RESEARCH ARTICLE

The auto-inhibitory domain and ATP-independent microtubule-binding region of Kinesin heavy chain are major functional domains for transport in the Drosophila germline

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ABSTRACT

The major motor Kinesin-1 provides a key pathway for cell polarization through intracellular transport. Little is known about how Kinesin works in complex cellular surroundings. Several cargos associate with Kinesin via Kinesin light chain (KLC). However, KLC is not required for all Kinesin transport. A putative cargo-binding domain was identified in the C-terminal tail of fungal Kinesin heavy chain (KHC). The tail is conserved in animal KHCs and might therefore represent an alternative KLC-independent cargo-interacting region. By comprehensive functional analysis of the tail during Drosophila oogenesis we have gained an understanding of how KHC achieves specificity in its transport and how it is regulated. This is, to our knowledge, the first in vivo structural/functional analysis of the tail in animal Kinesins. We show that the tail is essential for all functions of KHC except Dynein transport, which is KLC dependent. These tail-dependent KHC activities can be functionally separated from one another by further characterizing domains within the tail. In particular, our data show the following. First, KHC is temporally regulated during oogenesis. Second, the IAK domain has an essential role distinct from its auto-inhibitory function. Third, lack of auto-inhibition in itself is not necessarily detrimental to KHC function. Finally, the ATP-independent microtubule-binding motif is required for cargo localization. These results stress that two unexpected highly conserved domains, namely the auto-inhibitory IAK and the auxiliary microtubule-binding motifs, are crucial for transport by Kinesin-1 and that, although not all cargos are conserved, their transport involves the most conserved domains of animal KHCs.

KEY WORDS: Cell asymmetries, Body plan, Oogenesis, Intracellular transport, Cytoskeleton, Microtubules, Motor proteins

INTRODUCTION

The transport of cargos by motors contributes to cytoplasmic heterogeneity. The major motor Kinesin-1 (hereafter Kinesin) is responsible for the transport of cargos in most cell types and plays a crucial role in germline and neuronal polarization. Mutations in the Drosophila melanogaster force-generating subunit of Kinesin, Kinesin heavy chain (KHC) result in defects in axonal transport (Hirokawa et al., 2010), localization of developmental determinants (Gagnon and Mowry, 2011) and movement of lipid droplets (Welte, 2009). A mouse model has also implicated Kinesin in axonal process growth (Karle et al., 2012).

Biochemical investigations have elucidated important aspects of the walking mechanism of KHC (Gengerich and Vale, 2009), but how Kinesin discriminates among its cargos and which domains are involved in cargo interaction are not yet understood. Several cargos associate with Kinesin via Kinesin light chain (KLC), a major partner of KHC. KLC binds to coil-3 of the KHC stalk [amino acids (aa) 771-813 and 792-836 of human and Drosophila KHC; Fig. 1A] (Diefenbach et al., 1998; Loiseau et al., 2010) and mediates interaction of the motor with various cargos, including JNK-interacting protein (JIP) vesicles (Bowman et al., 2000; Gauger and Goldstein, 1993; Gindhart et al., 1998; Verhey et al., 2001) and the KASH proteins involved in nuclear migration (Meyerzon et al., 2009). However, KLC is not required for the association of all cargos with Kinesin. For example, in neurons the localization of mitochondria and FMRP (FMR1) occurs in a KLC-independent manner (Glater et al., 2006; Ling et al., 2004). In the case of Drosophila mitochondria, KHC binds Milton, which in turn binds Miro, a mitochondrial GTPase. Milton competes with KLC for its binding to KHC (Glater et al., 2006). In addition, some cargo adaptors seem to bind both KLC and KHC, as shown for DISC1 (Taya et al., 2007) and Sunday driver (Syd; Drosophila JIP) (Sun et al., 2011).

The mechanisms that target Kinesin to specific cargos outside of the neuron are less well understood. For example, in the Drosophila oocyte, neither KLC nor the KLC-like protein Pat1 [which is redundant with KLC (Loiseau et al., 2010)] plays a major role in the KHC-dependent localization of the developmental determinant oskar mRNA, in KHC-dependent positioning of the nucleus or in the induction of cytoplasmic streaming (Brendza et al., 2002; Duncan and Warrior, 2002; Januschke et al., 2002; Loiseau et al., 2010; Palacios and St Johnston, 2002). Studies on Neurospora crassa (which lacks KLCs) have identified a putative cargo-binding domain in the C-terminus of KHC, which is conserved in animal KHCs (aa 850-950, Fig. 1A, Fig. 5A) (Seiler et al., 2000). Furthermore, brain microsomes and GRIP1 bind to this region in sea urchin and mouse KHC, respectively (Setou et al., 2002; Skoufias et al., 1994; Yu et al., 1992). This region, which is known as the tail, might therefore represent an alternative cargo-binding domain that could account for some of the KLC-independent functions of KHC. In addition to the N. crassa putative cargo-binding domain, the tail has two other conserved regions, which comprise the auto-inhibitory IAK motif (Coy et al., 1999; Friedman and Vale, 1999; Stock et al., 1999) and an auxiliary ATP-independent microtubule (MT)-binding site (Hackney and Stock,
To provide details of the functional structure of the C-terminal region of KHC, as well as to gain further insight into how KHC carries out its various transport functions, we performed a structural/functional analysis of the motor (excluding the motor domains) in the Drosophila oocyte. The germline is a unique model system in that it permits the study of Kinesin in a living cell in which several cargos are known and easily detectable, and the assessment of the developmental impact of modifying Kinesin function. This is achieved by analyzing Kinesin function in oocytes that lack endogenous KHC and only express mutated versions of the motor (tagged to GFP). Studying eggs that arise from these mutant oocytes assesses the developmental impact of the mutated motor. To our knowledge, this is the first structural/functional study on animal KHC, adding data to the study performed in fungi (Seiler et al., 2000).

RESULTS

The tail of KHC is essential for localization of oskar mRNA but not for Dynein transport

The two most conserved regions at the C-terminal end of animal KHCs are the KLC-binding domain (aa 792-839 and 771-818 in Drosophila and human KHCs, respectively) and the tail domain (aa 850-975 and 829-929 in Drosophila and human KHCs, respectively). We first investigated cargo localization using a KHC that lacks the tail but contains the KLC-binding site (KHC1-849GFP, Fig. 1A) (Loiseau et al., 2010). A full-length motor (KHC1-975GFP) rescues all of the Khc27 null mutant phenotypes in the oocyte (Fig. 1B,C, Fig. 2E, Table 1, Fig. 6B; supplementary material Figs S1, S3). However, oskar mRNA (detected by Staufen antibodies) is never localized to the posterior pole in Khc mutant oocytes (Khc27 germline clones, GLCs) that express KHC1-849GFP (n=80, Fig. 1D), indicating that amino acids 850-975 are required for oskar transport. KHC1-849GFP has a similar expression level to, and dimerizes with, endogenous KHC (Loiseau et al., 2010) (supplementary material Fig. S2), and localizes to the posterior, with and without endogenous motor (Fig. 1D,E; data not shown).

In contrast to its inability to rescue oskar mRNA transport, KHC1-849 does rescue the transport of Dynein, which is found at the posterior in all KHC1-849 oocytes (n=10, Fig. 1E). Note that although Dynein is transported from the anterior to the posterior by KHC1-849, its posterior localization is not completely wild type. Since oskar mRNA, but not Dynein, requires the KHC tail for its transport to the posterior, this suggests that KHC has domain-specific functions in the germline.

Although KLC is not essential for KHC function in Drosophila oocytes (Loiseau et al., 2010; Palacios and St Johnston, 2002), it is unknown whether the KLC-binding site itself is required for the establishment of asymmetry. Oocytes expressing a truncated motor lacking the last 275 amino acids (KHC1-700GFP) have a Dynein localization phenotype indistinguishable from that of Khc null
oocytes (n=12, Fig. 1G) (Duncan and Warrior, 2002; Januschke et al., 2002; Palacios and St Johnston, 2002). This result, together with the posterior localization of Dynein in KHC1-849 oocytes, suggests that amino acids 701-849 (containing the KLC-binding site) are required for Dynein transport. KHC1-700GFP has a similar expression level to that of the endogenous motor and localizes to the posterior, with and without endogenous motor (Fig. 1F,G; supplementary material Fig. S2; data not shown).

The phenotypes observed in both KHC1-849GFP and KHC1-700GFP egg chambers demonstrate that KHC-mediated cargo transport is domain specific and not via a common mechanism.

**Both the tail and 701-849 region are required for positioning of the oocyte nucleus and establishment of the embryonic DV axis**

Nucleus positioning is required for a number of cellular and developmental events. The importance of this process is exemplified by the link between abnormal nucleus localization in muscle cells and myopathies. In *Drosophila*, the localization of the oocyte nucleus to the anterior-dorsal corner (Fig. 2A; supplementary material Fig. S1) is an early step in the establishment of the embryonic dorsal-ventral (DV) axis, since the dorsal determinant Gurken localizes around the nucleus and signals to the overlying follicle cells to take up a dorsal fate (supplementary material Fig. S1A). As a consequence, dorsal cells differentiate into two dorsal appendages (DAs) on the egg. When nucleus positioning or Gurken signaling is affected, the appendages are malformed or missing (Brendza et al., 2002). Only 14% of stage (st) 9 KHC1-849 oocytes have normal Gurken protein distribution, and in most oocytes Gurken is either not closely associated with the nucleus or shows diffuse expression. This is a stronger defect than the nucleus positioning defect. This is also the case in KHC1-700 oocytes (n=79, Fig. 2C). Oocytes expressing the tailless KHC1-849 show a mild improvement in nucleus placement, with nuclei aberrantly positioned in 60% of the mutant oocytes (n=107, Fig. 2D). The full-length KHC1-975 fully rescues the localization of the nucleus in Khc mutants (n=79, Fig. 2E).

To study the developmental impact of the mislocalization of the nucleus, we analyzed DA formation in KHC1-700 and KHC1-849 eggs. As with the nuclei, full-length KHC completely rescued the formation of the DAs (supplementary material Fig. S1), whereas 67% and 52% of the KHC1-700 and KHC1-849 eggs, respectively, have no DA (Table 1). Therefore, both the KHC tail and the region 701-849 are required for Kinesin to position the nucleus and to establish the DV axis.

Although there are more KHC1-849 eggs than KHC1-700 eggs with DAs, removing the tail blocks the formation of completely normal appendages, since only 3.5% of the KHC1-849 eggs have two fully formed DAs (Table 1). This suggests that Gurken signaling is strongly affected in KHC1-700, partially rescued by KHC1-849, but not fully rescued by any of these transgenes. This is confirmed by the observation that KHC1-849 oocytes are defective for Gurken localization, even when the nucleus seems properly positioned (supplementary material Fig. S1). This differential effect of KHC on the nucleus and on Gurken is also observed in *Khc* null oocytes (Brendza et al., 2002). Only 14% of stage (st) 9 KHC1-849 oocytes have normal Gurken protein distribution, and in most oocytes Gurken is either not closely associated with the nucleus or shows diffuse expression. This is a stronger defect than the nucleus positioning phenotype, suggesting that the DA defect of the tailless KHC is due to KHC1-849 having defective localization of both Gurken and nucleus.

These results indicate that both the tail and the KLC-binding regions are involved in proper nucleus and Gurken localization by KHC, and thus in establishing the embryonic DV axis.

**The nucleus positioning function of KHC requires its motor activity**

Motors might act as static anchors of cargos (Delanoue and Davis, 2005; Delanoue et al., 2007). Since oocytes with slow KHC show no defects in nucleus positioning, we investigated whether Kinesin requires its motor activity in order to ‘anchor’ the nucleus. We
studied nucleus positioning in Khc27 oocytes expressing KHC330-975GFP, a KHC that lacks the motor domain (Fig. 1A). This motorless Kinesin, in contrast to the posterior localization of wild-type KHC (Fig. 1B; supplementary material Fig. S3E,F), accumulates at the anterior/lateral cortex, where the minus ends of MTs are thought to be prevalent (supplementary material Fig. S3B,G,H) (Cha et al., 2002; Parton et al., 2011). Both nucleus positioning and DA formation are abnormal in KHC330-975 oocytes (supplementary material Fig. S3B,D), demonstrating that the motorless KHC is unable to sustain these processes. A motor that lacks the ATP-binding domain (KHC231-975) behaves equivalently to KHC330-975 (data not shown). KHC330-975 also phenocopies the Khc null mislocalization phenotype of Staufen and Dynein (supplementary material Fig. S3G,H). Although it is unknown how direct the action of KHC is on the positioning of the nucleus, it is interesting to note that KHC330-975GFP localizes to the oocyte nuclear membrane. This is also observed with full-length KHC, although with an additional punctate localization not seen with motorless KHC (supplementary material Fig. S3B,C).

More than one KHC dimer is present on posterior cargos
In the presence of endogenous Kinesin, KHC231-975 and KHC330-975 localize to the posterior (Fig. 3A; data not shown). This raises the question of how these motorless Kinesins reach this pole, as they cannot transport themselves there in the absence of KHC (Fig. 3B; supplementary material Fig. S3). Either they interact with cargos moved by wild-type Kinesin, or they form heterodimers with endogenous KHC and move by an unexpected ‘inchworm’ mechanism. To distinguish these hypotheses, we expressed both KHC231-975 and KHC1-604betaGal in a Khc null background. KHC1-604betaGal is a truncated form of KHC that moves on MTs and localizes to the posterior, but is without all known cargo-binding domains. If these two mutant Kinesins were able to heterodimerize and move (the inchworm model), both motors would be detected at the posterior. If, however, they cannot move together, then the motorless KHC should remain at the anterior whereas KHC1-604betaGal would appear at the posterior. Only KHC1-604betaGal was found at the posterior (Fig. 3, 100%, n=15), suggesting that the posterior localization of KHC231-975 requires a cargo moved by another KHC molecule. Therefore, we can conclude that motorless KHC, and by extrapolation KHC, can be moved to the posterior by binding to cargos moved by other active motors, and that more than one KHC dimer can bind to a cargo being moved to the posterior. This correlates with previous work on lipid droplet transport (Shubetia et al., 2008). Whether ‘hitchhiking’ is relevant to KHC activity remains to be seen.

Developmental differences in Kinesin function
The behavior of KHC tail truncations highlights that Kinesin has distinct mechanisms of action within the same cell. For example, the tail is important for oskar RNA localization and nucleus positioning but does not affect Dynein transport. To fully characterize Kinesin function, we studied another process that is dependent on KHC: streaming of the ooplasm. From mid-oogenesis, there is constant mixing of the ooplasm driven by KHC-dependent transport (Ganguly et al., 2012; Palacios and St Johnston, 2002; Serbus et al., 2005). At st9, the movement is slow (Table 2). At st11, the flows are faster and more organized (Fig. 4; supplementary material Movie 1) (Dahlgaard et al., 2007; Ganguly et al., 2012; Theurkauf, 1994). It is unknown to what extent streaming is relevant for cargo transport, but flows aid nanos RNA transport (Forrest and Gavis, 2003) and may help oskar localization (Ganguly et al., 2012).

In Khc mutants, streaming is completely absent at both mid- and late oogenesis. Both the early/slow and late/fast streaming are rescued by KHC1-975 (data not shown). When analyzing the streaming speed of KHC1-849 oocytes we observed a complex temporal phenotype whereby KHC1-849 cannot uphold streaming at st9 but by st11 streaming is of wild-type speed and appearance (Fig. 4, Table 2; supplementary material Movie 2). We observed a transition at st10B in KHC1-849 oocytes, in which there are regions

![Staufen and KHC localization in KHC231-975GFP oocytes](image1)

(A,B) Staufen (red in merge) in KHC231-975GFP (green in merge) oocytes, in the presence (A) or absence (B, Khc27 GLC) of endogenous KHC. KHC231-975GFP is transported to the posterior only in the presence of endogenous KHC.

![KHC1-604-betaGal and KHC231-975GFP localization](image2)

(C,D) Localization of KHC1-604-betaGal (red in merge) and KHC231-975GFP (green in merge) in the presence (C) or absence (D) of endogenous KHC. DAPI, blue. The presence of nuclear GFP is a consequence of the mutant clone selection protocol and is not related to KHC-GFP. Khc mutant cells lack nuclear GFP (e.g. germline in B and D).
Table 2. Streaming speeds in wild-type and mutant stage 9 and 11 oocytes

<table>
<thead>
<tr>
<th>Genotype</th>
<th>st9</th>
<th>st11</th>
</tr>
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<tbody>
<tr>
<td>Wild type</td>
<td>21.5±0.8 nm/s (n=21)</td>
<td>109±7.6 nm/s (n=9)</td>
</tr>
<tr>
<td>KHC1-849, Khc27 GLC</td>
<td>–</td>
<td>111.7±7 nm/s (n=6)</td>
</tr>
<tr>
<td>KHC1-604, Khc27 GLC</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Khc27 GLC</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>KHC330-975, Khc27 GLC</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

–, No discernible flows.

- of fast flows in the center of the oocyte, surrounded by regions where streaming is not observed (data not shown). This transition might correlate with the actin cytoskeleton re-organization that occurs at st10B, when a cytoplasmic actin mesh is seen to disintegrate, initiating from the center of the oocyte (Dahlgaard et al., 2007). Our findings show that removing the tail has a different impact on flows depending on the developmental stage, allowing cytoplasmic streaming at st11 but not at st9.

Novel in vivo role for the auto-inhibitory IAK domain

The tail is dispensable for Dynein transport or late streaming, but it is essential for oskar transport, DV axis and st9 streaming. The tail contains three conserved motifs: the auto-inhibitory IAK motif, the auxiliary ATP-independent MT-binding site (hereafter, AMB), and the N. crassa putative cargo-binding domain (Fig. 5A). To characterize the function of these domains in oskar transport, we deleted the last 65 amino acids of KHC, creating KHC1-910GFP, which lacks the IAK and the AMB domains, but still contains the N. crassa-like domain. Although KHC1-910 localizes efficiently to the posterior (Fig. 5B), and is expressed at similar levels to endogenous KHC (supplementary material Fig. S4), oskar ribonucleoprotein (RNP) is mainly found at the anterior/lateral cortex of KHC1-910 oocytes, similar to in Khc null oocytes (Fig. 5B, n=35). Upon close inspection of the phenotype, however, it seems that a small amount of Staufen reaches the posterior. This would suggest that KHC1-910 activity in oskar RNA transport is severely constrained.

To further investigate which of the two conserved domains removed in KHC1-910 (i.e. IAK or AMB) is responsible for oskar transport, we obtained oocytes that only express a KHC in which the IAK or AMB is responsible for this localization, KHC1-975ΔIAK or KHC1-975ΔAMB, respectively (supplementary material Fig. S4D), which might suggest that removing the IAK makes KHC less active in RNA transport. This result is also in agreement with the fact that a point mutation from IRS to QIAKS or from QIAKPIRS to QIAKPIRF results in inhibition, rather than overactivation, of some Kinesin-mediated transport (Moua et al., 2011).

We then analyzed how other KHC-dependent processes are affected when the IAK motif is removed. Interestingly, and in contrast to the weak defects observed for oskar localization, KHC1-975ΔIAK oocytes show a strong nucleus positioning phenotype (Table 3A, 30%). Accordingly, DA formation is also affected in KHC1-975ΔIAK eggs (Table 3B, 9% normal DAs). A striking Khc mutant phenotype is the presence of actin spheres close to the mislocalized nucleus (Januschk et al., 2002; Mische et al., 2007). This is a strongly penetrant Khc null phenotype, affecting 91% of Khc oocytes (Fig. 6). To fully describe the IAK function we looked more carefully at the formation of these aberrant actin spheres. Although never seen in wild-type or KHC1-975 oocytes (Fig. 6B; data not shown), these spheres are present in 84% of KHC1-975ΔIAK (Fig. 6C) and in 74% of KHC1-849 (Fig. 6D) oocytes. These spheres contain Rabenosyn-5 [a Rab5 effector protein (Tanaka and Nakamura, 2008)] (supplementary material Fig. S5), suggesting that vesicle trafficking is affected in Khc mutant oocytes. Interestingly, these ectopic vesicles seem to nucleate actin, as suggested when filming their behavior in the presence of Utrophin-GFP (supplementary material Fig. S5).

In vitro studies have shown that the IAK can interact with the motor domain to hinder ADP release and reduce processive movement. To distinguish whether the phenotypes observed in the KHC1-975ΔIAK oocytes are due to a lack of auto-inhibition or to the loss of function of the KHC1-975ΔIAK motor, we analyzed Staufen and DAs when amino acids 521-641 (Hinge2, Fig. 1A) are deleted (Barlan et al., 2013). The KHC auto-inhibited conformation is achieved by the motor folding in half at Hinge2, and deletion of

Fig. 4. Streaming phenotypes are developmentally regulated. Cytoplasmic streaming shows a stage-specific requirement for amino acids 849-975 (see also Table 2). (A,B) Streamline picture of one time point of wild-type (A, black) and KHC1-849 (B, red) st11 streaming. The cell is outlined (dotted line). (C) Correlation length distribution for wild-type versus KHC1-849 at st11 streaming. The correlation length is a statistical measure of the radii of the flow features (Ganguly et al., 2012). The guide line (green) aids visualization of the correlation length. Bars indicate s.e. A t-test (P=0.70) and a Kolmogorov–Smirnov test (P=0.53) indicate that the correlation lengths in wild-type and KHC1-849 late stages are statistically identical.
this ‘flexible’ sequence is sufficient to disrupt tail-mediated repression of Kinesin (Friedman and Vale, 1999). KHC1-975ΔHinge2 oocytes show weak oskar localization defects (Fig. 7A, n=43) and no aberrant actin spheres (n=24). Furthermore, most KHC1-975ΔHinge2 eggs have normal DAs (Table 4). It is thought that auto-inhibition might prevent the mislocalization of Kinesin and futile ATP depletion. Our data suggest that KHC auto-inhibition does not play a major role in the oocyte.

Together, these results show that the IAK has functions other than auto-inhibition. This motif is required for KHC to be fully functional, and it is important for cargos such as the nucleus and actin spheres/vesicles and for the establishment of the DV axis. However, it is dispensable for st9 streaming (Ganguly et al., 2012) and the transport of oskar mRNA. oskar localization is a function of Kinesin that is not rescued by KHC1-910, a truncated motor with the N. crassa-like domain but that lacks the AMB region. Therefore, we next investigated whether the AMB site affects RNA transport.

An ATP-independent MT-binding domain at the C-terminus is essential for oskar RNA transport

The deletion of the last 37 amino acids creates a motor (KHC1-938GFP) that contains all conserved domains within the tail (including the AMB site) except the IAK and an uncharacterized motif (aa 955-959, IRGGG, which is conserved from Drosophila to mammals). Similarly to KHC1-975ΔIAK, 33% of the KHC1-938 oocytes show aberrant nucleus positioning (Table 3A) and DA formation is strongly affected in KHC1-938 eggs (Table 4, 16% normal DAs). Also, as with KHC1-975ΔIAK, oocytes expressing KHC1-938 show the aberrant accumulation of actin-recruiting spheres (supplementary material Fig. S6O). Most importantly, Staufen is mainly found at the posterior in KHC1-938 oocytes (Fig. 7B) and not at the anterior/lateral cortex as in KHC1-910 oocytes (Fig. 5B). Specifically, the KHC1-938 oocytes show Staufen in a tight posterior crescent, but also in a posterior dot (Fig. 7B, 76% of oocytes with dots, n=25). This result shows that the addition of the AMB domain to KHC1-910 (resulting in KHC1-938) restores the capacity for KHC to transport oskar to the posterior. This suggests that the MT-binding site at the C-terminus of KHC (the AMB domain) is essential for oskar RNA transport, ascribing a novel function to this domain. Although oskar is not a conserved cargo, its transport involves one of the most conserved domains of animal KHCs (Kirchner et al., 1999b).

**DISCUSSION**

The oocyte allows the analysis of the C-terminal region of KHC in an in vivo context. Our results show that the interaction of Kinesin with its cargos and/or the regulation of the motor is complex and relies on more than one region. The tail (aa 850-975) is essential for all functions of KHC in the st9 oocyte except Dynein transport. These functions include the positioning of the nucleus and Gurken protein (and consequently establishment of the DV axis), the localization of oskar, the induction of streaming, and the distribution of actin-recruiting vesicles. Most of these tail-dependent KHC activities can be functionally separated from one another by further characterizing the conserved domains within the tail (supplementary material Fig. S7). The various functional domains are not necessarily involved in cargo binding, but their presence is required for wild-type cargo transport. In particular, our data show the following: (1) a temporal regulation of the impact of KHC activity on cytoplasmic streaming during oogenesis; (2) a novel essential role for the IAK that is distinct from its auto-inhibitory function; (3) that lack of auto-inhibition in itself is not necessarily detrimental to KHC function; and (4) that the AMB motif is required for oskar RNA localization.

**Table 3. Nucleus positioning and DA phenotypes of KHC tail domain mutants**

<table>
<thead>
<tr>
<th>A. Nucleus positioning phenotypes</th>
<th>Khc27 GLC plus:</th>
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<tr>
<td>KHC1-975</td>
<td>0 (79)</td>
</tr>
<tr>
<td>B. DA phenotype of mutant eggs</td>
<td>Normal (%)</td>
</tr>
<tr>
<td>KHC1-975, Khc27 GLC (79)</td>
<td>96.2</td>
</tr>
<tr>
<td>KHC1-975ΔIAK, Khc27 GLC (156)</td>
<td>9</td>
</tr>
<tr>
<td>KHC1-849, Khc27 GLC (401)</td>
<td>3.5</td>
</tr>
</tbody>
</table>
KLC and Pat1 are essential only for the KHC-dependent localization of Dynein

The localization of Dynein to the posterior requires Kinesin (Brendza et al., 2002; Duncan and Warrior, 2002; Januschke et al., 2002; Palacios and St Johnston, 2002). Here we show that deletion of the tail has a weak effect on the transport of Dynein, whereas further deletion of the region covering coil3 and half of coil2 renders a motor unable to localize Dynein. This observation correlates with the finding that KLC, which together with Pat1 mediates Dynein localization, interacts with coil3 of KHC in a tail-independent manner (Loiseau et al., 2010). It is then likely that Dynein is a posterior cargo of KHC, and that the Dynein complex interacts with KHC via KLCs. In C. elegans, the KLC-binding protein Jip3 binds Dynein light intermediate chain (Dlic) (Arimoto et al., 2011). Alternatively, KLC might bind the Dynein intermediate chain (DIC), as in mammals (Ligon et al., 2004). This observation, together with the fact that amino acids 795-839 (including coil3) are conserved in animal KHCs, makes it plausible that, in the oocyte, KHC localizes Dynein via a coil3-dependent KLC-DIC complex.

It is important to keep in mind that even though KLC and the KLC-like protein Pat1 are not essential for the localization of oskar and the nucleus, or for the induction of flows, they still contribute to these KHC-dependent processes, albeit in a minor manner. Pat1 mutants have slightly slower flows (Ganguly et al., 2012), and Pat1,Klc double mutants show mild oskar and nucleus localization defects in 78% and 9%, respectively, of the mutant oocytes (Loiseau et al., 2010) (data not shown). These nucleus anchoring defects might correlate with those seen in KHC1-700 oocytes, since KHC1-700 does not contain the KLC-binding domain; however, the nucleus phenotypes in KHC1-700 may not be statistically significantly different from those observed in KHC1-849 oocytes.

The tail domain of KHC is important for anterior-posterior and dorsal-ventral axes

oskar RNA is found at the anterior/lateral regions of the Khc mutant oocyte (Brendza et al., 2000). Similarly, Khc27 st9 oocytes show a mispositioned nucleus and an aberrant distribution of Gurken protein (Brendza et al., 2002; Duncan and Warrior, 2002; Januschke et al., 2002). Consequently, embryos resulting from Khc27 oocytes have an aberrant anterior-posterior (AP) and DV body plan. Deletion of the tail produces a motor that is unable to localize oskar RNA and thus is unable to support the establishment of the AP axis. Further characterization of the function of conserved domains within the tail suggests that RNA transport activity relies on the AMB site.

In addition, 96.5% of the embryos resulting from tailless KHC oocytes have aberrant DA formation. This DV axis defect might be due to more than the tail function in nucleus positioning, since the nucleus is not positioned in 60% of tailless KHC1-849 oocytes. We show that KHC1-849 oocytes are defective for Gurken protein localization, even when the nucleus seems properly positioned. Given that the oocyte nucleus is associated with one of the MT-organizing centers (Januschke et al., 2006), it is possible that the defects in Gurken signaling, and thus DV axis, in Kinesin mutants are a result of both nucleus mispositioning and the misorganization of the anterior MTs (Brendza et al., 2002). This is consistent with MT defects observed at the anterior of KHC1-849 and KHC1-700 oocytes (supplementary material Fig. S6,F,G,I, arrows). In wild-type and KHC1-975 oocytes, there is an obvious AP gradient of MTs, with a population of enriched MTs close to the anterior/lateral cortex (supplementary material Fig. S6,A,B). This gradient can also be seen in some KHC1-849 and KHC1-700 oocytes (supplementary material Fig. S6,E,H). However, most of these mutant oocytes show an extension of this anterior ‘bright’ MT network towards the posterior around the nucleus (supplementary material Fig. S6,F,G), as well as the misorganization of MTs in a pattern that resembles the aberrant vesicles often detected at the anterior of Khc mutant oocytes (supplementary material Fig. S6,F,I, arrows; vesicles in Fig. 6). The region encompassing the KLC-binding domain might also contribute to the establishment of the DV axis, since the number of oocytes with Gurken in an anterior-dorsal crescent drops from 14% in KHC1-849 oocytes to 0% in KHC1-700 oocytes (supplementary material Fig. S1).

Does KHC act directly on oocyte nucleus positioning and Gurken protein localization?

At first glance, it is unclear why there are nucleus and Gurken localization defects in the Khc null, when plus ends are biased towards the posterior (Parton et al., 2011). As nucleus positioning requires the Dynein complex, it follows that KHC function could be indirect for the anterior cargos, for example via the recycling of Dynein (Brendza et al., 2002; Duncan and Warrior, 2002; Januschke et al., 2002; Lei and Warrior, 2000; Swan et al., 1999; Swan and Suter, 1996; Zhao et al., 2012). However, we think that KHC could be acting directly on nucleus positioning. First, it cannot be
discounted that Dynein and Kinesin act independently: Dynein localization to the posterior is abolished in Pat1,Klc double mutants, whereas nucleus positioning is only weakly affected, suggesting that the coordinated action of the two motors is not necessarily required. Second, the MT network is complex, and there seem to be some plus ends towards the anterior cortex that Kinesin may harness (Parton et al., 2011). Third, KHC localizes at the nuclear envelope. Fourth, when KHC is missing, alpha-tubulin and Jupiter-GFP [a MT-associated protein fused to GFP (Ganguly et al., 2012; Karpova et al., 2006)] are found in dots at the nuclear envelope (data not shown) in a similar punctate pattern to that displayed by KHC.

All these preliminary observations might suggest that KHC is acting on a set of MTs that allows positioning of the nucleus in close proximity to the anterior membrane: when KHC is missing, these MTs seem to ‘collapse’ to the nuclear envelope and their stable existence is not maintained. Taking work on cultured cells (Splinter et al., 2010) into consideration, Kinesins might well bind to the nuclear envelope and transport the nucleus towards the plus ends. However, it is likely that the relative importance of different molecular links between the nuclear envelope and motors depends on the cell type (Splinter et al., 2010). For example, Drosophila SUN/KASH proteins (Msp-300, Klarsicht and Klaroid) have no existence is not maintained. Taking work on cultured cells (Splinter et al., 2010) into consideration, Kinesin may harness (Parton et al., 2011). Third, KHC localizes at the nuclear envelope. Fourth, when KHC is missing, alpha-tubulin and Jupiter-GFP [a MT-associated protein fused to GFP (Ganguly et al., 2012; Karpova et al., 2006)] are found in dots at the nuclear envelope (data not shown) in a similar punctate pattern to that displayed by KHC.

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There are other mutants that show nucleus positioning defects, including skittles (which encodes phosphatidylinositol 4,5-bisphosphate-synthesizing enzyme) (Gervais et al., 2008), trailer hitch (tral) and Bicaudal C (BicC). Among these, tral and BicC mutants have abnormal actin-covered vesicles that look similar to those present in Khc oocytes (Kugler et al., 2009; Snee and Macdonald, 2009). This similarity, together with our data showing that Rabenosyn-5 is present in Khc mutant vesicles, suggest that KHC is required for membrane trafficking in the oocyte. This correlates with the function of KHC in other cells and with the observation that, in Khc oocytes, Rab6 vesicles aggregate abnormally around the mispositioned nucleus (Januschke et al., 2007). The ectopic vesicles that we observe in Khc oocytes seem to nucleate actin, as seen in time-lapse movies of Utrophin-GFP. As suggested for tral and BicC, the formation of ‘actin spheres’ (as a readout of vesicle trafficking problems) in Khc oocytes might cause defects in Gurken signaling. In fact, Gurken is detected in close proximity to actin-recruiting vesicles in KHC1-938 oocytes (supplementary material Fig. S6O, arrow). These data stress that the anterior phenotypes observed in Khc mutant oocytes are likely to be the result of a complex relationship between vesicle trafficking, MTs and nucleus location. Ectopic sites of actin nucleation by aberrantly distributed vesicles. Ectopic vesicles at the posterior of the oocyte (GLC) containing KHC1-938GFP (green in merge). DAPI, blue. linked with the observation that, in Khc oocytes, Rab6 vesicles aggregate abnormally around the mispositioned nucleus (Januschke et al., 2007). The ectopic vesicles that we observe in Khc oocytes seem to nucleate actin, as seen in time-lapse movies of Utrophin-GFP. As suggested for tral and BicC, the formation of ‘actin spheres’ (as a readout of vesicle trafficking problems) in Khc oocytes might cause defects in Gurken signaling. In fact, Gurken is detected in close proximity to actin-recruiting vesicles in KHC1-938 oocytes (supplementary material Fig. S6O, arrow). These data stress that the anterior phenotypes observed in Khc mutant oocytes are likely to be the result of a complex relationship between vesicle trafficking, MTs and nucleus location. Ectopic sites of actin nucleation by aberrantly distributed vesicles.

**Novel in vivo functions for the IAK motif**

Auto-inhibition to limit the consumption of ATP/GTP by motors not bound to cargos is conserved in Myosins (Jung et al., 2008; Li et al., 2006; Umeki et al., 2009) and Kinesins (Al-Bassam et al., 2003; Imanishi et al., 2006; Seiler et al., 2000). As both protein families share a common ancestor, it is not unexpected that there is a common mechanism to this auto-inhibition, in which the tail folds back to the motor domain. It is clear from research on affecting

### Table 4. The DA phenotypes of wild-type and Khc mutant eggs

<table>
<thead>
<tr>
<th>Genotype (n)</th>
<th>Normal (%)</th>
<th>Fused/one (%)</th>
<th>None (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wild type (284)</td>
<td>97.5</td>
<td>1.4</td>
<td>1.1</td>
</tr>
<tr>
<td>KHC1-975ΔHinge2, Khc27 GLC (130)</td>
<td>77</td>
<td>18</td>
<td>5</td>
</tr>
<tr>
<td>KHC1-975ΔJAK, Khc27 GLC (156)</td>
<td>9</td>
<td>36</td>
<td>55</td>
</tr>
<tr>
<td>KHC1-938, Khc27 GLC (96)</td>
<td>16</td>
<td>30</td>
<td>54</td>
</tr>
</tbody>
</table>

KHC1-975ΔHinge2 and KHC1-975ΔJAK eggs do not have equivalent DA defects.
auto-inhibition in vivo that these motors cannot function correctly, leading to detrimental transport (Al-Bassam et al., 2003; Imanishi et al., 2006; Seiler et al., 2000). What was still unknown is whether the defects in transport are a consequence of a lack of inhibition or are due to alternative functions of the motifs involved. We have compared these two hypotheses directly for the first time.

Recently, the stoichiometry of the interaction between the IAK and motor domains has been determined, with one IAK motif per motor dimer required (Hackney et al., 2009). This has led to the suggestion that the other motif could be free to bind cargo or other regulators of KHC. A mutant IAK with two individual point mutations (IAK\textsuperscript{PIRS} to IAK\textsuperscript{PIRS}, IAK\textsuperscript{PIRS} to IAK\textsuperscript{PIRS}) shows weak defects in oskar transport and DA formation that are similar to those of Khc hypomorphic alleles, suggesting that these mutations result in inhibition rather than overactivation of transport (Moua et al., 2011). Similarly, the IAK seems to facilitate, rather than downregulate, axonal transport of mitochondria. However, these IAK point mutants did not constitute a full null of IAK activity, since when we mutagenize the entire motif the DA defects are much stronger than those observed in the point mutants. In addition, deletion of the IAK phenocopies the deletion of the tail regarding vesicle trafficking result in mild defects in cytoskeleton organization, involving various feedback loops (Tanaka et al., 2011; Tanaka and Nakamura, 2008; Vanzo et al., 2007). It is possible that defects in vesicle trafficking function of KHC. This idea is supported by our findings, since KHC1-975\DeltaIAK and KHC1-938 oocytes show aberrant actin spheres/vesicles (84% and 45% of KHC1-975\DeltaIAK and KHC1-938 oocytes, respectively) and dots/clouds of oskar adjacent to the posterior crescent. The relationship between oskar localization, MTs and endocytosis at the posterior is complex, involving various feedback loops (Tanaka et al., 2011; Tanaka and Nakamura, 2008; Vanzo et al., 2007). It is possible that defects in vesicle trafficking result in mild defects in cytoskeleton organization, since Rab11 and Rab6 mutant oocytes show mislocalized MTs. Thus, this inefficient oskar localization to a posterior crescent in mutant oocytes might indirectly result from mild cytoskeleton defects at the posterior. Alternatively, KHC1-975\DeltaIAK-dependent or KHC1-938-dependent ectopic Oskar protein and/or ectopic MT plus ends might result in aberrant endocytosis at the posterior.

It is interesting to note that although oskar RNA is not a conserved cargo its transport involves a highly conserved domain, i.e. the AMB domain. This, and our findings concerning the IAK domain, show that although not all cargos are conserved their transport involves the most conserved domains of animal KHCs. Thus, both the IAK and AMB domains might play a crucial role in the transport of cargos in other cell types and organisms.

**Materials and Methods**

**Stocks and germline clones**

Fly stocks: w\textsuperscript{y}, P\textsuperscript{y} [y\textsuperscript{hs};FLP]; P\textsuperscript{w\textsuperscript{'}}, FRT\textsuperscript{1}G13 ovar\textsuperscript{1}/Tp/Cyo, w\textsuperscript{'}P[w\textsuperscript{'}], FRT\textsuperscript{1}G13Khc\textsuperscript{1}/Cyo.P[w\textsuperscript{'}], mat-tub-a4::KHC1-975GFP]/TM6B,
TM6B, w–, P{w+,FRT}G13Khc27/CyO; P{w+,mat-tub-FLP/FRT system (Chou et al., 1993; Chou and Perrimon, 1996). Homozygous w–, P{w+,mat-tub-CyO, w–, P{w+,FRT}G13Khc27/CyO, w–, P{w+,mat-tub-FLP/FRT system (Chou et al., 1993; Chou and Perrimon, 1996). Homozygous w–, P{w+,mat-tub-CyO, w–, P{w+,FRT}G13Khc27/CyO, w–, P{w+,mat-tub-FLP/FRT system (Chou et al., 1993; Chou and Perrimon, 1996). Homozygous w–, P{w+,mat-tub-CyO.

performed and analyzed some experiments. S.G. analyzed flows by particle image velocimetry and discussed results. P.L. designed some of the transgenic constructs and performed and discussed early experiments.

Funding
L.S.W. and P.L. were supported by the Wellcome Trust and L.S.W. by the Cambridge Cancer Centre/Cancer Research UK, S.G. by the European Research Council, B.F.N. by Singapore Ministry of Education, and I.M.P. by the Royal Society and Cambridge University. Deposited in PMC for immediate release.

Supplementary material
Supplementary material available online at http://dev.biologists.org/lookup/suppl/doi:10.1242/dev.097592/-/DC1

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