Drosophila PAT1 is required for Kinesin-1 to transport cargo and to maximize its motility

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SUMMARY
Kinesin heavy chain (KHC), the force-generating component of Kinesin-1, is required for the localization of oskar mRNA and the anchoring of the nucleus in the Drosophila oocyte. These events are crucial for the establishment of the anterior-posterior and dorsal-ventral axes. KHC is also essential for the localization of Dynein and for all ooplasmic flows. Interestingly, oocytes without Kinesin light chain show no major defects in these KHC-dependent processes, suggesting that KHC binds its cargoes and is activated by a novel mechanism. Here, we shed new light on the molecular mechanism of Kinesin function in the germline. Using a combination of genetic, biochemical and motor-tracking studies, we show that PAT1, an APP-binding protein, interacts with Kinesin-1, functions in the transport of oskar mRNA and Dynein and is required for the efficient motility of KHC along microtubules. This work suggests that the role of PAT1 in cargo transport in the cell is linked to PAT1 function as a positive regulator of Kinesin motility.

KEY WORDS: Kinesin, Oocyte, Trafficking, Drosophila

INTRODUCTION
Kinesin is composed of two heavy chains (KHC) and two light chains (KLC), which are encoded by single genes in Drosophila melanogaster. KHC has an N-terminal motor domain, a dimeric coiled-coil domain (stalk) and a globular C-terminal tail. KLC binds through its N-terminal heptad repeats (HRs) to coil 3 of the KHC stalk (amino acids 771-813 of human KHC; see Fig. S1A in the supplementary material) (Diebenbach et al., 1998), and its C-terminal region contains six tetra-trico-peptide repeat (TPR) motifs. The first cargoes identified to bind KLC through the TPR motifs were the c-Jun N-terminal kinase (JNK)-interacting proteins (JIPs) (Bowman et al., 2000; Gauger and Goldstein, 1993; Gindhart et al., 1998; Verhey et al., 2001). Since cargo binding is required for the activation of KHC, this finding implied that KHC is essential for Kinesin activity. However, KLC is not required for the association of all cargoes with Kinesin, suggesting that KHC activation and its binding to some cargoes rely on other mechanisms. For example, Milton binds KHC and attaches it to mitochondria in a KLC-independent manner (Rice and Gelfand, 2006).

In Drosophila oocytes, KHC is required for the localization of oskar mRNA to the posterior pole, an essential step in anterior-posterior axis formation. KHC is also required for the posterior localization of Dynein, for ooplasmic flows and for the anchoring of the nucleus to the anterior-dorsal corner of the oocyte, a crucial event in the determination of the dorsal-ventral axis. Surprisingly, in the nucleus to the anterior-dorsal corner of the oocyte, a crucial event localization of Dynein, for ooplasmic flows and for the anchoring of posterior axis formation. KHC is also required for the posterior localization of Dynein and for all ooplasmic flows. Interestingly, oocytes without KHC light chain show no major defects in these KHC-dependent processes, suggesting that KHC binds its cargoes and is activated by a novel mechanism. Here, we shed new light on the molecular mechanism of Kinesin function in the germline. Using a combination of genetic, biochemical and motor-tracking studies, we show that PAT1, an APP-binding protein, interacts with Kinesin-1, functions in the transport of oskar mRNA and Dynein and is required for the efficient motility of KHC along microtubules. This work suggests that the role of PAT1 in cargo transport in the cell is linked to PAT1 function as a positive regulator of Kinesin motility.

MATERIALS AND METHODS
PAT1 sequence analysis and Pat1 mutant alleles
The Drosophila Pat1 gene (CG10695) is located on the X chromosome and encodes a predicted protein of 686 amino acids that shows 42% identity and 55% similarity with its human homolog. Structural analysis of the sequence (using Lasergene from DNASTar, Madison, WI, USA) shows that the protein is hydrophilic with no obvious signal sequence or membrane-spanning domains. Amino acids with high identity to human Pat1, amenable to functional analysis in Drosophila include the domains involved in APP binding, as well as the TPR motif.
We generated Pat1 mutants by imprecise excision of the P element *P[IE115664] inserted in the 5’UTR of *Pat1* (at position +37; see Fig. S1C in the supplementary material). PCR screening revealed a new *Pat1* allele with a 3-9 kb deletion within the gene, which was named *rob. In* antibodies against peptides from the N- and C-terminal regions of PAT1 did not recognize any fragments in *rob* oocyte extracts by western blot (see Fig. S1D in the supplementary material), indicating that no truncated proteins were produced. Furthermore, the same phenotypes were observed in *Pat1* knockout females or in females that were *Pat1*/*Pat1* heterozygous clones, or the *Pat1* homozygous clones, or the *Pat1* knockdown system, in which only homozygous *Pat1* OvoD1 homozygous clones, or the *Pat1* knockdown region, further supporting *Pat1* as a loss-of-function allele (data not shown).

**Fly strains and germline clones**

Fly stocks: *y,w;P[w+]*, *mat-tub-a4:GFP*staufen*, P[ry+; hs:FLP] (Palacios and St Johnston, 2002); w; P[w+], FRT42B *Khc*Δ27 and w; P[w+], FRT42B *Khc*Δ27 (Serbus et al., 2005); w; P[w+], FRT79D-F *Khc*Δ27 (Gindhart et al., 1998); P[EP10774]Pat1 E1554 and P[Bac(RB)Pat1]E102777 (Bloomington Stock Center); w; P[KZ503, Kin-βGal] (Clark et al., 1994); w; P[w+], *mat-tub-a4: Tau-GFP* (Micklem et al., 1997); w; P[w+], *GEN-KLC* (Gindhart et al., 1998); P[w+, ubiquitin promoter-c-myc-Khc] (generously provided by W. M. Saxton (Brendza et al., 2002b)); w; P[w+], *mat-tub-a4: KHC(1-975)*, w; P[w+], *mat-tub-a4: KHC(1-975)-GFP* and w; P[w+], *mat-tub-a4: KHC(1-849)-GFP*. Germline clones were generated by the FLP system (Chou et al., 1993; Chou and Perrimon, 1996) using the lack of GFP as a marker for homozygous oocytes, or the *OvoD1* system, in which only homozygous mutant oocytes develop after stage 4 of oogenesis. Third instar larvae were heat shocked at 37°C for 2 hours for 3 consecutive days.

**Molecular cloning**

For fly transgenic strains, the *Drosophila* KH region of interest (nucleotides 1-2925 for full-length and 1-2547 for tailless KHC) was cloned into pD277-GFP6 (van Eeden et al., 2001) to generate a construct in which the α-tubulin (αtub67C) promoter drives germline-specific expression of KHC fused to GFP6. Full-length KHC was also cloned into pD277 without GFP (Micklem et al., 1997). *Pat1* cDNA was amplified from the original pOT2 cDNA clone GH10889 and cloned into pD277, pD277 without GFP (Micklem et al., 1997). For transgenic fly strains, the *Pat1* cDNA was inserted in the 5’ UTR of *oskar* mRNA localization of *Pat1* knockout males, respectively (Fig. 1A-C; see Fig. S1B in the supplementary material). To test whether *Pat1* is required for KHC function, we studied the localization of *oskar* mRNA in *Pat1* mutant ovaries. In contrast to wild-type stage 9 oocytes, in which the transcript is localized in a posterior crescent, *oskar* mRNA and *Staufen*, a marker for the transcript, were found in an ectopic region in 22% (n=40) and 25% (n=140) of *Pat1* mutant oocytes, respectively (Fig. 1A-C; see Fig. 3C). Other KHC-dependent processes in the oocyte, such as the localization of Dynein and nucleus anchoring, were not affected in *Pat1* mutants (Fig. 1B,C). Similarly, ooplasmic streaming was still
Supplementary material). Absolutely required for these flows (Fig. 1D; see Fig. S2 in the supplementary material). Detectable in the absence of PAT1, showing that PAT1 is not absolutely required for these flows (Fig. 1D; see Fig. S2 in the supplementary material).

In wild-type stage 9 oocytes, oskar RNA is localized to the posterior pole, where it is anchored throughout the rest of oogenesis. It is possible, therefore, that the mislocalization of oskar RNA in Pat1 mutants is a consequence of PAT1 acting on the anchoring of oskar at the cortex. However, only 12.3% (n=61) of late Pat1 mutant oocytes (stage 11) presented an ectopic Staufen mislocalization, in contrast to 25% (n=140) of stage 9 Pat1 oocytes (P<0.0375 by Fisher’s test). This observation suggests that the anchoring of oskar mRNA at the posterior is unaffected in Pat1 oocytes. The oskar mRNA and Staufen localization defects in Pat1 females were rescued by the germline-specific expression of Pat1 cDNA (see Table S1 in the supplementary material), showing that Pat1 is required in the germline for the KHC-dependent transport of oskar mRNA to the posterior pole.

**Fig. 1. PAT1 is required for oskar mRNA localization, but not for Dynein transport or cytoplasmic flows.** (A) In situ hybridization for oskar mRNA at stage 9 of oogenesis in wild-type (left) and Pat1 mutant (right) Drosophila ovaries. In wild-type egg chambers, oskar mRNA localizes to the posterior pole of the oocyte, where it remains anchored throughout oogenesis. This localization is impaired in Pat1 mutant ovaries. Ectopic dots of oskar mRNA are found in 22% of Pat1 stage 9 oocytes (n=40), but in only 7% of wild-type oocytes (n=40). (B) Staufen protein (a marker for oskar mRNA) in wild-type (left) and Pat1 mutant (right) stage 9 egg chambers. As with oskar mRNA, Staufen is found in an ectopic region in 25% of the Pat1 oocytes (n=140; see Fig. 3). (C) Dynein heavy chain (green) and Staufen (red) in stage 9 Pat1 oocytes. Unlike Staufen, Dynein is not found as a dot in Pat1 mutants. (D) Particles that reflect 568 nm light (‘red’ particles) in wild-type (left) and Pat1 mutant (right) egg chambers. Each image results from a continuous confocal scan, averaged eight times using the Kalman function. Insets show representative streaks of dots, which are used as a qualitative measure of cytoplasmic streaming.

**PAT1 is not required for microtubule organization or regulation of Oskar translation**

The oskar mRNA localization defects observed in Pat1 mutants resemble the phenotype described for oskar-overexpressing oocytes, in which premature translation of Oskar protein results in the mislocalization of oskar RNA to an ectopic region (Zimyanin et al., 2007). To investigate whether the oskar mislocalization phenotype in Pat1 mutants is due to the premature translation of oskar, we analyzed the temporal regulation of oskar translation in wild-type and Pat1 mutant oocytes. In wild-type egg chambers, Oskar protein was not detected at stage 8 of oogenesis, and started accumulating at stage 9 (Fig. 2A). Similarly, the translation of oskar RNA did not take place in early Pat1 oocytes, and Oskar was only detected from stage 9 (Fig. 2A). We conclude that the mislocalization of oskar mRNA in Pat1 mutants is not due to its premature translation.

Neither the accumulation of Dynein at the posterior of the oocyte, nor the Dynein-dependent transport of the nucleus, was affected in Pat1 mutants, suggesting that PAT1 is not required for the organization of microtubules. To further test this, we analyzed the distribution of both Kin-β-Gal and the microtubule-binding protein Tau in wild-type and Pat1 oocytes. A GFP-tagged version of Tau showed that the overall morphology of the microtubules was not affected in Pat1 mutants (Fig. 2C). Kin-β-Gal is a fusion of β-galactosidase to amino acids 1-604 of KHC and, as with endogenous KHC, localizes to the posterior in wild-type oocytes (Brendza et al., 2002; Clark et al., 1994; Duncan and Warrior, 2002; Januschke et al., 2002; Palacios and St Johnston, 2002). This localization of Kin-β-Gal to the posterior pole is affected when cytoskeletal polarity is disrupted. However, the localization of Kin-β-Gal was normal in Pat1 oocytes, where it was found at the posterior, and not in the ectopic Staufen-containing dots (Fig. 2E). In addition, bicoid RNA and Gurken protein always showed a wild-type localization to the anterior cortex and anterior-dorsal corner, respectively (Fig. 2B,D). Thus, the Dynein-dependent localization of RNAs and the polarization of the microtubule cytoskeleton are not disrupted in Pat1 mutant oocytes.
PAT1 and KLC interact genetically to affect the transport of some cargoes

Since PAT1 is a KLC-like protein and oskar mRNA is mislocalized in only 22% of Pat1 mutants, we hypothesized that PAT1 and KLC might act redundantly in the transport of oskar mRNA. To test this, we analyzed the localization of Staufen in Pat1, Klc double-mutant egg chambers. As in Pat1 mutants, Staufen was mislocalized to an ectopic region in the posterior half of Pat1, Klc double-mutant oocytes (Fig. 3A,B). However, this phenotype was observed in 78.1% of the Pat1, Klc egg chambers, representing over three times the penetrance of the single-mutant phenotypes (Fig. 3C).

To study whether this genetic interaction between PAT1 and KLC applies to other cargoes of KHC, we analyzed the localization of the nucleus and Dynein in Pat1, Klc oocytes. Although the nucleus was always anchored at the anterior corner in the double-mutant oocytes, Dynein did not localize to the posterior in these egg chambers and was instead found at the anterior/lateral cortex (Fig. 3B).

These results indicate that PAT1 and KLC have a functional interaction in the localization of oskar mRNA and Dynein to the posterior of the oocyte. This genetic interaction between PAT1 and KLC, together with their sequence homology, raises the possibility that PAT1 and KLC might act in a redundant manner in the localization of cargos in the germline. To study this hypothesis further, we increased the KLC dosage by expressing a full-length KLC-encoding transgene (Gindhart et al., 1998) in Pat1 mutant oocytes. The Staufen mislocalization phenotype was fully rescued in these flies (see Table S1 in the supplementary material).

Pat1 mutants enhance the defects caused by a mutant form of KHC

To study whether Pat1 interacts functionally not only with KLC but also with KHC, we analyzed the effects of mutating Pat1 in egg chambers that express a mutant form of KHC. Expression of a truncated KHC that is missing the last 125 amino acids and fused to GFP [KHC(1-849) or ‘tailless’; see Fig. S1A in the supplementary material) induced the mislocalization of Staufen in 18% of the oocytes [KHC(1-849)-GFP/+; n=50; Fig. 4]. This effect on the localization of Staufen was specific for this tailless KHC, as the expression of full-length KHC showed no defects (n=20; Fig. 4A). How KHC(1-849) acts as a mutant form of KHC is not fully understood, but this truncated KHC was able to both efficiently dimerize with endogenous KHC and localize to the posterior pole (Fig. 4A; see Figs S3 and S4 in the supplementary material). Furthermore, a reduction of KHC dosage enhanced the Staufen mislocalization phenotype in flies expressing tailless KHC, whereas an increase in the KHC dosage reduced the Staufen phenotype (see Table S2 in the supplementary material). These observations suggest that KHC(1-849) might act as a mutant motor by titrating out full-length KHC, so reducing the number of oskar-
PAT1 is a positive regulator of Kinesin

PAT1 associates with Kinesin-1

To study whether PAT1 associates with Kinesin, we performed biochemical interaction studies. Since the quality of the KLC and PAT1 antibodies was not sufficient in our hands for interaction studies in oocyte extracts, we used MYC-tagged KLC, V5-tagged PAT1, and KHC(1-849)-GFP for immunoprecipitation experiments using cultured Drosophila cells. Endogenous KHC and KLC-MYC specifically co-purified with PAT1 when PAT1-V5 was immunoprecipitated using an anti-V5 antibody. As a control, the immunoprecipitation was performed with extracts that expressed empty V5, instead of PAT1-V5. The PAT1-KLC interaction was validated by performing similar pull-downs in the reverse direction, using cells that expressed KLC-MYC and PAT1-V5 (Fig. 5B). In this case, PAT1-V5 specifically co-purified with KLC-MYC using an anti-MYC antibody.

PAT1 has a strong functional interaction with the truncated KHC(1-849) protein. To study whether PAT1 associates with this tailless KHC, we immunoprecipitated KHC(1-849)-GFP by its GFP tag from cells that expressed PAT1-V5. As shown in Fig. 5C, PAT1 specifically co-purified with KHC(1-849)-GFP. As a control, we performed the same immunoprecipitation with extracts that expressed PAT1-V5 with GFP alone. The interaction of tailless KHC-PAT1 was validated by performing similar pull-downs in the reverse direction, using cells that expressed KHC(1-849)-GFP and either PAT1-V5 or empty V5 (Fig. 5D). KHC(1-849)-GFP specifically co-purified with PAT1 when PAT1-V5 was immunoprecipitated using an anti-V5 antibody.

These results show that PAT1 forms a complex with KHC in a tail-independent manner, similarly to the known interaction between KHC and mammalian KLC (Dienfench et al., 1998). To study whether Drosophila KLC also binds tailless KHC, we immunoprecipitated KLC-MYC from cells expressing KHC(1-849)-GFP. The KLC-binding domain was still present in tailless KHC and the Kinesin-1 complex was able to form (see Fig. S5 in the supplementary material).

Together, these results show that PAT1 forms a complex with Kinesin-1, and that this association between PAT1 and the motor does not require the tail domain of KHC. Whether this interaction is direct or is mediated by additional factors needs further study.

The velocity and run length of Kinesin are reduced in the absence of Pat1

As PAT1 interacts both biochemically and genetically with Kinesin, it is likely that the aberrant localization of oskar mRNA in Pat1 oocytes is due to defects in the transport of the transcript. If this is the case, what is the possible molecular mechanism of PAT1 function in oskar transport? The ectopic accumulation of oskar mRNA in Pat1 mutants partially resembles the oskar phenotype in Khc17 mutants (see Fig. S6 in the supplementary material) (Serbus et al., 2005). Khc17 is a hypomorphic allele caused by a missense mutation in the motor domain (S246F) that reduces the ATPase activity and velocity of KHC (Brendza et al., 1999). When we analyzed in detail the Staufen phenotype in Khc17 oocytes, we noticed that Staufen was distributed ectopically in a diffuse manner, as previously described (Serbus et al., 2005), but also in dot-like structures, similar to those found in Pat1 mutants (see Fig. S6 in the supplementary material). Also, similarly to Pat1, Khc17 enhanced the Staufen phenotype fivefold in KHC(1-849)-expressing oocytes (see Fig. S6 in the supplementary material). Whether this mislocalization of oskar RNA in Khc17 oocytes is linked to the lower motility of KHC or to some other property of the mutant motor is unknown, but the transcript is transported more slowly in this mutant (Zimyanin et al., 2007). Furthermore, a similar phenotype is observed in oocytes that are mutant for the Khc23 allele, a mutation that also results in a slower motor and slowed oskar RNA transport (see Fig. S6 in the supplementary material) (Serbus et al., 2005; Zimyanin et al., 2007).
To explore whether PAT1 has an effect on the velocity of Kinesin, we set up an in vitro assay to analyze the movement of KHC-GFP along microtubules in ovary extracts using total internal reflection fluorescence (TIRF) microscopy (Fig. 6A). A comparison of the behavior of Kinesin between control and Pat1 mutant extracts would address the effect of PAT1 on the motility of the motor, regardless of the details of the PAT1-KHC interaction.

First, we sought a KHC-GFP construct suitable for single-molecule analyses. Full-length KHC-GFP did not show frequent processive movement (data not shown), presumably owing to the C-terminal autoinhibitory domain (Coy et al., 1999; Friedman and Vale, 1999), and did not allow statistically reliable measurements of its motility. Conversely, KHC(1-849)-GFP showed slightly diffusive, but mostly unidirectional and processive movement along microtubules (Fig. 6B; see Movies 1 and 2 in the

Fig. 4. Loss of function of Pat1 enhances the phenotype of a mutant form of KHC. (A) Staufen (red) in Drosophila egg chambers that express one copy of KHC(1-975)-GFP (left), one copy of KHC(1-849)-GFP (middle), or one copy of KHC(1-849)-GFP but are also mutant for Pat1 (right). Top panels show the localization of the various KHC-GFP fusions. In contrast to oocytes expressing the full-length KHC, Staufen (red) is mislocalized in 18% of the KHC(1-849)-GFP-expressing oocytes (see B). This mislocalization is more severe and four times more penetrant in Pat1;KHC(1-849)-GFP oocytes than in the KHC(1-849)-GFP-expressing egg chambers. Arrows point to the region where Staufen is mislocalized. (B) Quantification of the Staufen mislocalization phenotype in stage 9 egg chambers that express one copy of tailless KHC fused to GFP, and that are either wild-type [KHC(1-849)-GFP/+] or mutant for Pat1 [Pat1;KHC(1-849)-GFP/+].
and dorsal-ventral axes, respectively. KHC is also essential for the localization of mRNA and the anchoring of the nucleus by KHC are crucial for the establishment of the anterior-posterior and dorsal-ventral axes, respectively. KHC is also essential for the posterior localization of Dynein and for all ooplasmic movements. However, oocytes that lack KLC show no major defects in these KHC-dependent processes, suggesting that KHC binds these cargoes and is activated by a novel mechanism. Here, we investigate the molecular mechanism of Kinesin function in the germline using a combination of genetic, biochemical and motor-FIG. 6. The velocity and run length of Kinesin are reduced in the absence of Pat1. (A) The in vitro assay used to study the motility of KHC in control and Pat1 ovarian extracts. KHC-GFP-expressing ovaries are dissected and added to immobilized Rhodamine-labeled microtubules in the presence of ATP. The motility of KHC is analyzed by TIRF microscopy, which allows single fluorophores close to the surface to be tracked when moving along an immobilized microtubule. (B) Representative kymographs of KHC in extracts that express tailless KHC-GFP, and that are either wild-type or mutant for Pat1. (C-F) The velocity and run length of KHC are reduced in Pat1 mutants. (C-E) Bar charts of association time (C), velocity (D) and run length (E) of the individual KHC-GFP particles moving along microtubules in control and Pat1 extracts. (F) Mean square displacements (MSDs) calculated from the consolidated data were plotted against time intervals (t) and fitted with quadratic curves MSD= v^2t+2Dt (v, velocity; D, diffusion coefficient). The velocity and run length of KHC are reduced by 20% and 42% in Pat1 extracts, respectively. A statistically significant difference between control and Pat1 extracts was seen in three independent experiments, although some variation occurred in the mean velocities. There was no significant difference in the diffusion coefficient (13,000±600 versus 13,400±600 nm^2/second).

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DISCUSSION

The localization of oskar mRNA and the anchoring of the nucleus by KHC are crucial for the establishment of the anterior-posterior and dorsal-ventral axes, respectively. KHC is also essential for the requirement for PAT1 as a positive regulator of KHC-mediated microtubule-association time. These findings suggest that the functional PAT1 could explain the mislocalization of oskar in ovaries expressing tailless KHC (Fig. 4). Therefore, any difference detected in the motility of this truncated KHC between the control and Pat1 mutant can be related to the role of PAT1 in vivo.

We compared the motility of KHC(1-849)-GFP in control and Pat1 extracts by automated tracking of the GFP signals along immobilized microtubules (Fig. 6C-E). In addition to measuring the duration and distance of individual processive runs (association time and run length), we analyzed particle velocity. This was achieved by assuming that processive runs consist of directional movement (with velocity v) and diffusive movement (with diffusion coefficient D) along the microtubule. Velocity and diffusion of a particle are then determined by fitting the mean square displacement (MSD) of a particle to the form MSD (t)=v^2t+2Dt (Okada and Hirokawa, 1999). In control extracts, the average of the velocities determined for individual particles was ~340 nm/second (337±8 nm/second, n=285), which is slightly lower than the velocity of purified Kinesin-1 in buffer, but similar to the speed of the motor in extracts (Blasius et al., 2007; Sung et al., 2008). In addition, we obtained mean values of 0.82±0.06 seconds for association time and 347±33 nm for run length. In Pat1 mutant extracts, KHC-GFP also showed processive motility along microtubules, with approximately the same association time (0.74±0.07 seconds; n=771, P=0.43; Fig. 6C). However, velocity and run length were significantly reduced from those in wild-type extracts; by 20% and 42%, respectively (271±4 nm/second and 202±8 nm, respectively; P<0.001; Fig. 6D,E). A similar reduction in velocity was also observed in Pat1 mutant extracts when MSD data for all trajectories were pooled and analyzed (control, 339±3 nm/second; Pat1, 246±4 nm/second; Fig. 6F). These results indicate that the velocity of Kinesin-1 is affected by loss of PAT1. A reduced efficiency of KHC motility in the absence of functional PAT1 could explain the mislocalization of oskar mRNA in mutant oocytes.

We conclude that PAT1 is important for the efficient trafficking of cargo by KHC along microtubules, and that the absence of PAT1 reduces the overall motility of KHC without affecting its microtubule-association time. These findings suggest that the requirement for PAT1 as a positive regulator of KHC-mediated transport relies on PAT1 function as a positive regulator of Kinesin motility.
tracking studies. We show that the KLC-like protein PAT1 interacts with Kinesin, functions in the transport of oskar mRNA and Dynein, and is required for the efficient motility of KHC along microtubules. We suggest that the role of PAT1 in the transport of cargoes in the cell correlates with PAT1 function as a positive regulator of Kinesin motility.

**PAT1 is specifically required for oskar mRNA localization**

Several lines of evidence suggest that the aberrant localization of oskar mRNA in Pat1 mutants is due to defects in the transport of the transcript. PAT1 is not required for any other step in oskar mRNA biogenesis, as Pat1 mutants do not affect its accumulation in the oocyte, its colocalization with Staufen or its translational regulation. Furthermore, the penetrance of the oskar mislocalization phenotype in Pat1 mutants is weaker at later stages of oogenesis, suggesting that the transcript is not physically detaching and that its anchoring at the posterior is normal. PAT1 is also not required for the polarization of the oocyte or the microtubule cytoskeleton, nor for the Dynein-dependent localization of RNAs such as bicoid.

Taking into account the homology of PAT1 to the cargo-binding domain of KLC (the TPRs) and the biochemical interactions between PAT1 and Kinesin-1, one possible model for the function of PAT1 in oskar transport is that PAT1 contributes to the binding of the transcript to KHC. Whether PAT1 associates with oskar mRNA is unknown, but it is interesting to note that mammalian Pat1 interacts with zipcode-binding protein 1 (also known as Igf2bp1) (J. B. Dietenberg and R. H. Singer, personal communication), the Drosophila homolog of which, IMP, binds oskar mRNA and localizes to the posterior (Munro et al., 2006). However, oocytes lacking IMP localize oskar mRNA normally, indicating that the putative binding of Pat1 to IMP is not the only mechanism that would mediate the binding of Pat1 to the oskar-localizing complex.

**Function of PAT1 and KLC in KHC-dependent transport**

If PAT1 contributes to the binding of cargo to KHC, it is possible that, at least for some cargoes, it does so in conjunction with KLC. This hypothesis is supported by several findings. Firstly, PAT1 and KLC have a similar domain organization, with high sequence similarity in the KHC- and cargo-binding domains. Secondly, PAT1 and KLC form a complex with KHC. Lastly, Dynein seems to localize normally to the posterior in Pat1 or Klc single mutants, but it accumulates at the anterior/lateral cortex when both genes are mutated, which is equivalent to the Dynein mislocalization phenotype observed in Khc-null mutant oocytes. These results suggest that PAT1 and KLC might redundantly mediate the interaction of Dynein with KHC that is required for its transport to the posterior.

This seems not to be the case for the transport of oskar mRNA to the posterior pole of the oocyte. Although the oskar mRNA mislocalization phenotype is more highly penetrant in Pat1, Klc double-mutant oocytes than in the single mutants, in contrast to Khc mutant oocytes, oskar mRNA is not found at the anterior/lateral cortex in these double mutants, but in the center and posterior of the oocyte. This suggests that PAT1 and KLC are not essential for KHC to bind oskar mRNA, and that other proteins must contribute to the interaction of oskar with the motor.

In contrast to the germline, where the absence of KLC results in no major defects in KHC-dependent processes, both Khc and Klc mutant larvae exhibit a neuronal phenotype in which axonal cargoes (e.g. synaptotagmin vesicles) accumulate in ‘clogs’ in the peripheral nerves (Hurd et al., 1996). Furthermore, Khc and Klc mutant larvae present locomotion defects, flip their posterior region upwards and paralyze progressively. Our preliminary data show that Pat1 mutant axons also exhibit a high number of clusters of synaptotagmin vesicles (see Fig. S8 in the supplementary material), suggesting that Pat1 is also required for KHC function in the nervous system. However, Pat1 mutants are viable and Pat1 larvae show no obvious phenotypes. This indicates that Kinesin-1 has Pat1-independent functions that are important for locomotion and viability. In contrast to Khc and Klc mutants, the axonal clogs are not observed in the proximal region of the Pat1 mutant peripheral nerves. This difference between Pat1 and Khc or Klc larvae might explain the absence of paralysis and lethality in Pat1 mutants. For further analysis of Pat1 function in the nervous system, it would be interesting to study whether the transport of molecules localized in a KLC-independent manner (e.g. FMRP or GRIP1) is disrupted in Pat1 or Pat1, Klc double-mutant neurons.

In vertebrates there are two partially functionally overlapping KLC isoforms. The present study suggests that Pat1 might be a second KLC isoform in Drosophila. In light of our results it would be interesting to analyze whether KHC can form various complexes with Pat1 and with KLC. These distinct complexes could have overlapping, but not identical, specificities, providing a possible explanation for how one motor coordinates the transport of its many cargoes.

**The velocity and run length of Kinesin are reduced in the absence of Pat1**

In vitro motility assays using purified molecules are powerful systems to obtain mechanistic insights into the function of motors, but they might eliminate physiologically relevant factors that regulate their functions (Cai et al., 2007b; Sung et al., 2008). The use of KHC-GFP ovary extracts on defined microtubule tracks allowed us to analyze active KHC with and without Pat1 under more physiological conditions. Our results show that the velocity and run length of KHC, but not its association time, are reduced in the absence of Pat1. Pat1 is the first protein shown to positively regulate Kinesin speed and run length, without affecting its association time, revealing a novel mechanism of Kinesin regulation.

In light of the homology of Pat1 to the HR motif of KLC, and because Pat1 is found in a complex with KHC and KLC in co-immunoprecipitation experiments, a simple hypothesis for how Pat1 stimulates KHC motility is by direct physical interaction. Although we have detected interactions between Drosophila KLC and mammalian Pat1 in a yeast two-hybrid assay (data not shown), we have failed to detect a direct interaction between Drosophila KHC and Pat1 in this assay. This result suggests that either the Pat1 binding to KHC is transient and/or regulated by additional factors [e.g. KLC, as suggested by our results and those of Hammond et al. (Hammond et al., 2008)], or the hypothesis is incorrect and Pat1 does not directly bind KHC.

The mechanistic details of how Pat1 facilitates Kinesin-dependent transport would be the focus of future research. A potential mechanism for Pat1 to affect the motility of KHC is through the regulation of the KHC oligomerization state. To test this, the fluorescence intensity and pattern of fluorescence decay for each particle tracked were analyzed (Cai et al., 2007b) (see Fig. S7 in the supplementary material). Although GFP fluorescence fluctuates, we estimate that most particles contained one or two active GFP molecules, indicating that each particle primarily
PAT1 is a positive regulator of Kinesin

PAT1 was first identified in human cells, where it weakly interacts with microtubules and with APP. This work in human cells showed that PAT1 appears to regulate APP trafficking and processing, although the molecular mechanism of this regulation is not understood (Kuan et al., 2006; Zheng et al., 1998). Our results support a model in which the role of PAT1 in APP processing is probably linked to PAT1 function in regulating Kinesin. This hypothesis is further supported by recent work showing that mammalian PAT1 is required for the transport of mRNAs in neurons (J. B. Dicktenberg and R. H. Singer, personal communication). Thus, the function of PAT1 as a novel regulator of Kinesin motility and cargo transport seems to be evolutionarily conserved.

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Competing interests statement

The authors declare no competing financial interests.

Supplementary material

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References


The complex, PAT1 does not seem to accumulate at the posterior and is found in oocytes. This hypothesis is supported by several observations. Analysis of the KHC conformation changes revealed by FRET on cells confirmed that Kinesin-1 is partially folded while undergoing microtubule-based transport (Cai et al., 2007a; Coy et al., 1999; Friedman and Vale, 1999; Hisanaga et al., 1989; Verhey et al., 1998). This conformation would allow the stalk, and consequently PAT1, to come into close molecular contact with the neck and motor domains. Once in close contact, PAT1 could induce a change in the structure of the motor domain, for example by affecting the proximity between the two heads, so that they are in proper proximity for processive motility (Adio et al., 2009; Cai et al., 2007a), or by optimizing the internal tension required for the coordinated activity of the two heads (Hackney et al., 2003; Yildiz et al., 2008). It is also conceivable that the interaction of PAT1 with Kinesin releases an inhibitory mechanism of motor activity, as it has been shown for JIP1 (APPL1) and UNC-76 (Blasius et al., 2007; Gindhart et al., 2003). In either case, these effects could be achieved directly by PAT1, or by an additional factor that is recruited to the motor in a PAT1-dependent manner, as has been described for the KHC-interacting protein Milton (Wang and Schwarz, 2009). Further biochemical and biophysical studies are needed to understand exactly how PAT1 achieves this novel regulation of KHC motility.

Whether PAT1 functions in both cargo binding and regulation of KHC motility is not clear. Genetic analyses suggest that PAT1 and KLC mediate the interaction of Dynein with KHC, as Dynein mislocalizes to the anterior/lateral cortex in a similar manner in Pat1, Klc double-mutant and Khc mutant oocytes (Brendza et al., 2000a; Brendza et al., 2002; Duncan and Warrior, 2002; Januschke et al., 2002; Palacios and St Johnston, 2002). In the case of oskar mRNA it is possible that the slower motility of KHC in the absence of PAT1 explains the mislocalization of this transcript in Pat1 oocytes. This hypothesis is supported by several observations. Firstly, in contrast to components of the oskar-localization complex, Pat1 does not seem to accumulate at the posterior and is diffuse in the cytoplasm of the germline (see Fig. S9 in the supplementary material). Secondly, the absence of Pat1 enhances the oskar mRNA mislocalization phenotype in oocytes expressing tailless KHC and it reduces the motility of this truncated motor. Thirdly, the oskar mRNA phenotype in Pat1 mutants is similar to that of Khc<sup>217</sup> and Khc<sup>234</sup>, which are mutant alleles that result in a less motile KHC. In these alleles, oskar mRNA localizes to the posterior pole, but there is a small amount that accumulates in the middle of the oocyte (Serbus et al., 2005). It was subsequently shown that this is due to a delay in the transport of oskar mRNA (Zimyanin et al., 2007). This correlation between slowed motor mechanochemistry and ectopic oskar accumulation as a result of slowed oskar transport supports the hypothesis that the oskar phenotype in Pat1 mutants is due to a slower KHC.

contained a single dimer of KHC in both control and Pat1 mutant extracts (see Fig. S7 in the supplementary material). Thus, the formation of higher-order oligomers is unlikely to account for the observed difference in velocity. Another possibility is that PAT1 affects Kinesin activity by binding microtubules, as PAT1 was identified in human cells as a weak microtubule-interacting protein (Zheng et al., 1998). However, we do not think this to be the case, as Drosophila PAT1 did not show a strong affinity for microtubules in sedimentation assays (data not shown).


