**Drosophila** Ataxin 2-binding protein 1 marks an intermediate step in the molecular differentiation of female germline cysts

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**SUMMARY**

In the *Drosophila* ovary, extrinsic signaling from the niche and intrinsic translational control machinery regulate the balance between germline stem cell maintenance and the differentiation of their daughters. However, the molecules that promote the continued stepwise development of ovarian germ cells after their exit from the niche remain largely unknown. Here, we report that the early development of germline cysts depends on the *Drosophila* homolog of the human ataxin 2-binding protein 1 (A2BP1) gene. *Drosophila* A2BP1 protein expression is first observed in the cytoplasm of 4-, 8- and 16-cell cysts, bridging the expression of the early differentiation factor Bam with late markers such as Orb, Rbp9 and Bruno encoded by arrest. The expression of A2BP1 is lost in *bam*, *sans-fille* (*snf*) and *mei-P26* mutants, but is still present in other mutants such as *rbp9* and *arrest*. A2BP1 alleles of varying strength produce mutant phenotypes that include germline counting defects and cystic tumors. Phenotypic analysis reveals that strong A2BP1 alleles disrupt the transition from mitosis to meiosis. These mutant cells continue to express high levels of mitotic cyclins and fail to express markers of terminal differentiation. Biochemical analysis reveals that A2BP1 isoforms bind to each other and associate with Bruno, a known translational repressor protein. These data show that A2BP1 promotes the molecular differentiation of ovarian germline cysts.

**KEY WORDS:** Ataxin 2-binding protein 1, *Drosophila*, Oogenesis, Ovarian tumor

**INTRODUCTION**

The development of naïve cells towards a terminally differentiated fate often proceeds through a number of distinct steps. Complex transcriptional and post-transcriptional hierarchies regulate transitions between these stages so that differentiation occurs in a temporal and tissue-specific manner. *Drosophila* ovarian germline cyst development has served as a useful platform for studying how diverse mechanisms coordinate to establish specific cell fates, particularly with regards to stem cells and their differentiating progeny.

Ovarian cyst development begins in the germarium with the asymmetric division of a germline stem cell (GSC) (for a review, see Wong et al., 2005). This division results in one of the daughters being displaced away from the cap cell niche. This cell, called the cystoblast, proceeds through four incomplete mitotic divisions to form an interconnected 16-cell cyst. Within this cyst, one cell becomes the oocyte, whereas the remaining cells become supportive nurse cells. Once encapsulated by follicle cells, the cyst buds off of the germarium to become an egg chamber.

Several molecular and morphological markers highlight changes within differentiating germline cysts. One widely used marker has been the fusome, a germline-specific organelle that has many properties of the endoplasmic reticulum (Lighthouse et al., 2008; Snapp et al., 2004). The fusome plays roles in regulating the mitotic cell cycle within germline cysts and in oocyte specification (Lin and Spradling, 1995; Lin et al., 1994). Within GSCs, the fusome appears small and round. During the incomplete mitotic divisions, the fusome becomes branched and runs through the ring canals of the interconnected cells within the germline cyst (de Cuevas and Spradling, 1998). The degree of fusome branching reflects the number of cells within a developing cyst and has served as a primary marker for evaluating germ cell differentiation within the germarium.

Expression of *bam* is both necessary and sufficient for the early differentiation of germline cysts. Cytoplasmic Bam is first observed within cystoblasts and persists through eight-cell cysts. Loss of *bam* results in a tumorous phenotype in which all germline cells remain as single cells in a pre-cystoblast state (McKearin and Ohlstein, 1995; McKearin and Spradling, 1990). The biochemical function of Bam remains unclear but recent findings show at least one of its roles is to repress *nanos* translation (Li et al., 2009).

**KEY WORDS:** Ataxin 2-binding protein 1, *Drosophila*, Oogenesis, Ovarian tumor

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Accepted 26 July 2010
A2BP1 is expressed in developing germline cysts

The initial differentiation of *Drosophila* ovarian germ cells depends on the expression of the *bam* gene. *bam* represses *nanos* translation through elements within the 3’UTR of *nanos* mRNA (Li et al., 2009). Once *Bam* levels decrease, *Nanos* expression re-emerges in 16-cell cysts. However, during the course of our studies, we

RESULTS

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confirmed the GFP sequence from the protein trap was spliced in translational start site (Fig. 1F) (Buszczak et al., 2007). RT-PCR of several available cDNA clones revealed at least three additional splice variants (Fig. 1F). Five of these isoforms have been previously detected in the cytoplasm of early multicellular germline cysts (bracket). (A2BP1 and human A2BP1 are 90% identical. (F) Structure of the A2BP1 gene and transposon insertions in the region. Scale bars: 20 μm.

Performing BLAST analysis of human A2BP1 sequence against the Drosophila genome showed CG32062 to be the closest homolog of A2BP1. Because of these similarities, we will refer to CG32062 as A2BP1 hereafter.

Human A2BP1 was first identified based on its association with human ataxin 2, a protein implicated in spinocerebellar ataxia type 2 (Shibata et al., 2000). Recent studies suggest A2BP1 may also contribute to several other human diseases, including cancer, autism and osteoarthritis (Cheung et al., 2008; Huang et al., 2009; Martin et al., 2007; Zhai et al., 2009). Previous molecular analysis of mammalian A2BP1 has focused on its role in alternative splicing (Auweter et al., 2006; Fukumura et al., 2009; Jin et al., 2003; Kuroyanagi et al., 2007; Lee et al., 2009; Minovitsky et al., 2005; Nakahata and Kawamoto, 2005; Underwood et al., 2005; Zhang et al., 2008; Zhou et al., 2007; Zhou and Lou, 2008). However, the localization of A2BP1 is not always restricted to the nucleus. In mammals, A2BP1 itself undergoes alternative splicing and several of the resulting isoforms localize to the cytoplasm, leaving open the possibility that the protein carries out additional functions (Nakahata and Kawamoto, 2005). Given the dynamic subcellular localization patterns of A2BP1 during oogenesis, we considered the possibility that Drosophila A2BP1 protein also has multiple functions relating to RNA metabolism.

A2BP1 protein is expressed in a novel pattern during early cyst development

We raised a polyclonal antibody against a region of the endogenous A2BP1 protein common to all annotated isoforms. Staining A2BP1/CC00511 heterozygotes with this A2BP1 antibody showed the GFP protein trap displayed the same expression pattern and subcellular localization as the endogenous protein (see Fig. S1A in the supplementary material). In situ hybridization suggested the expression of endogenous A2BP1 within the gerarium was regulated at the level of transcription (see Fig. S1B in the supplementary material).

To further define the spatial and temporal expression pattern of A2BP1, we compared its protein expression to a set of molecular markers that define different developmental stages during early cyst development (Fig. 2). The first two markers we examined were Nanos and Bam (Fig. 2A). Nanos is expressed in all GSCs occasionally noticed a delay in when high levels of Nanos expression reappeared after Bam antibody staining had decreased below the levels of detection (Fig. 1A). In addition, we observed a similar gap in when cysts express high levels of cytoplasmic Sxl and Bruno, two factors previously described as having mutually exclusive expression patterns (Fig. 1B) (Wang and Lin, 2007). Based on these results, we hypothesized that unidentified factors might function in four- and eight-cell cysts (Fig. 1C). To identify such genes, we screened a previously described protein trap collection (Buszczak et al., 2007). These efforts led to the identification of CC00511. GFP expression within CC00511 ovaries was first observed in the cytoplasm of early multicellular germline cysts (Fig. 1D). In region 3 of the gerarium, the GFP expression shifted from the cytoplasm to the nuclei of the germline cells where it remained for the rest of oogenesis. GFP was also observed in the nuclei of follicle cells beginning in region 2b of the gerarium.

Previous molecular analysis showed the CC00511 P-element was inserted in an intron of the CG32062 gene downstream of the translational start site (Fig. 1F) (Buszczak et al., 2007). RT-PCR confirmed the GFP sequence from the protein trap was spliced in frame to the first exon downstream of the element’s insertion site. The CG32062 locus covers ~79 kb and contains many splice variants (Fig. 1F). Five of these isoforms have been previously annotated (FlyBase). Sequencing several other available cDNA clones revealed at least three additional splice variants (Fig. 1F). The molecular function of CG32062 remains uncharacterized but is a recent large-scale RNAi screen implicated this gene in nervous system development (Koizumi et al., 2007). A2BP1 protein is expressed in a novel pattern during early cyst development (Fig. 2). The first two markers we examined were Nanos and Bam (Fig. 2A). Nanos is expressed in all GSCs
but largely repressed in dividing cysts (Wang and Lin, 2004). Nanos reappears at high levels in newly formed 16-cell cysts. By contrast, Bam expression is first observed in cystoblasts and persists up until the eight-cell cyst stage. Staining for these two proteins and A2BP1 revealed that A2BP1 exhibits a novel expression pattern. A2BP1 was not expressed in the earliest Bam-positive cells but Bam and A2BP1 expression overlapped in four- and eight-cell cysts. As A2BP1 levels increased in eight-cell cysts, Bam expression decreased. A2BP1 expression peaked in cysts after Bam expression was no longer observed and as Nanos expression began to re-emerge.

Next, we compared A2BP1 expression with Sxl and Mei-P26, two markers that label GSCs and early cysts (Fig. 2B). Others have shown Sxl is cytoplasmic in GSCs, the cystoblast and two-cell cysts (Bopp et al., 1993; Chau et al., 2009). In later cysts, Sxl cytoplasmic expression levels decrease and the protein moves into the nucleus. Double labeling with Sxl and A2BP1 antibodies revealed that cytoplasmic Sxl did not overlap with A2BP1 in the germarium (Fig. 2B). Like Sxl, Mei-P26 protein is first detected in GSCs (Liu et al., 2009; Neumuller et al., 2008). Mei-P26 expression continues to increase during cyst development, peaking in 16-cell cysts. Cytoplasmic A2BP1 expression overlapped with Mei-P26 expression and persisted in cysts even after Mei-P26 levels had fallen below the levels of detection (Fig. 2C).

Finally, we compared the expression of A2BP1 with Orb, Rbp9 and Bruno, the translational repressor encoded by the arrest gene (Fig. 2D-F). All three of these proteins exhibit very low levels of expression in GSCs and early cysts. The expression of these proteins dramatically increases in 16-cell cysts. We found A2BP1 expression preceded the highest levels of expression of Orb, Rbp9 and Bruno. Together, these data suggest A2BP1 exhibits a novel expression pattern that bridges the expression of the early differentiation marker Bam and the expression of late markers such as Orb, Rbp9 and Bruno.

A2BP1 germline expression depends on bam, mei-P26 and snf, but not on rbp9 or arrest
Although changes in fusome morphology reflect cell division (de Cuevas and Spradling, 1998), we reasoned that A2BP1 protein expression might provide a new molecular marker for evaluating germline cysts as they progress through differentiation. To test this idea, we examined A2BP1 antibody staining in ovaries from a variety of female sterile mutants. We also co-stained these samples with the 1B1 monoclonal antibody that labels fusomes and cell membranes. We first looked at A2BP1 expression in bam mutants that contain only single stem cell-like cells. As expected, given their early block in differentiation, bam mutant germline cells do not express high levels of A2BP1 (Fig. 3B). Next, we examined A2BP1 expression in snf, mei-P26, rbp9 and arrest mutant ovaries, all of which contain multicellular cysts of varying severity. We did not observe high levels of cytoplasmic A2BP1 staining in the germline cells of mei-P26 and snf mutant ovaries, despite the presence of multicellular cysts (Fig. 3C,D). By contrast, germline cells from rbp9 and arrest mutants both expressed readily detectable levels of A2BP1 at the appropriate stages (Fig. 3E,F). These data show, consistent with previous findings, that different ovarian tumor mutants arrest cyst development at distinct steps.
A2BP1 mutants display defects in early germline differentiation

In order to determine whether A2BP1 functioned during cyst differentiation, we sought to characterize A2BP1 mutant phenotypes. Previous transposon screens yielded a number of inserts in and around the A2BP1 locus (Fig. 1F). These included both P-elements (A2BP1CC00511, A2BP1KG06465) and piggyBac elements (A2BP1f03440, A2BP1f01889, A2BP1f02600) (Bellen et al., 2004; Buszczak et al., 2007; Thibault et al., 2004). We crossed these alleles to molecularly defined deficiencies that uncover the region and to each other (see Materials and methods). This complementation analysis revealed that some of these insertions resulted in a female sterile phenotype (see Table S1 in the supplementary material). To further characterize how A2BP1 mutations disrupt normal oogenesis, we stained ovaries with antibodies to specifically label germline cells and the 1B1 monoclonal antibody. This analysis revealed that both fertile and sterile A2BP1 mutants exhibited a range of related phenotypes (see Table S1 in the supplementary material; Fig. 4). Hemizygous and transheterozygous A2BP1CC00511 and A2BP1f02600 females were fertile but a large percentage of their egg chambers contained 31 nurse cells and one oocyte (Fig. 4B,C; see Fig. S2 in the supplementary material). In addition to cell counting defects, A2BP1f02600 mutant ovaries often appeared slightly tumorous and their egg chambers contained fusome remnants (Fig. 4C). Counting the number of ring canals within A2BP1CC00511 oocytes revealed that the extra nurse cells within these mutants arose from an extra round of mitosis prior to the egg chambers pinching off of the germarium (see Fig. S2 in the supplementary material). The same phenotype has been observed in encore mutants (Hawkins et al., 1996; Hawkins et al., 1997; Van Buskirk et al., 2000). The encore gene encodes a conserved protein that negatively regulates Bam protein expression during late cyst development. Interestingly, we observed an expansion of Bam expression in A2BP1CC00511 mutants (see Fig. S2D in the supplementary material). We also found that a bam null allele dominantly suppressed the extra nurse cell phenotype of A2BP1CC00511 mutant cysts (see Fig. S2E in the supplementary material). Moreover, the encoreΔ4 allele strongly enhanced the A2BP1CC00511 phenotype so that fusomes persisted in egg chambers well beyond the time when the organelle would normally be degraded (see Fig. S2F-H in the supplementary material). These findings suggested A2BP1 was required for the final maturation of 16-cell germline cysts within the germarium.

Stronger hypomorphic alleles of A2BP1 exhibited more severe phenotypes that further implicated A2BP1 as a crucial regulator of germline cyst development. Females homozygous and hemizygous for A2BP1fKG06463, A2BP1f01889 and A2BP1f03440 were sterile. Ovaries from these females were small and did not contain maturing egg chambers. Anti-Vasa and 1B1 staining revealed strong A2BP1 mutants displayed a tumorous phenotype (Fig. 4D,F). Germaria from these females had a large number of multicellular germline cysts, reminiscent of cystic tumors caused by mutations in mei-P26 and snf (Fig. 4D) (Chau et al., 2009; Page...
a strong hypomorphic allele of To characterize the molecular function of A2BP1, we tested whether meiotic transition Strong A2BP1 mutants arrest before the mitotic to germline during early cyst development. Nanos and Bam staining in wild-type and early and late markers within the germline. First, we compared homozygous for the A2BP1e03440 allele appeared normal through the early stages of oogenesis (data not shown). These results indicate that A2BP1 functions cell-autonomously within the germline during early cyst development.

Strong A2BP1 mutants arrest before the mitotic to meiotic transition To characterize the molecular function of A2BP1, we tested whether a strong hypomorphic allele of A2BP1 affected the expression of early and late markers in the germline. First, we compared Nanos and Bam staining in wild-type and A2BP1e03440 hemizygous ovaries. This analysis showed disruption of A2BP1 resulted in a dramatic expansion of Bam expression and a subsequent delay in late Nanos expression (Fig. 5A). The early expression of Nanos within GSCs remained unaffected, suggesting that A2BP1 mutations do not cause a GSC phenotype (see Fig. S3 in the supplementary material). Previous results have shown that Bam helps repress the translation of nanos mRNA (Li et al., 2009). We found expression of Nanos and Bam remained mutually exclusive from one another in A2BP1 mutant cysts. These data indicated that A2BP1 does not directly participate in the negative regulation of Nanos (see Fig. S3 in the supplementary material) and suggested that A2BP1 functions downstream of the initial steps of cyst differentiation.

In wild-type germaria, cytoplasmic Sxl and A2BP1 were expressed in mutually exclusive patterns (Fig. 2B). Given this relationship, we tested whether disruption of A2BP1 results in an expansion of cytoplasmic Sxl expression (Fig. 5B). Normally cytoplasmic Sxl expression is limited to the GSCs, cystoblasts and early multicellular cysts in the anterior region of the gerarium. However, A2BP1e03440 hemizygous mutants displayed cytoplasmic Sxl expression in germ cells throughout the gerarium, including in eight-cell and 16-cell cysts. Likewise, the expression of Mei-P26 appeared greatly expanded in A2BP1e03440 mutants (Fig. 5C). The expanded expression of both these markers indicated that A2BP1 mutants were unable to properly regulate gene expression during cyst development.

To further examine how mutations in A2BP1 affected gene expression during cyst development, we examined the expression of three late markers in control and A2BP1e03440 mutant ovaries: Orb (Fig. 5D), Rbp9 (Fig. 5E) and Bruno (Fig. 5F). Normally, early developing cysts express low levels of Orb, Rbp9 and Bruno. The expression of all three genes increases in 16-cell cysts. By contrast, A2BP1e03440 mutant ovaries displayed severe reductions in Orb, Rbp9 and Bruno expression, even though 16-cell cysts were present in the samples. These findings support the conclusion that A2BP1 promotes the expression of proteins needed for the final steps of cyst development.

A2BP1 mutant cysts appeared to remain mitotically active beyond the point when the meiotic program should normally be initiated. To test formally whether A2BP1 mutant germline cells displayed defects in the mitotic to meiotic transition, we stained control and mutant ovaries for C(3)G and Cyclin A (Fig. 5G). C(3)G is a component of the synaptonemal complex (Page and Hawley, 2001) and in wild-type samples accumulates at high levels after Cyclin A levels drop and cells have exited the meiotic cell cycle (Sugimura and Lilly, 2006). Hemizygous A2BP1e03440 mutants displayed defects in Cyclin A and C(3)G staining (Fig. 5G). Cyclin A expression persisted throughout the gerarium and robust C(3)G accumulation was not observed. Together, these experiments indicate that A2BP1 functions to promote changes in gene expression within four-, eight-cell and 16-cell cysts. The misregulation of these gene expression programs within A2BP1 mutants appears to block the normal transition from a mitotic cell cycle to a meiotic cell cycle.
A2BP1 isoforms associate with each other

We considered the possibility that different A2BP1 isoforms might form a functional complex together. To test this hypothesis, we performed a series of genetic and biochemical assays. Interestingly, our phenotypic analysis showed that the A2BP1KG06463 allele was fertile when placed over either of the other strong sterile alleles (A2BP1f01889 or A2BP1e03440) but not when placed over a small molecularly defined deficiency (see Table S1 in the supplementary material). However, careful examination revealed that germline cysts from A2BP1KG06463/A2BP1f01889 and A2BP1KG06463/A2BP1e03440 ovaries displayed counting defects at high penetrance and a mildly tumorous phenotype at low penetrance (see Fig. S4A,B in the supplementary material). Western blot analysis showed that these different mutations disrupt the expression of different A2BP1 isoforms, thus providing a possible explanation for their partial complementation (see Fig. S4C in the supplementary material). We tested for interactions between different isoforms using both yeast 2-hybrid and co-immunoprecipitation assays. The yeast 2-hybrid experiments revealed an interaction between A2BP1-PI and A2BP1-PE (see Fig. S4D in the supplementary material). Furthermore, co-immunoprecipitation experiments using epitope-tagged versions of different A2BP1 isoforms also indicated various A2BP1 isoforms associated with themselves and with each other (see Fig. S4E in the supplementary material; data not shown).

A2BP1 interacts with Bruno but not Rbp9

To further investigate the developmental function of A2BP1, we tested for genetic interactions between A2BP1 and several other mutants. We focused our efforts on rbp9 and arrest, two genes that function during the late stages of cyst development within the germarium. We reasoned that if A2BP1 worked together with rbp9 or arrest, mutations in these genes would enhance weak A2BP1 mutant phenotypes. To test this, we crossed single copies of rbp9 and arrest mutations into the A2BP1f02600/A2BP1e03440 background. A2BP1f02600/A2BP1e03440 transheterozygotes were weakly fertile.
but nearly all cyst cells from these mutants underwent an extra mitotic division so that the resulting egg chambers contained 32 germline cells. Of note, the presence of germline tumors and pseudo-egg chambers was extremely rare in this background (Fig. 6D). Interestingly, the \textit{rbp9\textsuperscript{1l}} and \textit{rbp9\textsuperscript{600}} alleles did not modify this weak \textit{A2BP1} mutant phenotype (Fig. 6B,D). These flies continued to lay eggs and there was little evidence of increased tumor formation (Fig. 6D). By contrast, the \textit{arrest\textsuperscript{672}} mutation dramatically enhanced the phenotype of \textit{A2BP1\textsuperscript{P2608}}/\textit{A2BP1\textsuperscript{P3460}} transheterozygotes (Fig. 6C). These flies were sterile and displayed a tumor phenotype similar to the strongest \textit{A2BP1} mutants. Moreover, we observed a marked increase in the number of pseudo egg chambers within these samples (Fig. 6D). These genetic interactions suggested a functional link between \textit{A2BP1} and \textit{arrest}.

The \textit{arrest} gene encodes the translational repressor Bruno. Previous studies have shown that Bruno protein binds to the 3' UTR of \textit{sxl}, \textit{Cyclin A} and other target mRNAs and represses their translation in the posterior region of the germarium (Sugimura and Lilly, 2006; Wang and Lin, 2007). Given the cytoplasmic localization of \textit{A2BP1} during cyst development and its genetic interaction with \textit{arrest}, we considered the possibility that \textit{A2BP1} might physically associate with Bruno. To test this, we made extracts from whole ovaries and conducted immunoprecipitation experiments using anti-\textit{A2BP1} antibodies (Fig. 6E; data not shown). In parallel, we treated separate extracts with RNase A to test whether any observed interactions were dependent on the presence of RNA. We probed the resulting immunoprecipitation pellets for the presence of Bruno. These experiments revealed that \textit{A2BP1} was associated with Bruno even in the absence of RNA.

Previous work has demonstrated interactions between mammalian \textit{A2BP1} and ataxin 2 (Atx2), and between \textit{Drosophila} Bruno and Cup (Nakamura et al., 2004; Shibata et al., 2000). To test whether \textit{Drosophila} \textit{A2BP1} interacted with these proteins, we cloned sequences corresponding to \textit{Drosophila} \textit{cup} and Atx2 into FLAG-tagged S2 cell expression vectors. We also placed the open reading frame of \textit{rbp9} into this vector. \textit{A2BP1-RE} sequence was cloned into a separate S2 cell expression vector that carried a Hemagglutinin (HA) tag. We expressed these proteins in S2 cells and performed immunoprecipitations on the resulting extracts using HA resin (Fig. 6F). The pellets were probed for the presence of FLAG-tagged proteins. These experiments confirmed that \textit{A2BP1} and Bruno physically associated with each other. However, we did not detect interactions between \textit{A2BP1} and FLAG-tagged Cup, Atx2 or Rbp9.

**DISCUSSION**

Here, we report the \textit{Drosophila} homolog of human \textit{A2BP1} promotes the differentiation of germline cells into 16-cell cysts. \textit{A2BP1} is expressed in a novel pattern during early cyst development and mutations in \textit{A2BP1} disrupt early oogenesis, resulting in the formation of cystic tumors. Our findings suggest that \textit{A2BP1} helps regulate changes in gene expression programs during the intermediate steps of germline cyst development.

\textbf{A2BP1 marks a distinct step in the molecular differentiation of germline cysts}

Past studies have sought to characterize the mechanisms that control \textit{bam} expression in germline stem cells and cystoblasts. These efforts led to the understanding that \textit{dpp} signaling from the cap cells initiates a phosphorylation cascade that results in the transcriptional repression of \textit{bam} in stem cells through a well-defined element within its promoter (Chen and McKearin, 2003a; Chen and McKearin, 2003b; Song et al., 2004; Xie and Spradling, 1998). Once a stem cell daughter leaves the niche, this repression subsides resulting in active \textit{bam} transcription. The expression of \textit{Bam} continues up until the eight-cell cyst stage whereupon it is again repressed (McKearin and Ohlstein, 1995). Given these findings and the lack of two-, four- and eight-cell cyst specific markers, the prevailing view has been that all Bam-expressing cysts are roughly equivalent on a molecular level. Subsequently, fusome branching has served as a widely used marker to track the progress of cyst differentiation. However, the expression of \textit{A2BP1} now shows that the number of mitotic divisions undertaken by a cyst does not necessarily reflect the underlying molecular state of these cells. In addition to undergoing successive rounds of incomplete mitotic divisions, cystoblasts, and two, four- and eight-cell cysts also exhibit distinct changes in their gene expression programs. For example, the cystoblast expresses both cytoplasmic \textit{sxl} protein and Bam. In two-cell cysts, \textit{sxl} expression begins to recede while Bam levels increase. In four-cell cysts, cytoplasmic \textit{sxl} protein is no longer detectable, Bam expression continues and \textit{A2BP1} protein expression is induced. In eight-cell cysts, Bam expression begins to decrease while \textit{A2BP1} expression continues to increase. Finally, in 16-cell cysts, Bam is absent, \textit{A2BP1} is present and the expression of other proteins such as Nanos, Orb, Rpb9 and Bruno is upregulated. These markers probably reflect much broader changes in gene expression during cyst development.

In situ hybridization suggests that the regulation of \textit{A2BP1} expression occurs at the level of transcription (see Fig. S1 in the supplementary material). However, given the complexity of the \textit{A2BP1} locus, we cannot completely rule out the possibility that alternative splicing and translational regulation also restrict \textit{A2BP1} expression. Examining \textit{A2BP1} protein expression in various mutant backgrounds has allowed us to further subdivide cystic tumors. Consistent with previous phenotypic characterization, \textit{A2BP1} expression shows that \textit{mei-P26}, \textit{snf}, \textit{rbp9} and \textit{arrest} tumors are arrested at different stages of cyst differentiation. Loss of \textit{mei-P26} and \textit{snf} blocks the molecular differentiation of cysts prior to the induction of \textit{A2BP1} expression. The absence of \textit{A2BP1} expression within \textit{mei-P26} and \textit{snf} mutant germline cysts indicates that mitotic divisions can continue in the absence of molecular differentiation. These findings suggest \textit{mei-P26}, \textit{snf} and, by inference, \textit{sxl} help drive cyst development to a point defined by \textit{A2BP1}. In turn, \textit{A2BP1} promotes cyst progression towards a terminally differentiated state marked by reduced levels of Bam and \textit{sxl} and increased levels of late markers such as Rbp9 and Orb.

\textbf{Progressive germline differentiation depends on the ability to repress earlier programs}

What is the developmental function of \textit{A2BP1}? A number of mutations that result in germline tumors have been isolated. Some of these mutations disrupt genes involved in the regulation of sex-specific splicing and germline sexual identity. However, the issue of why defects in sexual identity result in tumorous phenotypes remains largely unresolved (Casper and Van Doren, 2009). Other mutations such as \textit{mei-P26} and \textit{arrest} do not have a clear role in establishing sexual identity, suggesting that disruption of other molecular pathways can also block cyst differentiation. Our data, together with previous findings, suggests cysts must turn off earlier programs of gene expression to move to the next stage of differentiation. For example, Bam expression must be repressed in 16-cell cysts. In \textit{encore} and \textit{A2BP1} mutants, the expansion of Bam expression results extra mitotic divisions and a subsequent delay in meiosis (Hawkins et
A2BP1 regulates ovarian cyst differentiation

The molecular function of A2BP1
A2BP1 contains a highly conserved RNA recognition motif. The mammalian homolog of A2BP1 was first identified based on its association with ataxin 2. We find little evidence that A2BP1 physically or genetically interacts with Drosophila Ataxin 2 in S2 cell extracts or during early cyst development (Fig. 6; data not shown). However, this conclusion is based on negative data and the findings that A2BP1 functions during nervous system development (Koizumi et al., 2007) leaves open the possibility that these two proteins may interact in different contexts.

Our studies suggest a functional link between A2BP1 and Bruno. Interestingly, high levels of A2BP1 expression precede high levels of Bruno expression. However, there are detectable levels of Bruno within four- and eight-cell cysts. These low levels of Bruno expression may be sufficient to coordinate with A2BP1 to promote cyst development. A2BP1 may also have additional functions that do not require interaction with Bruno. Differences between A2BP1 and arrest mutant phenotypes may reflect these separate functions. However, it is important to note that the Drosophila genome encodes three highly related Bruno-like proteins (FlyBase). Genetic redundancy between these genes may mask other functions during early cyst development. Regardless, the observed genetic and physical interactions between A2BP1 and Bruno support a model in which these two proteins cooperate to regulate germline cyst differentiation.

Mammalian A2BP1 binds to UGCAUG RNA elements within introns and regulates the alternative splicing of specific messages (Jin et al., 2003; Lee et al., 2009; Underwood et al., 2005). Given the RRM domain in A2BP1 is 90% identical to its mammalian homologs, A2BP1 may also bind to similar elements. The original study that defined the A2BP1 RNA binding sites in vitro showed that the protein associated with GCAUG sites with a slight bias for UGCAUG and AGCAUG sequences (Jin et al., 2003). Further work showed A2BP1 bound preferentially to UGCAUG sites in vivo (Underwood et al., 2005). The cytoplasmic localization of A2BP1 protein in four-, eight- and 16-cell cysts and its association with Bruno suggests it may participate in translational repression. Examination of annotated sequences (FlyBase) reveals that a small number of Drosophila transcripts contain multiple UGCAUG and AGCAUG sites within their 3’UTRs. For example, sxl-RH 3’UTR has five AGCAUG sites but none of the preferred UGCAUG sites. The functional significance of these elements remains uncertain. Interestingly, Bruno has also been implicated in alternative splicing (Park et al., 2004). Therefore, identifying in vivo mRNA targets of A2BP1 will help clarify its molecular functions and further enhance our understanding of the complex genetic hierarchies that control germline cyst development.

Acknowledgements
We thank T. Schübich, H. Salz, R. S. Hawley, J. Knoblich, P. Lasko, H. Lin, M. Lilly, A. Nakamura, J. Kim-Ha, R. Dubreuil, the Developmental Hybridoma Bank, the Bloomington Stock Center and the Harvard Stock Center for reagents. We thank Dhananjay Chaturvedi, Robin Hiesinger and Nevine Shalaby for comments on the manuscript. This work was supported by the E.E. and Greer Garson Fogelson Endowment (UTSW Medical Center) to M.B. and by the National Institutes of Health grant GM045820 to D.M. Deposited in PMC for release after 12 months.

Competing interests statement
The authors declare no competing financial interests.

Supplementary material
Supplementary material for this article is available at http://dev.biologists.org/supplemental/10.1242/dev.0050575-DC1

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