Different mechanisms link gain and loss of kinesin functions to axonal degeneration

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♦ Please, note that Y.-T.L. is the key contributor to this work as part of her PhD thesis (Liew, 2018). Unfortunately, we have not been able to establish contact for over two years, so that direct consent by this author to publication of this work has not been given. However, consent is assumed from prior discussions we had.

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Abstract

Axons are the slender, often meter-long projections of neurons that form the biological cables wiring our bodies. Most of these delicate structures must survive for an organism's lifetime, meaning up to a century in humans. Long-term maintenance and sustained functionality of axons requires motor protein-driven transport distributing life-sustaining materials and organelles to places of need. It seems therefore plausible that loss of motor function can cause axon degeneration; however, also gain-of-function conditions were linked to disorders including motor neuron disease or spastic paraplegia. To understand this phenomenon, we studied ~40 genetic manipulations of motor proteins, cargo linkers and regulators of reactive oxygen species in one standardised *Drosophila* primary neuron system. Using axonal microtubule bundle organisation as a relevant readout reflecting the state of axon integrity, we found that losses of Dynein heavy chain, KIF1A/Unc-104 and KIF5/Kinesin heavy chain (Khc) all cause bundle disintegration in the form of chaotically curled microtubules. Detailed functional studies of Khc and its adaptor proteins revealed that losses of mitochondrial or lysosomal transport cause ROS dyshomeostasis, which is a condition that inducing MT-curling in fly and mouse neurons alike. We find that hyper-activated Khc induces the same MT-curling phenotype, not through ROS but directly through enhanced mechanical forces. Studies with loss of Unc-104 and expression of an ALS-linked mutant form of the human Khc orthologue KIF5A suggest that the two mechanisms apply to motors beyond Khc. We discuss a model which can explain the surprising common outcome of both conditions and examine its relevance for understanding motor-linked neurodegeneration.

Introduction

Axons are the long and slender processes of neurons which form the biological cables that wire the
nervous system and are indispensable for its function. In humans, axons can be up to 2 metres
long whilst displaying diameters of only 0.1-15µm (Prokop, 2020). Most of these delicate cellular
processes must survive for an organism's lifetime, meaning up to a century in humans.
Unsurprisingly, mammals lose about 40% of their axon mass towards high age (Calkins, 2013;
Coleman, 2005; Marner et al., 2003). This rate is drastically increased in hereditary forms of
axonopathies (Prokop, 2021; Smith et al., 2023).

A prominent group of axonopathy-inducing mutations affects motor proteins, especially
dynein/Dynactin, kinesin-1 and kinesin-3 family members and some of their associated adaptor
proteins, which are actively involved in the live-sustaining axonal transport of RNAs, proteins, lipids
and organelles (Guedes-Dias and Holzbaur, 2019; Hirokawa et al., 2010; Smith et al., 2023). The
loss of such transport was shown to affect axon growth, function and regeneration (Guerra San
Juan et al., 2024); it can be expected to lead to systemic collapse of axonal structure and
physiology, hence axonopathy, in the longer term, and explain the reported links to Charcot Marie
Tooth diseases, hereditary sensory neuropathies or ataxias (for a detailed list of links listed in the
Online Mendelian Inheritance in Man® database, see Smith et al., 2023). Surprisingly, disease-
relevant mutations of motors do not only cause loss-of-function, but some mutations cause over-
activation of motors (Baron et al., 2022; Chiba et al., 2019; Gabrych et al., 2019; Pant et al., 2022;
Pino et al., 2023). This poses the question of how opposing mutational effects can cause very
similar outcomes.

To address this question, we used an experimental approach based on two strategic decisions:
Firstly, we used axonal microtubules (MTs) as our main readout. These MTs are arranged into
loose bundles that run all along axons; they are required for axonal morphogenesis and they form
the essential highways for axonal transport (Prokop, 2020). Accordingly, aberrations of MT bundles
are sensitive indicators of axonal pathology, with disorganised curling of MTs being an often-
observed pathological phenotype (Fig.1; Hahn et al., 2019; Prokop, 2021; Smith et al., 2023).

Secondly, we used *Drosophila* primary neurons as a cost-effective model system, where
mechanistic complexity can be addressed with fast and efficient genetic strategies (Hahn et al.,
2021; Prokop et al., 2013; Qu et al., 2017). Loss-of-function analyses in *Drosophila* are facilitated
by the fact that key factors, such as Kinesin heavy chain (Khc, kinesin-1), Kinesin light chain (Klc)
or Milton, are each encoded by a single gene in *Drosophila*, as opposed to three, four or two in
mammals, respectively. Furthermore, genetic tools are readily available to manipulate virtually any
gene in question - and all these functional approaches can be combined with efficient and well-
established readouts reflecting axonal physiology (Hahn et al., 2016; Prokop et al., 2013; Prokop et
al., 2012; Sánchez-Soriano et al., 2010).

Here we show that the losses of three motor proteins, the Kif5 homologue Kinesin heavy chain
(Khc; kinesin-1), the Kif1A/Bβ homologue Unc-104 (PH domain-containing kinesin-3), and the
DYNC1H1 homologue Dynein heavy chain 64C (Dhc64C), all cause MT-curling and reduced
numbers of mitochondria and synaptic dots in axons. Refined genetic analyses of Khc and its
various adaptor proteins revealed two very different mechanisms that cause MT-curling: Firstly,
loss of Khc-mediated transport of mitochondria and lysosomes causes harmful reactive oxygen
species (ROS) which, in turn, induce MT-curling in fly and mouse neurons alike. Secondly, loss of
the adaptor protein Kinesin light chain (Klc) causes overactivation of Khc as a ROS-independent

curl-inducing mechanism mimicked by hyperactivating mutations of Khc; MT curling in these
conditions occurs likely through direct force-mediated damage. Further experiments suggest that
these fundamental mechanisms apply to other transport motor proteins. We discuss a conceptual
model that can explain our findings and provide explanations for neurodegeneration in the wider
sense.

Results

<u>Losses of Khc, Unc-104 or Dhc cause axonal microtubule curling</u>

To start our investigation, we assessed whether functional loss of motor proteins would cause
measurable changes of axonal microtubule (MT) bundles as well-established indicators of axonal
health (Okenve-Ramos et al., 2024; Prokop, 2020; Smith et al., 2023). We assessed MT bundle
organisation in axons of neurons deficient for a range of transport motor proteins: (a) Dynein heavy
chain (Dhc) is the obligatory motor-bearing subunit of the dynein/Dynactin complex essential for
most, if not all, MT-based retrograde transport (Reck-Peterson et al., 2018); (b) Klp64D is one of
two obligatory subunits of heterodimeric kinesin-2 (KIF3 homologue), reported to mediate
anterograde axonal transport of acetylcholine-related synaptic enzymes or olfactory receptors
(Baqri et al., 2006; Jana et al., 2021; Kulkarni et al., 2017; Ray et al., 1999); (c) the PX-domain-
containing type 3 kinesin Klp98A (KIF16B homologue) was shown to mediate autophagosome-
lysosome dynamics and endosomal Wingless transport in non-neuronal cells but is also strongly
expressed in the nervous system (Mauvezin et al., 2016; Witte et al., 2020; flybase.org:
[FBgn0004387](#)); (d) the PH-domain-containing type 3 kinesin Unc-104 (Kif1A homologue) is
essential for synaptic transport in *Drosophila* axons (Pack-Chung et al., 2007; Voelzmann et al.,
2016); (e) Kinesin heavy chain/Khc is the sole kinesin-1 in *Drosophila* (KIF5A-C homologue)
involved in multiple transport functions in *Drosophila* neurons (see details below; e.g. Bowman et
al., 2000; Gindhart et al., 2003; Glater et al., 2006; Loiseau et al., 2010; Rosa-Ferreira et al., 2018;
Saxton et al., 1991).

We cultured primary neurons obtained from embryos homozygous for loss-of-function mutant
alleles of these motor proteins (see Methods) and analysed them at 5DIV (days *in vitro*). These
analyses revealed that especially the losses of Dhc, Khc and Unc-104 caused enhanced MT
bundle disintegration displaying as areas where MTs are disorganised into curled, criss-crossing
arrangements (from now on referred to as MT curling; curved arrows and enlarged insets in
Fig.1,B,F-H).

To assess whether MT curling phenotypes were accompanied by transport defects, we analysed
additional sub-cellular markers in *Khc[8]*, *unc-104[170]* and *Dhc64C[4-19]* homozygous mutant neurons.
First, using the pre-synaptic protein Synaptotagmin (Syt) as a crude but easy to assess indicator of
vesicular transport (Voelzmann et al., 2016), we found reduced presynaptic spots within axons of
neurons mutant for any one of these three motor proteins (Fig.2A-D,O). Second, also the axonal
number and distribution of mitochondria (visualised with mitoTracker; Klionsky et al., 2012), was
significantly reduced in neurons lacking either Khc, Unc-104 or Dhc64C function (Fig.2H-K,P).
Third, in *Khc[8]* mutant neurons, we also assessed the distribution of endoplasmic reticulum (ER)
using a genomically GFP-tagged allele of Rtnl1, a constituent of axonal smooth ER (O'Sullivan et
al., 2012). In wild-type neurons, ER is distributed evenly along the entirety of the axon (inset in
Fig.S1A); loss of Khc does not affect this continuity, but about three quarters of neurons show an
abnormal prominent accumulation of Rtnl-1::GFP label at their tips (details in legend of Fig.S1B).

In conclusion, our data strongly suggest that the three motor proteins that display MT curling
mediate the transport of axonal components in primary neurons.

Khc displays strong maternal effects

We next focussed analyses on Khc, because many independent genetic tools are available
enabling us to dissect sub-functions of Khc's transport roles (Fig.3B). As the first step, we
validated Khc's MT-curling phenotype using the additional mutant allele Khc^{27}, crossing Khc^8 and
Khc^{27} over a deficiency, and through RNAi-mediated knockdown of Khc (using pan-neuronal *elav-*
Gal4). In all cases we found strong MT curling phenotypes at 5DIV confirming our initial finding
(Fig.S2A,B).

However, the MT phenotypes were not evident at earlier stages as revealed by analyses of $Khc^{8/Df}$
mutant neurons at 6 hours *in vitro* (HIV) or 3DIV (Fig.S2B,D): either phenotypes accumulate
gradually over time (as observed for loss of Efa6; Qu et al., 2019), or mutant phenotypes are
masked by maternal *Khc* gene product deposited during oogenesis by the heterozygous mothers
(as previously observed for Eb1; Alves-Silva et al., 2012; Prokop, 2013).

To distinguish between these two possibilities, we used a pre-culture technique where neurons are
kept in centrifuge tubes for 5 days to deplete maternal gene product, before growing them in
culture (Prokop et al., 2012; Sánchez-Soriano et al., 2010). $Khc^{8/Df}$-mutant neurons pre-cultured in
this way, displayed prominent MT curling already 12 hrs after plating (Fig.S2C,E), suggesting that
Khc has a prominent maternal contribution that persists for more than 3 days. Similar observations
were made when pre-culturing the Khc^{1ts} mutant allele (details in Fig.S2C).

MT sliding functions of Khc do not link to MT-curling

We next tested potential mechanisms of Khc that might cause curling when abolished. For
example, Khc might contribute to MT bundle maintenance by sliding MTs to achieve their even
distribution along axons. Khc' MT-sliding function is made possible by its C-terminal MT-binding
site which, together with the MT-binding motor domain, enables it to cross-link MTs and move
them against each other (Fig.3Bi; Andrews et al., 1993; Jolly et al., 2010; Lu et al., 2013; Lu et al.,
2015; Winding et al., 2016).

To test whether Khc-mediated sliding contributes to MT bundle regulation we used the lethal
Khc^{mutA} mutant allele that specifically abolishes the binding of the Khc C-terminus to MTs but not
other cargoes (Fig.3A; Winding et al., 2016). Khc^{mutA}-mutant neurons were cultured in different
ways: either as embryo-derived neurons cultured for 1DIV after 5d pre-culture, or as embryo-
derived neurons cultured for 5DIV without pre-culture. In both cases, these neurons failed to show
enhanced MT curling (Fig.3Ci), suggesting that the *Khc* mutant phenotype is not caused by the
loss of its MT sliding function.

Losses of Milton, Miro and Arl8 cause MT-curling phenotypes

Next, we focussed on organelle transport functions of Khc including mitochondria, peroxisomes
and lysosomal compartments. The axonal transport of mitochondria requires the linker protein
Milton and its binding partner Miro (a small GTPase) which bind to the C-terminus of Khc
(Fig.3A,Biii; Harbauer, 2017; Misgeld and Schwarz, 2017; Sheng, 2017; Smith and Gallo, 2018).
Miro has also been reported to mediate the transport of peroxisomes (Castro et al., 2018; Covill-

Cooke et al., 2020; Okumoto et al., 2018; Tang, 2018). We therefore tested the loss-of-function
mutant alleles *milt^{92}*, *Miro^{Sd32}* and *Miro^{B682}*, which all caused prominent increases in MT curling at
5DIV (Fig.3Ciii) suggesting that defective mitochondrial transport can trigger MT curling.

To determine whether MT-curling is more likely to correlate with aberrant mitochondrial or
peroxisomal transport, we labelled peroxisomes using Gal4/UAS-mediated expression of
PTS1::YFP (Faust et al., 2014) and mitochondria with mitoTracker (Voelzmann and Sánchez-
Soriano, 2022) and assessed their axonal abundance. Peroxisomes mainly restricted to neuronal
cell bodies (on average >10 peroxisomes) with axons displaying only an average of two (Fig.S3A-
D). This is consistent with neurons in the fly brain which were reported to harbour low numbers of
peroxisomes versus a much higher abundance in glial cells (Chung et al., 2020). Since the culture
medium we used contains only trace amounts of fatty acids (Else, 2020; Prokop et al., 2012;
Schneider, 1964), peroxisomes are unlikely contributors to energy metabolism hence not needed
in high numbers (Wanders et al., 2020). Preliminary analyses suggested that loss of Khc has little
impact on peroxisome distribution in axons (see details in Fig.S3E), and loss of peroxisomes
(deletion of the biogenesis factor Pex3) did not at all increase MT curling (Fig.S3F).

In contrast, mitochondria numbers in axons were clearly reduced upon loss of Miro and Milt
(Fig.2L,M,O), in agreement with observations made *in vivo* (Glater et al., 2006; Guo et al., 2005;
López-Doménech et al., 2018; Russo et al., 2009; Vagnoni et al., 2016). This phenotype was
strongest in *milt^{92}* mutant neurons where mitochondria were frequently restricted to cell bodies and
proximal axon segments (Fig.2L,O). The milder phenotype of Miro is consistent with findings in fly
neurons *in vivo* as well as in mouse neurons (Glater et al., 2006; Guo et al., 2005; López-
Doménech et al., 2018; Russo et al., 2009; Vagnoni et al., 2016; see also Mattedi et al., 2023).

Finally, we tested Khc-mediated transport of lysosomes and their derivatives. This requires Arl8
(ARL8A/B homologue; a small GTPase of the Arf family) in conjunction with SKIP/PLECHM2
(potential orthologue of Prd1 or Plekhm1 in fly) and the BORC complex (present in *Drosophila*;
flybase.org; Fig.3Biv; Keren-Kaplan and Bonifacino, 2021; Rosa-Ferreira and Munro, 2011; Rosa-
Ferreira et al., 2018). Using a loss-of-function mutant allele of Arl8 in homozygosis or over
deficiency, we observed strong MT curling at 5DIV (Fig.3Civ). This suggests that impairing
anterograde lysosome transport causes MT curling - although Arl8 has recently been suggested to
contribute to a certain degree also to retrograde lysosome transport (Paumier and Gowrishankar,
2024).

We conclude that aberration of peroxisomes and their distribution is unlikely to explain MT curling,
whereas aberrant mitochondrial and lysosomal transport are much more likely causes.

<u>Excessive ROS triggers MT-curling in fly and mouse neurons</u>

Reduced numbers of mitochondria or their wrong localisation are likely to impair important aspects
of local axon homeostasis. Expected changes might include the regulation of calcium, ATP, Krebs
cycle-derived metabolites, protein quality control, and signalling including reactive oxygen species
(ROS; Glynn, 2017; Misgeld and Schwarz, 2017; Paupe and Prudent, 2018). Of these, energy
depletion and ROS were shown to affect MT networks (Conze et al., 2024; Park et al., 2013;
Shields et al., 2024a). Since both mitochondrial and lysosomal dysfunction are known to cause
oxidative stress (Kurz et al., 2008; Zhang et al., 2016), we tested ROS as a potential common
nominator leading to MT curling.

For this, we first applied DEM (diethyl maleate) which causes ROS increase by inhibiting the anti-
oxidant compound glutathione ('blue arrowhead' in Fig.4A; Albano et al., 2015; Dasgupta et al.,

2012; Pompella et al., 2003). When applying 100 µM DEM for 12hrs before fixation (from 4.5 to
5DIV) we observed robust MT curling (Fig.4F). To validate these findings, we genetically
manipulated the function of ROS-regulating enzymes ('red arrowheads' in Fig.4A); this included the
use of a null allele of the peroxidase Catalase (*Cat^{n1}*; Walker et al., 2018), loss and gain-of-function
of Superoxide dismutase 1 (*Sod1^{n1}*, *Sod1^{n64}*, *elav>Sod1*; converting O_2^- into H_2O_2; Palma et al.,
2020b), targeted expression of *Nox* (NADPH oxidase; enhancing O_2^- levels), of *Sod1* (to reduce
O_2^- levels and enhance H_2O_2, and of *Duox* (Dual oxidase; to increase H_2O_2 levels; Anh et al., 2011;
Bedard and Krause, 2007; Zelko et al., 2002). All these manipulations caused increased MT
curling (Fig.4F). Of these, the observed effects upon loss of Catalase might be surprising when
considering that peroxisomes (as its preferred sites of localisation) are in low abundance; but
Catalase was reported to localise in the cytoplasm when peroxisomes are absent (Kleinecke et al.,
2017; Zhou and Kang, 2000).

Finally, we tested whether the MT curl-inducing effects are conserved with mammalian neurons.
For this, we applied either 100 or 200 µM DEM to cultured mouse primary cortical neurons. Also
these neurons displayed a robust increase in MT-curling (Fig.7).

Taken together, dyshomeostasis of ROS clearly triggers MT-curling in fly and mouse neurons
alike. Upregulation of either O_2^- or H_2O_2 seems to cause this effect, although O_2^- is perhaps more
likely to elicit its effects through conversion into H_2O_2 (Bedard and Krause, 2007; Palma et al.,
2020a).

<u>MT-curling downstream of Khc, Milt and Arl8 deficiency seems mediated by harmful ROS</u>

To assess whether harmful ROS might be responsible for linking aberrant organelle transport to
MT-curling, we treated Khc-, Milt- and Arl8-deficient neurons with Trolox (6-hydroxy-2,5,7,8-
tetramethylchroman-2-carboxylic acid). Trolox is an α-tocopherol/vitamin E analogue that displays
beneficial antioxidant effects in many cell systems, including neuronal models of
neurodegeneration; it inhibits fatty acid peroxidation and quenches singlet oxygen and superoxide
(Chow et al., 1994; Giordano et al., 2020; Janc and Müller, 2014). To first validate its effect, we
treated neurons with DEM to induce MT-curling; we observed that this phenotype was abolished
upon co-application of Trolox (Fig.5A; see also Shields et al., 2024b).

We next treated *Khc^8*, *milt^{92}* and *Arl8^{e00336}* mutant neurons with 100µM Trolox and found a robust
suppression of the MT-curling phenotype in all three conditions (Fig.5B-D), suggesting that
absence of their function causes harmful ROS as a key mediator of their MT-curling phenotypes
(Fig.S5B,C). This also agrees with reports that rat neurons depleted of the Khc homologue KIF5C
are more vulnerable to H_2O_2 application (Iworima et al., 2016).

<u>Klc causes MT curling independently of its role in vesicular transport</u>

We next tested, whether also the transport of non-organelle cargoes might cause MT-curling. For
example, Pat1 (Protein interacting with APP tail-1) was shown to link Khc to non-vesicular
transport in *Drosophila* oocytes (Fig.3Bii; Loiseau et al., 2010). Pat1 is also strongly expressed in
the *Drosophila* nervous system (flybase.org: [FBgn0029878]) but its potential neuronal cargoes are
unknown. However, when assessing Pat1-deficient primary neurons, there was no convincing MT-
curl-inducing effect (Fig.3Cii).

We further tested loss of Khc-mediated vesicular cargo transport which requires a complex of
various factors including Kinesin light chain (Klc; homologue of KLC1-4) and Sunday driver (Syd, a

JNK-Interacting Protein; Fig.3Bv; Gindhart et al., 2003; Horiuchi et al., 2005; Koushika, 2008).
Functional losses of Klc, Syd or Khc were shown to affect vesicular transport in larval axons to
similar degrees, suggestive of mutual requirements (Bowman et al., 2000; Füger et al., 2012;
Gauger and Goldstein, 1993; Gindhart et al., 1998; Hurd and Saxton, 1996; Pilling et al., 2006).
Using primary neurons, we found that the number of synaptic Syt-labelled dots was reduced upon
the losses of Khc, Klc and Syd, far less upon loss of Milt or Miro, whereas loss of Unc-104 showed
the strongest depletion (Fig.2P). These data agree with the existence of Khc/Klc/Syd-mediated
vesicular transport in *Drosophila* primary neurons, in parallel to known functions of Unc-104 in
synaptic transport (Pack-Chung et al., 2007; Voelzmann et al., 2016).

However, despite their very similar inhibitory effects on vesicular transport, neurons lacking Syd
showed no convincing increase in MT-curling, whereas loss of Klc caused a very strong phenotype
(Fig.3Cv). These findings might suggest that MT-curl-inducing effects upon loss of Klc do not relate
to vesicular transport. This notion was supported by knock-down of GAPDH (glyceraldehyde-3-
phosphate dehydrogenase), an enzyme required for glycolysis; its loss in *Drosophila* was
previously shown to inhibit the axonal transport of vesicles but not of mitochondria (details in
Fig.S4A,B; Zala et al., 2013). Consistent with these reports, knock-down of GAPDH in primary
Drosophila neurons caused robust reduction of synaptic dots and a far more moderate effect on
mitochondrial numbers (Fig.S4C,D). However, GAPDH knock-down did not cause any increase in
MT curling phenotypes (Fig.S4C), further supporting our conclusion that reduced vesicular
transport is not a MT-curl-inducing condition.

To explore potential alternative mechanisms underlying the Klc-deficient MT-curling phenotype, we
tested the potential involvement of ROS. When applying Trolox, the MT-curling phenotype in Klc-
deficient neurons was not at all suppressed (Fig.5E), clearly differing from loss of Khc, Milt or Arl8
(Fig.5B-D). This finding further suggested the involvement of a very different mechanism.

<u>Excessive pools of active Khc might explain the Klc-deficient MT-curling phenotype</u>

To gain a mechanistic understanding of Klc's role in MT regulation, we started by performing
genetic interaction studies. These studies assessed the potential occurrence of MT-curling when
combining heterozygous conditions of independent genes in the same animals or cells (referred to
as trans-heterozygous condition); phenotypes occurring upon trans-heterozygosis are suggestive
of a direct or indirect functional interaction between the tested genes. Unfortunately, the genetic
interactions we tested were not robust enough to draw clear conclusions, but they showed
meaningful trends. When combining $Klc^{8ex94/+}$ with $milt^{92/+}$, the trans-heterozygous condition does
not exceed the sum of the single heterozygous conditions; this suggests absence of genetic
interaction in agreement with their potential mechanistic dichotomy (Fig.S6A). In contrast, the
combination of $Khc^{8/+}$ and $milt^{92/+}$ caused a phenotype that seemed stronger than the sum of the
single heterozygous conditions (Fig.S6B), mildly suggestive of genetic interaction and agreeing
with their common function in mitochondrial transport. Finally, $Khc^{8/+}$ and $Klc^{8ex94/+}$ showed a trend
towards a negative interaction (Fig.S6C), as if Khc acts as a mediator of the Klc-deficient
phenotype.

The latter finding might point at reported roles of Klc in the inactivation of Khc. Thus, Khc
molecules not engaged in transport transit into an auto-inhibited, MT-detached Λ configuration
where the C-terminus binds intramolecularly to the N-terminus ('stippled blue line' in Fig.3A); Klc
further promotes this inactive stage (Figs.3Bvi; Bowman et al., 2000; Chiba et al., 2022; Koushika,
2008; Verhey and Hammond, 2009; Verhey et al., 1998; Weijman et al., 2022; Wong and Rice,

2010; Yip et al., 2016). In non-neuronal cells, overriding auto-inhibition of the Khc-Klc complex
causes severe MT-curling (Paul et al., 2020; Randall et al., 2017).

To test whether Klc-deficient MT-curling in neurons might involve excessive pools of active Khc
(Fig.S6D), we first targeted the expression of GFP-tagged Khc constructs to neurons. Full-length
Khc^{FL}::GFP was homogeneously distributed along axons as similarly reported for its homologue
KIF5A (Cozzi et al., 2024); it did not cause a MT-curling phenotype at 5DIV (Fig.6A,C). Next we
expressed, the deletion construct Khc$^{1-850}$::GFP (indicated as grey bar in Fig.3A) which lacks the C-
terminal region required for auto-inhibition, cargo transport and MT sliding. Khc$^{1-850}$::GFP
accumulated at axon tips (Fig.6B), as is typical of non-inactivating kinesins (Nakata and Hirokawa,
2003; Niwa et al., 2013; Seiler et al., 2000), and it caused a modest MT-curling phenotype
(Fig.6D). These results might suggest that free-running, non-inactivating Khc can harm axonal MT
bundles, unlike Khc^{FL} which inactivates and detaches from MTs when unengaged with cargo
(Fig.S5F,G).

Since Khc$^{1-850}$::GFP cannot bind cargo, it likely imposes less force on MTs than a loaded kinesin.
We therefore tested the genomically engineered *Khc^{E177K}* and *Khc$^{E177R, R947E}$* mutant variants which
are non-inactivating but still able to transport cargo: the E177 and R947 residues are essential for
the C- to N-terminal interaction ('blue asterisks' in Fig.3A; Kaan et al., 2011; Kelliher et al., 2018);
their mutation suppresses auto-inhibition and causes lethality and distal accumulations of Khc, but
does not affect the ability to transport cargo (Brendza et al., 1999; Kelliher et al., 2018). When we
cultured *Khc^{E177K}* and *Khc$^{E177R, R947E}$* homozygous mutant neurons, they displayed robust MT-curling
when tested at 3DIV (Figs.6E, S5E). Surprisingly, this is at a stage at which Khc-deficient neurons
do not show a phenotype yet (Fig.S2B), as became even clearer when testing *Khc$^{E177R, R947E}$*
mutant neurons at 1DIV which resulted in robust MT-curling (Fig.6F). This strongly suggests that
the E177K and R947E point mutations cause dominant phenotypes, overriding the wild-type
maternal protein present during the first days of development (Fig.6G).

Finally, we tested whether phenotypes observed upon Klc loss and Khc non-inactivation are
functionally related. Firstly, as observed in Klc-deficient neurons, Trolox failed to suppress the
Khc$^{E177R, R947E}$ mutant MT-curling phenotype (Fig.5E,F). Secondly, the trans-heterozygous
combination of *Klc$^{8ex94/+}$* with *Khc$^{E177R, R947E/+}$* in primary neurons, revealed a very strong and
convincing genetic interaction that supports synergetic contributions of Klc and intramolecular loop
formation during Khc auto-inhibition (Fig.6H).

Taken together, we conclude that MT-curling observed upon loss of Klc is due to failed inactivation
of Khc. This represents a very different pathological mechanism from that observed with losses of
Khc, Milt, Miro or Arl8, although the MT-curling phenotype of all these conditions looks surprisingly
similar.

<u>Unc-104 deficiency and heterologous KIF5A mimic MT-curling induced by loss- and gain of Khc</u>
<u>function</u>

So far, our studies of the *Drosophila* kinesin-1 Khc suggest that MT-curling can be due to gain-of-
function through failed auto-inhibition, or caused by loss-of-function through harmful ROS caused
by impaired organelle transport. We next asked whether these two pathways might be more widely
applicable. For this, we assessed the PH domain-containing *Drosophila* kinesin-3 Unc-104 and the
human kinesin-1 KIF5A.

As explained above, Unc-104 causes MT-curling (Fig.1F,H). Previous research in larval nerves
failed to resolve whether Unc-104 transports mitochondria (Barkus et al., 2008). We now found that

axonal mitochondria numbers in *unc-104[170]* mutant neurons at 3DIV and 5DIV are reduced to
similar degrees as observed upon loss of Khc (Fig.2J,O), suggesting a direct or indirect role in
mitochondrial motility. We speculated therefore that Unc-104 might cause ROS dyshomeostasis.
This notion was confirmed when applying Trolox, which suppressed the MT-curling phenotype in
unc-104[170] mutant neurons to wild-type levels, as similarly observed for loss of Khc (Figs.5B,G).

To assess whether also over-activation of Unc-104 causes MT-curling, we wanted to make use of
the non-inactivating *unc-104[bris]* mutant allele (Kern et al., 2013; Niwa et al., 2024), but we could no
longer track down this mutant fly stock. Instead, we used overexpression of wild-type and mutant
KIF5A: the KIF5A[Δexon27] mutant isoform is an aberrant splicing product linked to ALS; it displays a
small C-terminal truncation substituted by a 39 amino acid neopeptide (orange in Fig.S6I); this
weakens its ability to auto-inactivate, it promotes aberrant protein interactions trapping other
mutant or wild-type KIF5A molecules, and causes a decrease of protein lifetime in a proteasome-
dependent manner (Fig.S5I; Baron et al., 2022; Carrington et al., 2024; Cozzi et al., 2024; Nakano
et al., 2022; Pant et al., 2022; Pino et al., 2023). Its overexpression might therefore cause curling
either through gain-of-function by being over-activated, or loss-of-function by trapping endogenous
kinesins.

We started our KIF5A investigation by expressing a C-terminally GFP-tagged wild-type version
(KIF5A[wt]::GFP; Pant et al., 2022). GFP fluorescence was above detection level in 67% of cells but
often occurring in aggregates, with 83% of fluorescent cells showing accumulations at axon tips
(Fig.S7A,A'). Tip localisation suggested reduced auto-inhibition, as was further supported by a
(non-significant) bias to cause MT-curling, very similar to results obtained with the Khc[1-850]::GFP
construct (Fig.6D,I). Although cargo linker-binding regions of KIF5A appear reasonably well-
conserved (Fig.S8), our findings might suggest that KIF5A's C-terminus fails to interact in the
heterologous context of fly neurons causing the motor to be free-running as observed for Khc1-
850::GFP (Fig.S5G,H) .

We next analysed expression of Kif5A[Δex27]::GFP which also occurred in aggregates, with over 70%
of fluorescent neurons showing tip localisation as a potential indicator of over-activation
(FigS7B,C). However, the number of neurons displaying GFP above detection levels was below
50% when expressing Kif5A[Δex27]::GFP, as compared to 70% for KIF5A[wt]::GFP. This reduction
might reflect the previously reported shorter protein lifetime of Kif5A[Δex27] mentioned above (Baron
et al., 2022; Cozzi et al., 2024; Pino et al., 2023). Despite this reduction, expression of the mutant
isoform displayed strong and robust MT-curling in *Drosophila* primary neurons at 3DIV (Fig.6I). To
test whether this phenotype is due to over-activation of KIF5A, or to loss-of-function by trapping
endogenous motors, we applied Trolox. We found that blocking ROS did not only fail to suppress
the curling phenotype, but curling was consistently and robustly increased in two independent
experiments. Increased MT-curling correlated with the observation that also the number neurons
with detectable GFP was increased from ~50% without Trolox to ~70% with Trolox. Although this
correlation might not be causative, it might suggest a positive role of ROS signalling involved in
Kif5A[Δex27] degradation which is suppressed by Trolox - and this might have implications in the ALS
disease context.

In conclusion, the experiments with Unc-104 and KIF5A suggest that loss- and gain-of-function-
mediated MT-curling is not specific to Khc, but is likely to apply also to other transport motors.

Discussion

<u>A standardised *Drosophila* primary neuron system reveals potential patho-mechanisms linked to axonal transport</u>

Transport motors and their linker proteins mediate the correct delivery and relocation of molecules and organelles required to maintain axonal physiology and function, yet their links to axonopathies remain poorly understood and speculative (Coleman, 2005; Guo et al., 2020; Kawaguchi, 2013; Sleigh et al., 2019). True understanding of axonal transport is confounded by various factors, such as the parallel or even interdependent involvement of different motor protein classes, or the involvement of many different cargo adaptor proteins that may interact promiscuously with different cargos and/or motors (Cason and Holzbaur, 2022; Hancock, 2014; Hirokawa et al., 2010).

Here we embraced this complexity using one standardised *Drosophila* primary neuron system amenable to efficient combinatorial genetics, combined with MT-curling as an efficient readout. Previous studies had already shown that *Drosophila* primary neurons provide powerful means to overcome redundancy or the complexity of genetic networks (e.g. Beaven et al., 2015; Gonçalves-Pimentel et al., 2011; Hahn et al., 2021; Qu et al., 2017). Here we used this system to investigate how aberrant axonal transport may cause neurodegeneration. This involved analyses of 38 different genetic loss- or gain-of-function conditions covering 17 different genes, partly in combination or applying different experimental regimes, and further complemented by the use of DEM and Trolox. Our loss-of-function studies were enormously facilitated by the lower genetic redundancy as compared to vertebrates (e.g. Khc/Kif5: 1 paralogue in fly *vs.* 3 paralogues in mammals; Miro/RHOT: 1 *vs.* 2; Milt/TRAK: 1 *vs.* 2; Klc: 1 *vs.* 4; Unc-104/Kif1: 1 *vs.* 2; Arl8 1 *vs.* 2) rendering the need of double- or triple-mutant approaches obsolete.

MT-curling is, in our view, a good indicator of lost axon integrity; MT bundles form the life-sustaining transport highways required for almost every cell biological process and provide a crucial means to communicate with the neuronal cell body; all of these features are prone to collapse upon MT-curling (Prokop, 2020; Smith et al., 2023), which then negatively impacts axon health (Okenve-Ramos et al., 2024). Importantly, MT-curling is a feature conserved with mammalian axons, easy to quantify in either system (Fig.7; Prokop et al., 2013; Smith et al., 2023). It is similarly observed during pathology of non-neuronal cells (Smith et al., 2023), for example in a model of chemotherapy-induced peripheral neuropathy (Rozario et al., 2021).

Using MT-curling as a readout upon genetic and pharmacological manipulations in the standardised *Drosophila* primary neuron system, we found that phenotypes upon loss of Khc, Unc-104 and even Dhc are comparable with respect to enhanced MT curling and the reduction in axonal numbers of mitochondria and synaptic dots (Figs.1, 2). This functional overlap agrees with reports that these three motors collaborate during transport or display a degree of mutual dependency (Arpağ et al., 2019; Cason and Holzbaur, 2022; Zahavi et al., 2021). It is therefore not unlikely that the three motors might link to axonopathy through comparable mechanisms. To gain insights into these mechanisms, we focussed on kinesin-1 where our strategy delivered data suggesting two distinct mechanistic pathways: Firstly, Milt/Miro- and Arl8-mediated transport is required to uphold ROS homeostasis (Fig.5B-D), and our studies with DEM, Trolox and ROS-regulating enzymes showed that harmful ROS is indeed a strong inducer of MT curling (Fig.4). Trolox rescue of the Unc-104 mutant phenotype (Fig.5G) shows that loss of ROS homeostasis is caused also by the loss of other transport motors. Secondly, we found that MT-curling can also be induced by increased transport movement of Khc (Fig.6), and expression of KIF5A$^{\Delta ex27}$ seems to cause curling in the same way suggesting wider applicability of this mechanism. Both mechanisms will be discussed in the following.

Mitochondria regulate ROS homeostasis required for MT bundle maintenance

Our finding that harmful ROS is a key trigger of MT curling is consistent with reports in other
systems: ROS can oxidise cysteins in both α- and β- tubulin (Landino et al., 2002; Löwe et al.,
2001; Luduena and Roach, 1991) or lead to functional modifications of MT-regulating proteins such
as MAP2, MAP1B, tau or the collapsin response mediator protein 2 (CRMP2; Conze et al., 2024;
Landino et al., 2004; Mattson et al., 1997; Miglietta et al., 1991; Sultana et al., 2013). ROS-induced
modifications disrupt MT organisation in non-neuronal cells (Goldblum et al., 2021; Wilson et al.,
2016; Wioland et al., 2021) and were reported (1) to inhibit axon growth and be causative in
neurodegeneration (Neely et al., 1999; Wali et al., 2016), (2) to induce axon swellings in models of
Parkinson's disease, multiple sclerosis or motor neuron disease (Czaniecki et al., 2019; Nikić et al.,
2011; Song et al., 2013) and (3) to block axonal transport and cause axonal MT disorganisation
that could be reverted with ROS scavengers (Nikić et al., 2011; Shields et al., 2024b; Sorbara et
al., 2014).

Our data suggest that ROS-dependent MT-curling is caused by aberrant transport of mitochondria
or lysosomes (Fig.3). In the case of lysosomes, this might be the indirect consequence of protein
stress caused by failed protein removal, or their direct involvement in the prevention of oxidative
stress (Paumier and Gowrishankar, 2024; Zhang et al., 2016). ROS production upon aberrant
mitochondrial transport, is far less clear. For example, our parallel work in *Drosophila* primary
neurons revealed that ROS-mediated MT-curling can be caused by aberrant mitochondrial
metabolism (which is unlikely to be affected by aberrant transport), whereas genetic aberration of
mitochondrial fission and fusion (potentially depending on motor proteins) did not cause MT-curling
(unpublished). As a further confusing observation, *milt* mutant neurons showed strong ROS-
induced MT-curling in axons, although mitochondria frequently remain in cell bodies (Figs.2L,O
and 3Ciii). Any excessive ROS generated by these somatic mitochondria would hardly reach far
into the axon due to the presence of abundant ROS-buffering systems (Fundu et al., 2019; Kükürt
et al., 2021; Oswald et al., 2018). Therefore, even the absence of mitochondria from axons might
affect ROS homeostasis, suggesting they may play an active role in cytoplasmic ROS regulation
(e.g. via Sod2-mediated H_2O_2 signalling; Palma et al., 2020a).

A further puzzling aspect of *milt* mutant neurons is that the reduction in axonal mitochondria is far
greater than upon loss of any motor protein (Fig.2O). This might suggest Milt as a potential 'master
regulator' of mitochondrial transport in fly neurons. Milt is known to link to Khc and Dynein in both
flies and mammals (Russo et al., 2009; van Spronsen et al., 2013), whereas no such reports exist
for Unc-104. So far, only the weak Unc-104 orthologue KIF1Bα (lacking a PH domain) was shown
to be involved in mitochondrial transport, mediated by the linker protein KIFBP (Kif1 binding
protein; Nangaku et al., 1994; Wozniak et al., 2005 - with KIFBP being involved also in the
inactivation of all kinesin-3 paralogues; see below). Therefore, our observed involvement of Unc-
104 in mitochondrial transport and the 'master regulator' role of Milt lack mechanistic explanations;
but understanding may eventually arise from future studies of the above-mentioned intricate
collaboration and interdependence of kinesin-1, kinesin-3 and dynein during axonal transport.

Motor hyperactivation as a further factor leading to MT-curling

Our findings that motor hyperactivation causes MT-curling aligns well with published *in vitro*
experiments demonstrating kinesin-1-induced MT damage (Andreu-Carbó et al., 2021; Budaitis et
al., 2021; Dumont et al., 2015; Triclin et al., 2021; VanDelinder et al., 2016), MT curling observed
in kinesin-1-based gliding assays *in vitro* (Hahn et al., 2019; Lam et al., 2016), and the dramatic

curling observed upon kinesin-1 activation in non-neuronal cells (Paul et al., 2020; Randall et al., 2017). Furthermore, MT-curling at the fringe of cultured epithelial cells was suggested to be caused by anterograde transport (Bicek et al., 2009).

That hyperactive motors are potentially damaging, is demonstrated by the fact that neurons dispose them into glia cells (Xie et al., 2024) and by the fact that hyperactivating mutations of KIF5A and of *Drosophila* Khc cause ALS or lethality, respectively (Baron et al., 2022; Kaan et al., 2011; Kelliher et al., 2018; Pant et al., 2022; Pino et al., 2023). Furthermore, KLC2 has been linked to neuropathy (SPOAN; #609541) and KLC4 mutations have recently been reported to cause excessive axon branching (Haynes et al., 2022), and hyperactivation of kinesin-1 may be an underlying cause.

Also kinesin-3 motors undergo inactivation involving intramolecular loop formation and the KIFBP linker (Cong et al., 2021; Kevenaar et al., 2016; Niwa et al., 2024; Solon et al., 2021).   Non-inactivating mutations of Kif1A cause axonopathy (spastic paraplegia; Chiba et al., 2019; Gabrych et al., 2019); KIFBP mutations impair axon growth, are disruptive to axonal MT bundles (Lyons et al., 2008) and cause the devastating neurological Goldberg-Shprintzen syndrome (GOSHS; Chang et al., 2019; Hirst et al., 2017). These observations seem to mirror those with hyperactivation of Khc/KIF5A and loss of Klc/KLC, suggesting common underlying concepts.

Conclusion

The key outcome of our studies is that one common phenotype of MT-curling (as an indicator of axon decay) can be generated through two distinct mechanisms: a physiological mechanism involving ROS dyshomeostasis upon motor protein loss or a mechanical mechanism due to hyperactivation of motor proteins. Our findings have essentially contributed to the formulation of the "dependency cycle of axon homeostasis" model (Prokop, 2021; Smith et al., 2023; details in Fig.YY8). It proposes that kinesins trailing along MT bundles during axonal transport ('2' in Fig.YY8) pose a mechanical challenge that leads to MT-curling ('3'); this challenge is enhanced upon hyperactivation of motors ('large red arrow' in Fig.8). Active machinery of MT-regulating proteins and support through the cortical actin-spectrin sleeve is required to prevent disintegration and maintain axon bundles long-term ('4'). However, this machinery of MT bundle maintenance is itself dependent on materials and physiology provided by axonal transport ('5'); this aspect of the cycle is affected by loss of (organelle) transport ('large green arrow' in Fig.8). This establishes a cycle of mutual dependency where interruption at any point will have a knock-on effect on all other aspects of axon physiology and function (Prokop, 2021; Smith et al., 2023). Apart from explaining MT-curling in the context of this work, this cycle can explain MT-curling upon loss of other groups of genes (Hahn et al., 2021; Qu et al., 2022) and offers potential explanations for why the same classes of axonopathies can be caused by a wide range of genes involved in very different cellular functions (Prokop, 2021; Shields et al., 2024a; Smith et al., 2023).

Conflict of Interest

None of the authors has a conflict of interest.

Acknowledgements

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Methods

Fly stocks

All human homology statements are based on information listed on flybase.org (Marygold et al., 2016; Millburn et al., 2016), all statements about genetic links to human diseases on information provided by www.omim.org (Online Mendelian Inheritance in Man®; Amberger et al., 2015). The following stocks were used in this study (reference and source provided in brackets; BL indicates Bloomington Drosophila Stock Collection): null mutant alleles (unless indicated differently) we used were

- *Arl8^{e00336}* (*PBac(RB)Arl8e00336*; BDSC #17846; Rosa-Ferreira et al., 2018)
- *Arl8^{Df}* (*Df(3R)D7*; BL #1898; Rosa-Ferreira et al., 2018)
- *Cat^{n1}* (Mackay and Bewley, 1989; Matthias Landgraf)
- *Dhc64C$^{4-19}$* (Gepner et al., 1996; BL #5274)
- *Khc^{8}* (Saxton et al., 1991; BL #1607)
- *Khc^{27}* (Saxton et al., 1991; Isabel Palacios)
- *Khc^{1ts}* (Saxton et al., 1991; BL #31994; a temperature-sensitive allele which is homozygous viable at 18ºC but usually kept over balancer)
- *Khc^{mutA}* (Winding et al., 2016; Vladimir Gelfand; confirmed by lethality of hetero-allelic *Khc$^{mutA/8}$* animals)
- *Khc^{E177K}* and *Khc^{E177K,R947E}* (Kelliher et al., 2018; Jill Wildonger)
- *Df(Khc)* (*Df(2R)BSC309*; Cook et al., 2012; BL #23692)
- *Klc^{8ex94}* (Gindhart et al., 1998; BL #31997)
- *Df(Klc)* (Bloomington #7596)
- *Klp64D^{k1}* (Ray et al., 1999; hypomorphic allele; BL #5578)
- *Klp64D^{n123}* (Perez and Steller, 1996; BL #5674)
- *Klp98A^{Δ47}* (Derivery et al., 2015; Marcos Gonzalez-Gaitan)
- *milt^{92}* (Cox and Spradling, 2006; Stowers et al., 2002; Tom Schwarz)
- *Df(milt)* (*Df(2L)ED440, P{w[+mW.Scer\FRT.hs3]=3'.RS5+3.3'}ED440*; Ryder et al., 2004; Kyoto #150498)
- *Miro^{Sd32}* (Guo et al., 2005)
- *Miro^{B682}* (Guo et al., 2005; BL #52003)
- *Df(Miro)* (*Df(3R)Exel6197*; Parks et al., 2004; BL #7676)
- *Pat1^{grive}* and *Pat1^{robin}* (Loiseau et al., 2010; Isabel Palacios)
- *Pex3^{2}* (Faust et al., 2014; BL#64251)
- *Sod1^{n1}* (Phillips et al., 1989; BL #24492)
- *Sod1^{n64}* (Phillips et al., 1995; BL #7451)
- *syd^{z4}* (Bowman et al., 2000; BL #32016)
- *Df(3L)syd^{A2}* (Bowman et al., 2000; deleting C-terminus; BL #32017)
- *unc-104^{170}* (Pack-Chung et al., 2007; Tom Schwarz)

Gal4 driver lines used were the

• *elav-Gal4* (BDSC #8765)
• *tubP-Gal4* (Lee and Luo, 1999; Liqun Luo)
UAS lines
• *UAS-Duox* (Ha et al., 2005; Matthias Landgraf)
• *UAS-Gapdh-IR* (*Gapdh1^{GD7467}*; VDRC #31631)
• *UAS-Khc^{FL}::GFP* (3rd, unpublished; Isabel Palacios)
• *UAS-Khc1-850-GFP* (Loiseau et al., 2010; Isabel Palacios)
• *UAS-Khc-RNAi* (Lu et al., 2013; Vagnoni et al., 2016; BL #35770)
• *UAS-hKIF5A^{wt}-GFP* (Pant et al., 2022; Devesh Pant)
• *UAS-hKIF5A$^{\Delta exon27}$-GFP* (Pant et al., 2022; Devesh Pant)
• *UAS-Nox* (Liew et al., 2021)
• *UAS-Sod1* (J. Hu and J.P. Phillips, unpublished)
• *UAS-YFP-PTS1* (BL #64248; Faust et al., 2014)
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Cloning of *UAS-Nox-YPet*
10xUAS-IVS-Nox::YPet was generated by using the *pJFRC12-10XUAS-IVS-myr-GFP*
vector (Addgene 26222; Pfeiffer et al., 2010) as a backbone which was modified by substituting
GFP with YPet (Nguyen and Daugherty, 2005) plus an N-terminal flexible linker, amplified from
dFlex_YPet_phase0 (Gärtig et al., 2019) using primer ML1 and ML2, and inserted by the Klenow
Assembly Method (https://tinyurl.com/4r99uv8m) into the XbaI/BamHI sites producing Vector 1:
pJFRC12-10xUAS-IVS-myr-linker-YPet. Nox cDNA was amplified from a DGRC (*Drosophila*
Genomics Resource Center) cDNA library clone using primers ML5 and ML6, located in a *pOTB7*
vector backbone, and inserted into BamHI/XhoI sites of Vector 1. Constructs were sent to FlyORF
for transgenesis, and targeted via PhiC31-mediated site-specific insertion to the *PBac{y$^+$-attP-*
3B}VK00040 landing site (Bloomington line #9755) on the third chromosome (3R, 87B10).
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ML1	gacatcatcagaccacgcggatccggctccgccggctccgccgccggctccggcgagttcgtgtccaagggcgag
ML2	gttccttcacaaagatcctctagattacttgtacagctcgttcatgccc
ML5	ggagccggcggagccggatccgaagcactccttacgaaaggcaaatccgt
ML6	cttcaggcggccgcggctcgagaatcaaaatgaacgcggaccaggagtc

Drosophila primary cell culture
Drosophila primary neuron cultures were performed as published previously (Prokop et al., 2012;
Qu et al., 2017). In brief, stage 11 embryos were treated for 1 min with bleach to remove the
chorion, sterilized for ~30 s in 70% ethanol, washed in sterile Schneider's/FCS, and eventually
homogenized with micro-pestles in 1.5 centrifuge tubes containing 21 embryos per 100µl
dispersion medium and left to incubate for 5 min at 37°C. Cells were washed with Schneider's
medium (Gibco), spun down for 4 mins at 650g, supernatant was removed and cells re-suspended
in 90µl of Schneider's medium containing 20% fetal calf serum (Gibco). 30µl drops were placed on
cover slips. Cells were allowed to adhere for ~2hrs either directly on glass or on cover slips coated
with a 5 µg/ml solution of concanavalin A, and then grown as a hanging drop culture for hours or
days at 26°C as indicated in each experiment.

To abolish maternal rescue of mutants, i.e. masking of the mutant phenotype caused by deposition
of normal gene product from the healthy gene copy of the heterozygous mothers in the oocyte
(Prokop, 2013), we used a pre-culture strategy (Prokop et al., 2012; Sánchez-Soriano et al., 2010)
where cells were kept for 5 days in a tube before they were plated on a coverslip.

Cells were treated with 100 µM Trolox (97% purity, Thermo Scientific or Sigma; stepwise diluted
from a 100 mM stock solution in ethanol) in 100% ethanol. For controls (vehicle treatment),
equivalent concentrations of vehicle (100% ethanol) were diluted in cell culture medium. In later
experiments, cells were treated with 100µM Trolox or 100µM diethyl maleate (DEM) dissolved
directly into neuronal culture medium; where necessary, the solution was incubated at 26 °C and
periodically agitated to ensure it is fully dissolved. The solution was then filter-sterilised. The
treated cells were grown in this medium for the entire culture period whereas control cells were
grown in Trolox/DEM-free medium. All reagents were purchased from Sigma-Aldrich, unless
otherwise stated.

For visualisation of mitochondria, cell cultures were incubated with 400nM MitoTracker Red
CMXRos (Invitrogen; Klionsky et al., 2012) for 30min at room temperature (RT) before fixation;
stock solutions were prepared in DMSO and diluted in cell culture medium to the final
concentration. Following incubation, cultures were then fixed and stained following the procedures
below.

Immunohistochemistry
Primary fly neurons were fixed in 4% paraformaldehyde (PFA) in 0.05M phosphate buffer (PB; pH
7–7.2) for 30min at room temperature (RT). Antibody staining and washes were performed with
PBT. Staining reagents: anti-tubulin (clone DM1A, mouse, 1:1000, Sigma; alternatively, clone
YL1/2, rat, 1:500, Millipore Bioscience Research Reagents); anti-Syt (1:1000; rabbit; Sean
Sweeney); anti-GFP (1:500, rabbit, ab290, Abcam); Cy3-conjugated anti-HRP (goat, 1:100,
Jackson ImmunoResearch); FITC-, Cy3- or Cy5-conjugated secondary antibodies (1:200; donkey,
purified, Jackson Immuno Research); F-actin was stained with Phalloidin conjugated with
TRITC/Alexa647, FITC or Atto647N (1:200; Invitrogen and Sigma). Specimens were embedded in
ProLong Gold Antifade mounting medium.

Mouse cell culture

Mice (C57/BL6) were housed, bred, and treated in compliance with the Animal (Scientific
Procedures) Act 1986 at the Biological Support Unit, University of Nottingham. Primary cortical
neuron cultures were prepared from time-mated embryos at embryonic day 16.5 (E16.5). The
brains were removed, placed in Hanks' Balanced Salt Solution (HBSS; Sigma-Aldrich), and the
cortices isolated under a dissection microscope, with meninges removed using forceps. The tissue
was transferred to a Nunc™ dish with 2 ml of HBSS and mechanically dissociated. Trypsin (1
mg/ml; Sigma-Aldrich) and DNAse I (50 µg/ml; Sigma-Aldrich) were added, followed by incubation
at 37°C (5% CO_2) for 30 minutes. Soybean trypsin inhibitor (0.05%; Sigma-Aldrich) was then
added. The tissue was mechanically dissociated further, and cells were re-suspended in
Neurobasal® medium (Gibco) with 1% GlutaMAX™ (Gibco) and 2% B-27™ supplement (Gibco).
Cells were plated at a 1:144 dilution (10-12 x 10^6 cells/ml) on 12-well plates (Corning) with 19 mm
glass coverslips (Fisher Scientific) coated with 50 µg/ml poly-L-ornithine (Sigma-Aldrich), incubated
overnight, and washed twice with dH2O before use. 100µM or 200µM of diethyl maleate (DEM;

Sigma) were dissolved directly in culture medium, which was then filter-sterilised and added to the
cultured cells on day 3.

4% PFA in PBS (Thermo Scientific™) was used to fix the neurons on day 4, 24 hours after DEM
application. The cell culture medium was discarded, and coverslips were rinsed with PBS before
being incubated in PFA for 30 minutes at room temperature. The PFA was discarded, and
coverslips were washed with PBS (3 x 5 minutes) and Buffer 1 (10mM glycine in PBS; 3 x 5
minutes). They were then incubated in Buffer 2 (10mM glycine and 0.2% Triton™ X-100 in PBS)
for 30 minutes at room temperature, followed by washing with Buffer 3 (0.1% Triton™ X-100 in
PBS; 3 x 5 minutes). Coverslips were incubated in PBS with 3% BSA for 30 minutes, then placed
onto 25 μl droplets of primary antibody (anti-acetylated tubulin, 1:300 in BSA 3% in a humidified
chamber at 4°C overnight. The next day, coverslips were washed with Buffer 3 (3 x 5 minutes) and
placed onto droplets containing the secondary antibody (488-coupled goat anti-mouse, 1:300 in
BSA 3%, Invitrogen) and DAPI (1:300 in BSA 3%; Sigma-Aldrich) for 2 hours at room temperature.
Coverslips were then washed with Buffer 3 (3 x 5 minutes) and stored in PBS until mounting. They
were mounted onto Epredia™ SuperFrost™ slides (Fisher Scientific) using 12 μl VectaShield®
HardSet™ mounting media (Vector Laboratories) per coverslip and stored at 4°C until imaging.

Microscopy and data analysis

Standard documentation was performed with AxioCam monochrome digital cameras (Carl Zeiss
Ltd.) mounted on BX50WI or BX51 Olympus compound fluorescent microscopes. To determine the
degree of MT disorganisation in axons we used the "MT disorganisation index" (MDI) (Qu et al.,
2017): the area of disorganisation was measured using the freehand selection tool in Fiji/ImageJ;
this value was then divided by axon length (see above) multiplied by 0.5 μm (typical axon
diameter, thus approximating the expected area of the axon if it were not disorganised). To
quantify the number of synaptic densities in mature neurons in culture, we used ImageJ, first
thresholding to select synaptic densities from axons of single isolated cells, followed by particle
analysis. For statistical analyses, Kruskal–Wallis one-way ANOVA with *post hoc* Dunn's test or
Mann–Whitney Rank Sum Tests were used to compare groups. The data used for our analyses
will be made available on request from the authors. Experiments were repeated at least once, data
pooled. MDI data were usually not normally distributed but nevertheless plotted as mean ± SEM to
avoid misleading median values of zero. Most experiments had only two groups and were
assessed using Mann–Whitney Rank Sum tests, for experiments with more then two groups we
applied Kruskal–Wallis one-way ANOVA with *post hoc* Dunn's test. Means of single slides were
used to generate super-plots (Lord et al., 2020) and assessed using standard t-tests. The data
used for our analyses will be made available on request.

Ethical statement

An ethical statement is not required.

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Figures

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Fig.1 Deficiencies of three transport motor proteins cause MT curling. **A-G**) Examples of neurons of different genotype (as indicated top right) and stained for tubulin at 5DIV; asterisks indicate cell bodies, arrow heads axon tips, curved arrows areas of MT curling, white rectangles shown as twofold-magnified yellow-emboxed insets; scale bar in A represents 20µm in all images. **H**) Quantification of MT curling phenotypes measured as MT disorganisation index (MDI) and normalised to wild-type controls (red stippled line); mean ± SEM is indicated left of data points. Single data points are shown as dark-red dots and the means of replicates (independent coverslips from usually two experimental repeats) are shown as blue circles with their statistical significance (established using t-tests) indicated as blue asterisks; numbers of assessed neurons are shown in orange, their p values relative to controls (established by Mann-Whitney tests) in black or grey; the intensity of the brown bar colour reflects the degree of significance of the increased values.

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Fig.2 Impacts of motor protein and linker mutations on numbers of axonal mitochondria and
Synaptotagmin-labelled spots. **A-N**) Examples of neurons of different genotype (indicated top right)
and stained at 5DIV for tubulin (tub, magenta) and either Synaptotagmin (Syt, green in A-G) or with
mitoTracker (green in H-N); scale bar in A represents 20µm in all images. **O,P**) Quantification of
axonal numbers of Syt-positive spots (O) or mitochondria (P), all normalised to wild-type controls
(red stippled line). Graphs are organised as indicated in Fig.1, only that significance of decreased
values is indicated by blue bar colour.

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Fig.S1 Upon loss of Khc, the endoplasmatic reticulum tends to accumulate at axon tips, independent of MT curling. **A-D**) Primary neurons at 5 DIV either being wild-type (A,C) or homozygous mutant for the *Khc^8* (B) or *Dhc64C$^{4-19}$* (D) mutant alleles. MTs are labelled in magenta (tub) and the endoplasmic reticulum (ER) in green: either via fluorescence of the genomically tagged *Rtln1-YFP* allele (del Castillo et al., 2019; O'Sullivan et al., 2012) or using anti-PDI staining; white boxes are shown as 2-fold magnified, yellow-framed insets showing only the MTs; cell bodies are indicated by asterisks, axon tips with/without strong ER accumulation by white/open arrowheads; as can be seen, there is no correlation between MT curling and ER accumulation. **E,F**) Control measurements indicate that the MT-curling phenotypes are reliably present in the neurons analysed for ER tip accumulation (for further explanation of graphs see legend of Fig.1); note that analyses of *Khc^8* Rtnl1::YFP mutant neurons were repeated in 2016, 2017 and 2022 with reproducible results (see also H). **G,I**) Quantification of no/weak/strong ER accumulation at axonal tips (indicated by light/medium/dark blue) in Rtnl1::YFP or wt controls and in *Khc^8* Rtnl1::YFP or *Dhc64C$^{4-19}$* mutant neurons; the P value of X^2 tests is shown above bars, the number of analysed neurons indicated in red. **H**) The pink triangles differently display the data from G representing the respective percentages of 5 independent experiment between 2016 and 2022 compared by t-tests, indicating a consistent increase in tip localisation upon loss of Khc. This increase is surprising contradicting reports in mouse neurons (Farías et al., 2019). We reasoned this to be caused by loss of Khc-dependent Dynein transport to axon tips (Moughamian et al., 2013; Twelvetrees et al., 2016), but loss of Dhc unexpectedly causes the opposite phenotype.

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Fig.3 Khc subfunction deficiencies that cause MT-curling. **A)** Schematic representation of
Drosophila Khc drawn to scale. Domains are colour-coded and start/end residues are indicated by
numbers: motor domain (red; according to Sablin et al., 1996), coiled-coil domains required for
homo- and/or heterodimerisation (green; as predicted by Ncoils in ensembl.org), the C-terminal
ATP-independent MT-binding motif (blue; according to Winding et al., 2016), and the C-terminal
auto-inactivation domain (dark grey; according to Kaan et al., 2011); the grey line above the protein
scheme indicates the three expression constructs used in this study; below the protein scheme
further details are shown: the sequence of the C-terminal MT-binding domain (*mutA* mutations

indicated in orange; Winding et al., 2016), the sequence of the auto-inactivation domain (indicating
the IAK motif and R947E mutation; Kelliher et al., 2018), the binding areas (darker green coiled-
coils) of Klc (according to Veeranan-Karmegam et al., 2016) and Milt (known to overlap with Klc;
Glater et al., 2006; Verhey et al., 1998). **B**) Schematic representation of some sub-functions of Khc
(details and abbreviations in main text; red and stippled black lines indicate processive transport):
via a C-terminal MT-binding domain Khc can slide MTs (i); by associating with Pat1 (and potentially
Klc) it is expected to transport non-vesicular cargoes including mRNA (ii); with Milt and Miro it
mediates transport of mitochondria and potentially peroxisomes (iii); its interaction with Arl8 is
required to drive the transport of lysosomes and its derivatives (iv); a protein complex containing
Klc and Syd is required for vesicular transport (v); in the absence of such associations Khc is auto-
inhibited and detaches from MTs assisted by Klc (vi); to interfere with these subfunctions in this
study, different genes were genetically removed (orange crosses) or specific *Khc* mutant alleles
used (italic orange text). **C**) Quantified effects on MT curling caused by specific mutations affecting
Khc sub-functions (numbers in grey circles indicate which function in A is affected); for details of
graph organisation refer to the legend of Fig.1.

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Fig.S2 Validation of Khc's MT phenotype and demonstration of maternal contribution. **A-C**)
Quantification of MT-curling phenotypes measured as MT disorganisation index (MDI) and
normalised to internal wild-type of *elav-Gal4/+* controls (red stippled line). A) shows data for *Khc27*
in homozygosis (*27*) or over deficiency (*27/Df*), for Khc knock-down (*elav>Khc-IR*). B) shows data
for *Khc8* over deficiency (*8/Df*) at different culture times (HIV, hours *in vitro*; DIV, days *in vitro*); C)
shows data for *Klc8/Df* and *Klc1ts* at 12HIV or 1DIV following 5d pre-culture; note that *Klc1ts* is a
temperature-sensitive allele (see methods) and was pre-cultured at 26ºC and cultured at 29ºC. For
further graph descriptions refer to the legend of Fig.1. **D,E**) Examples of neurons at different times
in culture (D; relating to data in B) and after pre-culture (E; relating to C); asterisks indicate cell
bodies, arrow heads axon tips, curved arrows areas of MT curling; scale bar in D represents 20µm
in D and E.

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Fig.4 ROS enhancing manipulations cause MT curling phenotypes. **A**) Scheme illustrating the complexity of ROS-regulating systems (for molecular details refer to Smith et al., 2023); reactive oxygen species are highlighted in yellow, manipulated enzymes are indicated by red arrow heads and ROS-inducing DEM/diethyl maleate with a blue arrowhead. **B-E**) Examples of neurons, either wild-type (wt), expressing Sod1 or Duox (driven by *elav-Gal4*), or homozygous for *Cat^{n1}*, all cultured for 1DIV and stained for actin (act, magenta) and tubulin (tub; green); asterisks indicate cell bodies, arrow heads axon tips, curved arrows areas of MT curling; yellow emboxed areas are shown as 1.5-fold enlarged insets (green channel only); scale bar in B represents 20µm in B-E. **F**) Quantification of MT curling phenotypes measured as MT disorganisation index (MDI) and normalised to wild-type controls (red stippled line); for further explanations of graph organisation refer to the legend of Fig.1.

Fig.S3 Analyses of peroxisomes in *Drosophila* primary neurons. **A-C)** Images of *Drosophila* primary neurons at 5DIV without (A) or with (B,C) expression of PTS1::YFP, stained for tubulin (magenta); asterisks indicate cell bodies, arrowheads tips of axons; arrows point at labelled peroxisomes; scale bar in A represents 10µm in all images. **D)** Quantification of peroxisome numbers classified by cell compartments: soma, total axon, proximal axon, mid axon and distal axon. **E)** Distribution of peroxisomes in axons in either controls (*elav/+*) or upon Khc knock-down (*elav>Khc^{IR}*). **F)** Quantification of MT-curling in Pex3-deficient neurons; for explanations of the graph structure, refer to Fig.1.

Fig.5 Ameliorating effects of Trolox on mutant MT-curling phenotypes. Each graph shows the results of separate experiments quantifying MT-curling phenotypes (measured as MT disorganisation index; MDI and normalised to wild-type controls (red stippled line); in each experiment, wild-type neurons with or without Trolox and mutant or DEM-treated neurons with or without Trolox treatment are shown; further culture conditions are indicated: which are either pre-culture (pre), or culture for 1 or 3DIV. Further explanations of graph organisation can be taken from the legend of Fig.1.

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Fig.S4 Phenotypes upon *Gapdh1* knock-down in primary neurons at 5 DIV. **A**) Illustration of the
NADH- and ATP-generating steps of glycolysis; names of proteins are shown in bold, other
molecules in italics: GAPDH (glyceraldehyde-3-phosphate dehydrogenase), PGK
(phosphoglycerate kinase), GAP (glyceraldehyde-3-phosphate), 1,3 BPG (1,3-
biphosphoglycerate), 3-PGA (3-phosphoglycerate). **B**) GAPDH and PGK are present on
transported vesicles together with other factors relevant for glycolysis (Hinckelmann et al., 2016;
Zala et al., 2013) providing ATP to drive kinesin-mediated processive transport (red and stippled
black lines). **C-D**) In the absence of Gapdh1, the transport of synaptic vesicles but not
mitochondria is impaired (assessed via anti-Syt and mitoTracker staining; see Fig.2). **E**) Absence
of GAPDH does not cause MT curling. For explanations of graph organisation, refer to the legend
of Fig.1.

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Fig.6 Impacts of activated Khc on MT curling. **A,B**) Examples of neurons at 5DIV expressing different Khc constructs (indicated bottom left; compare Fig.3A) and stained for tubulin (tub, magenta) and GFP (green), also shown as greyscale single channel images on the right; asterisks indicate cell bodies, arrow heads axon tips, curved arrows areas of MT curling; scale bar in A represents 20µm in all images. **C-G,I**) Quantification of MT curling phenotypes measured as MT disorganisation index (MDI) and normalised to wild-type controls (red stippled line); genotypes are shown below, also indicating the culture period (5DIV, 3DIV); for descriptions of graph organisation, refer to Fig.1. **H)** Illustration of the maternal Khc[wt] product (green dots) deposited in the eggs by heterozygous mothers and decaying over ~5 days; in *Khc[8]* mutant neurons, the phenotype (yellow star) appears upon maternal product depletion (top); in non-inactivating *Khc[act]* mutant neurons, the phenotype occurs early, suggesting that the Khc[act] protein (blue dots) overrides the healthy function of Khc[wt].

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Fig.7 DEM induces MT-curling in primary mouse cortical neurons. **A-C)** Mouse primary neurons
stained for tubulin, either untreated, or treated with 100μM or 200μM DEM, as indicated; asterisks
indicate cell bodies, arrow heads axon tips; yellow boxes correspond to the areas shown as 2-fold
magnified insets. **D)** Quantification of MT-curling data obtained; for explanations of graph
organisation, refer to the legend of Fig.1.

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Fig.S5 Graphical summary of key findings in this paper. A-I each represent one genotype: in each case, the top section lists the genotype, the second section indicates whether this condition permits auto-inhibition (N/A, not applicable), the third section lists the impact on transport (the number of green arrows reflects the amount of transport, organelles with low transparency indicate affected transport) or harmful ROS production, the bottom section indicates whether MT-curling is increased (size of blue arrow reflects the degree).

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1434 **Fig.S6** Genetic interaction studies involving Khc, Milt and Klc. Each graph represents a separate
1435 genetic interaction experiment showing wild-type controls, the two single-heterozygous conditions
1436 followed by the trans-heterozygous condition; in D also the homozygous mutant conditions for
1437 *shot³* and *Khc⁸* are shown. For further explanations of graph organisation, refer to the legend of
1438 Fig.1.

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Fig.8 Mapping findings of this work on the dependency cycle of local axon homeostasis. The numbered green arrows and red T-bar make up the previously published 'dependency cycle of local axon homeostasis' (Prokop, 2021; Shields et al., 2024a; Smith et al., 2023): 1) axonal transport provides materials, components and organelles required for axon function; 2) this transport requires MT bundles as the essential highways; 3) this live-sustaining transport damages MT bundles; 4) MT-binding proteins (MTBPs) support and maintain MT bundles (emboxed names a factors were shown to be involved in MT bundle-maintenance; Alves-Silva et al., 2012; Hahn et al., 2021; Qu et al., 2019); 5) bundle maintenance requires transport-dependent components and physiology, thus closing the circle. Hyperactivation of motor proteins enhances MT bundle damage (vibrating red arrow listing the genetic tools in support). Loss of function of Khc, Milt, Miro, Unc-104 and Dhc contribute to mitochondrial transport (large green arrow, top right). Mitochondria harbour Sod2 that can quench harmful ROS and signal to the cytoplasm to regulate ROS levels (green T-bar); various independent pharmacological and genetic manipulation of ROS regulation (bottom right) demonstrated that dysregulation of ROS causes MT curling (dashed red arrow).

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Fig.S7 Examples of neurons expressing normal and mutant versions of human KIF5A. *Drosophila* primary neurons at 3DIV expressing *elav-Gal4*-driven KIF5A^{wt}::GFP or KIF5A$^{\Delta ex27}$::GFP (as indicated top right) and stained for tubulin, treated with Trolox in C,C'; asterisks indicate cell bodies, arrow heads axon tips, open curved arrows areas of MT curling, white arrow distal GFP aggregates; scale bar in A represents 20μm in all images.

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KIF5A:    7  ECSIKVLCRFRPLNQAEILRGDKFIPIFQGD---DSVVIGGKPYVFDRVFPPNTTQEQVY   63
             E SIKV+CRFRPLN +E    G KF+   F +    + + I GK Y+FD+VF PN +QE+VY
Khc:     10  EDSIKVVCRFRPLNDSEEKAGSKFVVKFPNNVEENCISIAGKVYLFDKVFKPNASQEKVY   69

KIF5A:   64  HACAMQIVKDVLAGYNGTIFAYGQTSSGKTHTMEGKLHDPQLMGIIPRIARDIFNHIYSM  123
             +  A   IV DVLAGYNGTIFAYGQTSSGKTHTMEG + D     GIIPRI  DIFNHIY+M
Khc:     70  NEAAKSIVTDVLAGYNGTIFAYGQTSSGKTHTMEGVIGDSVKQGIIPRIVNDIFNHIYAM  129

KIF5A:  124  DENLEFHIKVSYFEIYLDKIRDLLDVTKTNLSVHEDKNRVPFVKGCTERFVSSPEEILDV  183
             + NLEFHIKVSY+EIY+DKIRDLLDV+K NLSVHEDKNRVP+VKG TERFVSSPE++ +V
Khc:    130  EVNLEFHIKVSYYEIYMDKIRDLLDVSKVNLSVHEDKNRVPYVKGATERFVSSPEDVFEV  189

KIF5A:  184  IDEGKSNRHVAVTNMNEHSSRSHSIFLINIKQENMETEQKLSGKLYLVDLAGSEKVSKTG  243
             I+EGKSNRH+AVTNMNEHSSRSHS+FLIN+KQEN+E ++KLSGKLYLVDLAGSEKVSKTG
Khc:    190  IEEGKSNRHIAVTNMNEHSSRSHSVFLINVKQENLENQKKLSGKLYLVDLAGSEKVSKTG  249

KIF5A:  244  AEGAVLDEAKNINKSLSALGNVISALAEGTKSYVPYRDSKMTRILQDSLGGNCRTTMFIC  303
             AEG VLDEAKNINKSLSALGNVISALA+G K+++PYRDSK+TRILQ+SLGGN RTT+ IC
Khc:    250  AEGTVLDEAKNINKSLSALGNVISALADGNKTHIPYRDSKLTRILQESLGGNARTTIVIC  309

KIF5A:  304  CSPSSYNDAETKSTLMFGQRAKTIKNTASVNLELTAEQWKKKYEKEKEKTKAQKETIAKL  363
             CSP+S+N++ETKSTL FG+RAKT+KN    VN ELTAE+WK++YEKEKEK    K + KL
Khc:    310  CSPASFNESETKSTLDFGRRAKTVKNVVCVNEELTAEEWKRRYEKEKEKNARLKGKVEKL  369

KIF5A:  364  EAELSRWRNGENVPETERLAGEEAALGAELCEETPVNDN-------------SSIVVRI   409
             E EL+RWR GE V    E++  E+    +   E                      +++   +
Khc:    370  EIELARWRAGETVKAEEQINMEDLMEASTPNLEVEAAQTAAAEAALAAQRTALANMSASV  429

KIF5A:  410  APEERQKYEEEIRRLYKQLDDKDDEINQQSQLIEKLKQQMLDQEELLVSTRGDNEKVQRE  469
             A  E+ +    E  RLY+QLDDKD+EINQQSQ  E+LK+Q+++QEEL + + R + E +Q E
Khc:    430  AVNEQARLATECERLYQQLDDKDEEINQQSQYAEQLKEQVMEQEELIANARREYETLQSE  489

KIF5A:  470  LSHLQSENDAAKDEVKEVLQALEELAVNYDQKSQEVEEKSQQNQLLVDELSQKVATMLSL  529
             ++ +Q EN++AK+EVKEVLQALEELAVNYDQKSQE++ K++    L +EL QK +    +
Khc:    490  MARIQQENESAKEEVKEVLQALEELAVNYDQKSQEIDNKNKDIDALNEELQQKQSVFNAA  549

KIF5A:  530  ESELQRLQEVSGHQRKRIAEVLNGLMKDLSEFSVIVGNGEIKLPVEISG-------AIEE  582
              +ELQ+L+++S HQ+KRI E+L  L++DL E    + GE + + +++S           +EE
Khc:    550  STELQQLKDMSSHQKKRITEMLTNLLRDLGEVGQAIAPGESSIDLKMSALAGTDASKVEE  609

KIF5A:  583  EFTVARLYISKIKSEVKSVVKRCRQLENLQVECHRKMEVTGRELSSCQLLISQHEAKIRS  642
             +FT+ARL+ISK+K+E K++ +RC  +E  Q + ++K+      ++L    +LLISQHEA+++S
Khc:    610  DFTMARLFISKMKTEAKNIAQRCSNMETQQADSNKKISEYEKDLGEYRLLISQHEARMKS  669

KIF5A:  643  LTEYMQSVELKKRHLEESYDSLSDELAKLQAQETVHEVALKDKEPDTQDADEVKKALELQ  702
             L E M+   E KKR LEE  DSL +E AKL+A E V  V  ++K    Q A+E++   + Q
Khc:    670  LQESMREAENKKRTLEEQIDSLREECAKLKAAEHVSAVNAEEK----QRAEELRSMFDSQ  725

KIF5A:  703  MESHREAHHRQLARLRDEINEKQKTIDELKDLNQKLQLELEKLQADYEKLKSEEHEKSTK  762
             M+   REAH RQ++ LRDEI  KQ  +DE+KD++QKL L  +++ ADYEK++ E+ EKS++
Khc:    726  MDELREAHTRQVSELRDEIAAKQHEMDEMKDVHQKLLLAHQQMTADYEKVRQEDAEKSSE  785

KIF5A:  763  LQELTFLYERHEQSKQDLKGLEETVARELQTLHNLRKLFVQDVTTRVKKS-AEMEPEDSG  821
             LQ +     ER EQ+++DLKGLE+TVA+ELQTLHNLRKLFVQD+  R++K+    E E+ G
Khc:    786  LQNIILTNE▮RREQARKDLKGLEDT▮VAKELQTLHNLRK▮LFVQDLQQRIRKNVVNEESEEDG  845

KIF5A:  822  GIHSQKQKISFLENNLEQLTKVHKQLVRDNADLRCELPKLEKRLRATAERVKALEGALKE  881
             G  +QKQKISFLENNL+QLTKVHKQLVRDNADLRCELPKLEKRLR T ERVKALE ALKE
Khc:    846  GSLAQKQKISFLENNLDQLTKVHKQLVRDNADLRCELPKLEKRLRCTMERVKALETALKE  905

KIF5A:  882  AKEGAMKDKRRYQQEVDRIKEAVRYKSSGKRGHSAQIAKPVRPGH                926
             AKEGAM+D++RYQ EVDRIKEAVR K  G+RG  AQIAKP+R G
Khc:    906  AKEGAMRD▮RKRYQYEVDRIKEAVRQKHLGRR▮GPQAQIAKPIRSGQ               950
```

Klc-binding: **XXX**; Milt-binding: **XXX**; MT-binding: **XXX**; loop-forming: **XXX**

Fig.S8 Sequence alignment of KIF5A and Khc. Alignment of KIF5A-202 (ENST00000455537.7, 5779bp,1032aa) and Khc-PA (FBtr0087184, 3718bp, 975aa) according to the BLAST function of flybase.org. C-terminal functional regions of Khc indicated in Fig.3A are highlighted as indicated in the box at the bottom. Degree of identity: 562 / 945 (59.5%); degree of similarity: 718 / 945 (76%); gaps = 29 / 945 (3.1%).