattB plasmid. hid CR was amplified by PCR from pUAST-hidMF plasmid (a gift from H. Steller) with forward primer Hid_CR_For, 5′-ATG GCC GTG CCC TTT TAT TTG CCC GAG GGC GGC GCCG-3′, and reverse primer Hid_CR_HA_Rev2, 5′-TCA AGC GTA GTC TGG GAC GTC GTA TGG GTA TCG CGC CGC AAA GAA GCC ACA GCCC-3′. The PCR fragment was ligated into pGEM T Easy vector, and the insert was further digested with EcoR1 and cloned into EcoR1, digested, and calf intestinal alkaline phosphatase (CIP) treated with pUASTattB to generate pUASTattB hid CR. hid 3′ UTR was amplified by PCR from pUAST-hidMF plasmid (a gift from H. Steller) with forward primer Hid3′UTR_For, 5′-GGA CTAGtAAG CGC AGG AGA CGT GTA ATCG-3′, and reverse primer Hid3′UTR_Rev , 5′-GGA CTA GTG TAT TTA TTT TTT GCT TGT TTG TC-3′. Similarly, rpr with its 3′ UTR was amplified by PCR from reaper-HA3-PUA ST plasmid (a gift from H. Steller) with forward primer Rpr5_For, 5′-TCA TTG AAT AAG AGA GAC ACC AGAA-3′, and reverse primer Rpr_3′UTR_Rev , 5′-CCC AAG CTT TTC GAC TCA TCT TCG-3′.

PCR fragments of grim and rpr were ligated into pGEM T Easy vector, and the inserted were further digested with EcoRI and cloned into EcoRI, digested, and calf intestinal alkaline phosphatase (CIP) treated with pUASTattB to generate pUASTattB híd FL. To generate pUASTattB-hid-3′UTR-Mut, site-directed mutagenesis (Stratagene) was used to mutate two bantam recognition sites in hid-3′ UTR (1041ATC = GCA and 1233ATC = GCA) with primers Bantam2 mut_For, 5′-TGG AAA TTA ATG AAA ATT GGC ATC CGC AGC TAG CC-3′, Bantam2 mut_Rev , 5′-GGC TAG CTG CGG ATG CCA ATT TTC ATT AAT TTC CA-3′, Bantam3 mut_For, 5′-CCA ATT CCC AAA AAT CGC ATT GGC ATC ATG GAT TTA TAC-3′, and Bantam3 mut_Rev , 5′-GTAAATCCATGATGCCAATT GCCATTTTGTAGGATTG-3′.

grim with its 3′ UTR was amplified by PCR from pUAST-grimMF plasmid (a gift from H. Steller) with forward primer Grim_CR_For, 5′-ATGGCCATCGGCATTTCATCCAGG-3′, and reverse primer Grim_3′UTR_Rev , 5′-GGCTAGCTGGATGCAATTTTATATTTCGCA-3′. Similarly, rpr with its 3′ UTR was amplified by PCR from reaper-HA3-PUAST plasmid (a gift from H. Steller) with forward primer Rpr5_For, 5′-TCA TTG AAT AAG AGA GAC ACC AGAA-3′, and reverse primer Rpr_3′UTR_Rev , 5′-CCC AAG CTT TTC GAC TCA TCT TCG-3′.

PCR fragments of grim and rpr were ligated into pGEM T Easy vector, and the inserted were further digested with EcoRI and cloned into EcoRI, digested, and CIP treated with pUASTattB to generate pUASTattB-grim and pUASTattB-rpr, respectively. The sequence of all DNA constructs described above was verified by DNA sequencing.

Drosophila stocks

Flies were raised at 25°C on standard cornmeal molasses agar medium freshly prepared in our laboratory. Crosses for the inducible GAL4/UAS TARGET system (McGuire et al., 2004)
were set up and maintained at 18°C until eclosion. Adults were placed in vials (20 males and 20 females per vial), kept at 29°C, and flipped every 2 d thereafter. Control and experiments were set and tested at the same time. Fly strains used in this research were w^1118, control Tub-GFP sensor, Tub-bantam-GFP sensor, Tub-hid-3′UTR reporter, Tub-grim-3′UTR reporter (S.M. Cohen; Brennecke et al., 2003), Tub-miR-9a-GFP sensor (E.C. Lai; Bejarano et al., 2010), control Ubi-GFP sensor, Ubi-miR-277-GFP sensor (K. Förstemann; Esslinger et al., 2013), upd-GALA4 (T. Xie), upd-GALA4;GAL80^{TS} (D.L. Jones) UAS-dcr1RNAi lines (24667 and 4106041; VDRC), and UAS-pashaRNAi and UAS-hid-RNAi (40118 and 31210; VDRC). To simultaneously knockdown hid and dcr1, we generated a recombinant line on the third chromosome (Rec#1, UAS-hid RNAi, UAS-dcr1RNAi) PUAS-grh.B12M (Bloomington Drosophila Stock Center; Baumgardt et al., 2009). The esg-GAL4, UAS-gfp, GAL80ts was made from esg-GAL4, UAS-gfp, and GAL80ts (Loza-Coll et al., 2014). pUASTattB-hid FL, pUASTattB-hid-3′UTRmut, pUASTattB-rpr, and pUASTattB-grim were injected into yw; attP2 (third chromosome; 8622; Bloomington Drosophila Stock Center) with BestGene.

Immunofluorescence TUNEL and stem cell counting
Wholemount testes from adult Drosophila were dissected in PBS and placed in Terasaki plates in 10 µl fixed solution of 2% PFA in PLP buffer (0.075 M lysine and 0.01 M sodium phosphate buffer, pH 7.4) for 1 h at RT, rinsed, and washed twice in PBST (0.5% Triton X-100), followed by standard immunofluorescence staining. Primary antibodies used in this study were as follows: polyclonal rabbit anti-Vasa (1:200; d-260; Santa Cruz Biotechnology), rabbit anti-Fas3 (1:10; 7G10; Developmental Studies Hybridoma Bank). anti-Hid (1:50; d-300; Santa Cruz Biotechnology), and mouse primary antibodies were as follows: polyclonal rabbit anti-Vasa (1:200; d-260; Santa Cruz Biotechnology), rabbit anti-Dcr1 (1:100; PA5-19429; Thermo Fisher Scientific), rabbit anti-Hid (1:50; d-300; Santa Cruz Biotechnology), and mouse anti-Fas3 (1:10; 7G10; Developmental Studies Hybridoma Bank). Secondary antibodies were obtained from Jackson Immunoresearch Laboratories. For TUNEL labeling, testes were refixed, washed, and labeled with the In Situ Cell Death Detection kit (Roche) according to the manufacturer’s instructions. Samples were mounted in Vectashield mounting medium with DAPI (Vector Laboratories).

Microscope image acquisition
Images were taken from samples at RT on a Zeiss AxioImager M2 microscope equipped with an ApoTome2 Optical sectioning device. The image shown in Fig. S1 A was taken with objective Plan Achromat 20×/0.8 M27; all the other images in the manuscript were taken with objective Plan Achromat 63×/1.40 oil M27. All images in all figures were single sections that were taken with high-resolution microscopy camera AxioCam HRm Rev.3 FireWire using Zen acquisition software and were processed with Adobe Photoshop CS6. GSCs were counted from multiple z stacks as Vasa-positive cells that were in direct contact with the hub that was marked with anti-Fas3.

X-ray irradiation
WT (w^1118) or upd-dcr1RNAi that were maintained for 6 d at 29°C were irradiated with 4,000 rads, and then recovered for 4 or 24 h or 17 d at 25°C. After recovery, testes were dissected and subjected to immunofluorescence and TUNEL labeling.

RNA extraction
Testes of 100 flies (~200 testes) of each phenotype and age were dissected in PBS diethyl pyrocarbonate. Testes were collected and pooled in 100 µl TRizol reagent and stored at −80°C until RNA extraction. To maximize RNA extraction, frozen samples were thawed at 37°C and refrozen in liquid nitrogen (~80°C) five times followed by five cycles of 30-s vortex and rest. Then, 100 µl of 99% ethanol was added to the samples, and total RNA was extracted using Direct-zol RNA miniprep kit (Zymo Research) with DNase treatment according to the manufacturer’s instructions. The RNA was eluted in 50 µl preheated DNase- and RNase-free water and kept at ~80°C for future use. RNA quality was measured by a BioAnalyzer, and samples were used for miRNAome, transcriptome, or qRT-PCR.

Transcriptome analysis and statistics
Illumina cDNA libraries were prepared with TruSeq RNA V2/Illumina kit from 1 µg total RNA extracted from testes of four RNA samples each in two biological repeats. The four samples were conditional dcr1RNAi males (upd-GALA4,GAL80^{TS};UAS-dcr1RNAi) and age-matched controls (upd-GALA4,GAL80^{TS} outcrossed to w^1118) that were raised at 29°C for 6 and 8 d. Libraries were prepared and sequenced with Illumina HiSeq 2500 at the Technion Genome Center. Raw reads were filtered for Illumina adapters, and low-quality reads, using Trimmomatic. Filtered reads were aligned to the Drosophila genome (dm6, FlyBase 6.05) using STAR (settings: alignIntronMax = 25,000; genomeSAindexNbases = 9.15; sjdbGTFfile). Gene expression levels were quantified using htseq-count, and differential expression was analyzed using edgeR. Differential expression data were filtered based on fold change (1.3 < FC < −1.3) and significance cutoff (P ≤ 0.05). We then searched the list for apoptotic genes that showed differential expression in conditional dcr1RNAi males versus control in both testes from 6 and 8 d.

miRNAome analysis and statistics
Total purified RNA samples (0.5 µg at 100 ng/µl) of WT w^1118 in three biological repeats were used to determine the identity and levels of miRNAs with NanoString Technologies (nCounter miRNA expression kit). Raw data were normalized using nCounter software and compared with a list of in silico predicted miRNAs for the nine apoptosis-associated genes (TargetScan Fly; Ruby et al., 2007).

qRT-PCR and statistics
1 µg RNA was reverse transcribed with random hexamer mixture and the High-Capacity cDNA Reverse Transcription Kit (Thermo Fisher Scientific) according to manufacturer’s instructions. Quantitative real-time PCR was performed with a StepOnePlus Real-time PCR System using TaqMan Gene Expression Assay (Applied Biosystems). Relative hid (assay ID: Dmo1823031_m1) levels were compared with Ribosomal Protein L32 (RPL-32; assay ID: Dmo2151827_g1). For other genes, we used SYBR Green PCR Master mix (Applied Biosystems), and the efficiency of the target and reference amplification was approximately equal. Specific primers for qRT-PCR of testes were gnr forward, 5′-CGAGGAAGT GTGCACAA-3′, and reverse, 5′-GAACCGAATGTGATCTTG-3′;
arrt forward, 5′-AGCTACATTATTCTGATGCAC-3′, and reverse, 5′-GCG GAT ACT GGA AGA TTT GC-3′; debcl forward, 5′-AGT TTG AGC CCT TTC AGT TTA GGC-3′; atg7 forward, 5′-TAA  GGA TTG TG-3′; and blm forward, 5′-AAT  CAA TAA ACT GGC TTC CCT TTT CCC GGC ACT GAAC-3′, and reverse, 5′-TCAGTGAAGCAAATTGAGCA-3′. Levels were compared with the average of two normalizing genes: act24A forward, 5′-TTCTAAGGCGGGTATCG-3′, and reverse, 5′-ATGGCGGCACAATTTCAC-3′; and sdhA forward, 5′-GCT GTC GCG ATA TGT CCA TCG ATT TTG-3′, and reverse, 5′-CTT  CGA TAT CTT GTC CGG ATC-3′. Real-time PCR results were analyzed using StepOne software (Applied Biosystems), and significance was determined using Student’s t test. An average of three experiments (each performed in triplicate measurements) is shown (mean ± SD).

Statistical analysis
For quantification of GSCs and hub cell number, the mean ± 95% confidence interval and the number (n) of testes examined are shown. P values were generated after a two-tailed Student’s t test or determined by one-way ANOVA, and post hoc analysis was performed with Tukey multicomparison test if samples were normally distributed and had equal variances; * P ≤ 0.01; ** P ≤ 0.005. The Shapiro–Wilk test, which is appropriate for small sample sizes (<50 samples), was used with SPSS software to determine normality.

Online supplemental material
Fig. S1 shows that updf5 drives expression only in the hub cells of the entire testis. Fig. S2 illustrates that impaired miRNA biogenesis in the hub leads to apoptosis but does not affect the viability of germ and cyst cells. Fig. S3 provides verification for the transcriptome analysis. Table S1 presents the miRNAs that are expressed in the Drosophila testis, and Table S2 shows the potential antiapoptotic miRNAs that are expressed in the hub cells.

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Author contributions: M. Volin, M. Zohar-Fux, and O. Gonen designed and performed the in vivo experiments. M. Volin and L. Porat-Kuperstein performed the qRT-PCR and transcriptome analysis. M. Volin and O. Gonen performed the miRNAome analysis. H. Toledano designed the study, coordinated the project, and wrote the manuscript with input from all authors.

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