RESEARCH ARTICLE

Genome-wide RNAi screen for nuclear actin reveals a network of cofillin regulators

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ABSTRACT

Nuclear actin plays an important role in many processes that regulate gene expression. Cytoplasmic actin dynamics are tightly controlled by numerous actin-binding proteins, but regulation of nuclear actin has remained unclear. Here, we performed a genome-wide RNA interference (RNAi) screen in Drosophila cells to identify proteins that influence either nuclear polymerization or import of actin. We validate 19 factors as specific hits, and show that Chinmo (known as Bach2 in mammals), SNF4Ay (Prkag1 in mammals) and Rab18 play a role in nuclear localization of actin in both fly and mammalian cells. We identify several new regulators of cofillin activity, and characterize modulators of both cofillin kinases and phosphatase. For example, Chinmo/Bach2, which regulates nuclear actin levels also in vivo, maintains active cofillin by repressing the expression of the kinase Cdi (Tesk in mammals). Finally, we show that Nup98 and lamin are candidates for regulating nuclear actin polymerization. Our screen therefore reveals new aspects of actin regulation and links nuclear actin to many cellular processes.

KEY WORDS: Actin, Nucleus, Cofilin, RNA interference

INTRODUCTION

Actin is a multifunctional protein in both the cytoplasm and the nucleus. In the cytoplasm, the dynamic regulation of actin polymerization into filaments and depolymerization into monomers, which is mediated by numerous actin-binding proteins (ABPs), is the key for its many functions during, for example, cell motility, intracellular transport and cell shape maintenance (Pollard and Cooper, 2009).

In the nucleus, actin is generally linked with protein complexes that are involved in all stages of gene expression (Grosse and Vartiainen, 2013). Actin specifically regulates the activity and localization of megakaryocytic acute leukemia protein MAL (also known as MKL1), a transcriptional coactivator of serum response factor (SRF) (Vartiainen et al., 2007). In addition, actin associates with the Brm-associated factor (BAF) chromatin remodeling complex (Kapoor et al., 2005). The polymerization status of nuclear actin under physiological conditions is still debatable, although mounting evidence suggests that various forms of actin operate in the nucleus and might account for the diverse functions of actin in this compartment. For example, nuclear actin polymers have been shown to mediate de-repression of Toll-like receptor response genes through the actin filament-binding protein coronin 2A, a component of the nuclear receptor co-repressor (NCoR) complex (Huang et al., 2011). Similarly, nuclear actin polymerization has been linked to the activation of occluded pluripotent genes during somatic nuclear reprogramming in the Xenopus laevis oocyte (Miyamoto et al., 2011). Recently, formin-regulated nuclear actin polymerization has been visualized for the first time and shown to regulate gene expression through the MAL–SRF pathway (Baarlink et al., 2013). By contrast, actin is kept monomeric at least in the yeast INO80 chromatin remodeling complex (Kapoor et al., 2013), and earlier studies have shown that polymeric actin associates with the Brm-associated factor (BAF) chromatin remodeling complex in a phosphatidylinositol-dependent manner (Rando et al., 2002). A recent report that utilized fluorescent probes based on known actin-binding domains showed that actin monomers are present in nuclear speckles, whereas actin polymers appeared to exclusively concentrate in interchromatin spaces (Belin et al., 2013). Despite the fact that numerous actin regulators are present in the nucleus (Rajakyla and Vartiainen, 2014), the mechanisms and signaling pathways that control nuclear actin polymerization are still unclear.

Although the detailed mechanisms through which actin regulates gene expression processes are lacking, the above findings strongly suggest that actin is an important protein in the nucleus. Indeed, decreased nuclear actin levels do not support maximal transcription in cells (Dopie et al., 2012). Moreover, low levels of nuclear actin seem to promote quiescence (Spencer et al., 2011), whereas increased nuclear actin has been linked to differentiation of HL60 cells towards macrophages (Xu et al., 2010). Nuclear actin levels might therefore play an important role in transcriptional regulation, and might even be used to elicit specific transcriptional programs, and thus cell fate decisions. This suggests that nucleo-cytoplasmic shuffling of actin must be tightly controlled. Actin appears to utilize active nuclear import (Dopie et al., 2012) and export (Stuven et al., 2003) mechanisms, although the size of actin (42 kDa) is close to the limit of passive diffusion. Nuclear export of actin is mediated by the transport factor exportin 6, and the small ABP profilin aids the interaction between actin and the exportin (Stuven et al., 2003). Another family of small ABPs, cofilins (represented by Tsr in


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Drosophila), plays a role in importin-9-dependent nuclear import of actin (Dopie et al., 2012). The signaling pathways regulating nuclear actin levels have remained largely unclear. A previous genome-wide screen in cultured Drosophila cells, followed by targeted screens in mouse and human cells, revealed that CG7597 and Hyx (known as Cdc73 and Cdc215, respectively, in mammals) are new regulators of nuclear actin (Rohn et al., 2011). Depletion of these factors by RNA interference (RNAi) caused the accumulation of actin in the nucleus, with a phenotype resembling exportin 6 depletion. In S2R+ cells this increased nuclear actin manifests as a phalloidin-stainable actin bar, and therefore these factors are candidates for acting either as nuclear export regulators of actin, or as negative regulators of nuclear actin polymerization. Importantly, the function of these proteins was conserved from flies to mammals (Rohn et al., 2011).

Here, we performed a genome-wide RNAi screen in cultured Drosophila cells to reveal new regulators of nuclear actin polymerization and proteins that influence nuclear actin levels by regulating its nuclear import. We confirm and validate the hits, and identify 19 specific regulators of nuclear actin, further demonstrating that a subset of these hits is also conserved in mammalian cells. Our results uncover new regulators of cofillin activity, which act at different levels to modify the phosphorylation status of this key actin regulator. We describe the transcriptional repressor Chinmo (Bach2 in mammals) as an in vivo regulator of nuclear actin levels, highlighting the importance of appropriate regulation of cofillin activity in this process.

RESULTS

Genome-wide screen in cultured Drosophila cells to identify new nuclear actin regulators

One issue that has clearly hampered nuclear actin studies has been the difficulties associated with its visualization (Grosse and Vartiainen, 2013). The amounts of nuclear actin in most cells are very low compared to cytoplasmic actin, and therefore the nuclear signal is easily obscured by the strong cytoplasmic staining. Silencing of the nuclear export receptor for actin, exportin 6, results in nuclear accumulation of actin (Stuven et al., 2003). In cultured Drosophila S2R+ cells, this increased nuclear actin manifests as a phalloidin-stainable (i.e. filamentous) actin bar, and the number of cells containing this bar are easy to quantify by microscopy (Fig. 1A,B) (Dopie et al., 2012). Of note, these bars are exclusively found within the cell nucleus, as we showed in a previous confocal microscopy study (Dopie et al., 2012), and as demonstrated by electron microscopy (supplementary material Fig. S1A). Using this method to visualize nuclear actin, we recently identified Twinstar (Tsr), the Drosophila cofillin, as a regulator of nuclear localization of actin. Silencing Tsr suppresses the nuclear accumulation of actin, and therefore leads to disappearance of the nuclear actin bar caused by exportin 6 RNAi (Fig. 1A,B) (Dopie et al., 2012). In general, bar formation can be prevented either by inhibiting nuclear import of actin or impairing formation of the nuclear actin bar e.g. nuclear actin polymerization. This assay therefore represents an excellent tool to identify new proteins that regulate nuclear actin.

To identify all genes whose depletion prevents the bar formation in the absence of exportin 6, we performed a genome-wide RNAi screen in cultured Drosophila S2R+ cells. In brief (for details see Materials and Methods), cells were seeded in 384-well plates containing both the Drosophila RNAi Screening Center (DRSC) double-stranded RNA (dsRNA) library 2.0 targeting 13,900 Drosophila genes and the dsRNA targeting exportin 6. DsRNA against Tsr was used as a positive control. After 5 days of RNAi, cells were fixed and stained with phalloidin and DAPI. The acquired images were processed and analyzed using both a customized Matlab algorithm (see Materials and Methods, Fig. 2A,B; supplementary material Fig. S1B) and visual inspection. Using the fraction of cells with bars per well as a readout, we identified the dsRNAs that caused a reduction in the number of cells with actin bar in the nucleus. Data was normalized per plate and the replicates were compared to each other (Fig. 2A,B). Hits (supplementary material Table S1) were then annotated using the Flybase (www.flybase.org) and DRSC (www.flyrnai.org) databases, revealing that the proteins were involved in a large spectrum of biological processes (Fig. 2C). Importantly, among the hits were proteins that we had previously shown to regulate the nuclear localization of actin, including Tsr, the Tsr phosphatase Slingshot (Shh) and the small GTPase Ran (supplementary material Table S1) (Dopie et al., 2012), demonstrating that our assay was operational also in a genome-wide format. Of note, we also observed several potential hits that increased the number of nuclear actin bars (supplementary material Table S2). These hits are candidates for acting as negative regulators of nuclear actin export and depolymerization, complementing those identified earlier in the absence of exportin-6 co-depletion (Rohn et al., 2011). However, for the present work, we decided to
concentrate on the hits displaying decreased numbers of nuclear actin bars.

We selected dsRNAs targeting 200 genes for retesting with the same dsRNA used in the genome-wide screen (supplementary material Table S3). At least one dsRNA from each biological function category (Fig. 2C) was included. Subsequently 113 putative hits (supplementary material Table S4) were retained for secondary screening using dsRNAs targeting different amplicons of the same genes. A total of 28 dsRNAs (supplementary material Table S5) also prevented the formation of the actin bar in the cell nucleus in this assay and the genes targeted were studied further.

Identification of specific regulators of nuclear actin

We next aimed to exclude those hits that caused the disappearance of the nuclear actin bar in an unspecific manner (e.g. those not directly related to either actin nuclear import or polymerization). In some hits phalloidin staining seemed lower than in control cells. Reduced actin expression would explain also the lack of nuclear actin, and we therefore determined the levels of actin and Tsr proteins by western blotting. Indeed, some dsRNAs, such as those against Fs(1)h and CG40451, caused a notable decrease in actin protein levels, whereas others, such as CycE and Nej affected Tsr expression (supplementary material Fig. S2A–C). Our primary RNAi screening identified core components of the RNAi pathway, such as Argonaute 2 and Dicer 2, as putative hits in our assay (supplementary material Table S1). Their depletion can result in ineffective RNAi silencing and implies that dsRNAs that affect components of the RNAi machinery are potential false positives in our assay. However, none of the remaining hits significantly impaired the exportin 6 silencing efficiency (data not shown).

We have previously shown that depletion of Ran, which provides the energy gradient for active nucleo-cytoplasmic shuttling, can prevent the exportin 6 depletion induced nuclear accumulation of actin (Dopie et al., 2012). This suggests that some of the identified dsRNAs could affect nuclear-cytoplasmic shuttling in a general manner, and not be involved in actin-specific processes. To eliminate such dsRNAs from our candidates, we expressed an import substrate, NLS–GFP–pyruvate-kinase, which uses the SV40 large T-antigen nuclear localization signal (NLS) to enter...
the cell nucleus through importin α and β (Kalderon et al., 1984). We examined the nuclear–cytoplasmic distribution of this construct in cells treated with candidate dsRNAs compared to Ketel (the Drosophila importin-β) dsRNA-treated cells. Whereas depletion of Ketel efficiently retained the NLS–GFP-pyruvate-kinase in the cytoplasm, the majority of tested dsRNAs showed prominent nuclear localization of this construct (supplementary material Fig. S3A,B), indicating that they do not cause gross defects in general protein import into the nucleus. This assay demonstrated that CG6686, CycE, Mov34 and Probeta5 might have scored in our screen due to their unspecific effects on nuclear import (supplementary material Fig. S3B). Surprisingly, neither Nup358 nor Nup98, which are components of the nuclear pore complex (Hetzer and Wente, 2009) caused a significant block in nuclear import (Fig. 3A). Quantification of the nuclear actin signal revealed that cells depleted of Capt, Lam (the Drosophila lamin) and Nup98 had significantly increased levels of nuclear actin (Fig. 3B), despite the absence of the actin bar. These proteins are therefore candidates for regulating nuclear actin polymerization, whereas the other hits are more likely to operate in nuclear import of actin.

To further probe the requirement for Capt, Lam and Nup98 in nuclear actin polymerization, we measured the intranuclear mobility of GFP–actin by using a fluorescence recovery after photobleaching (FRAP) assay (Fig. 3C). The recovery curves exhibited two phases of recovery (see Materials and Methods for details). The first phase, which likely corresponds to actin monomer mobility, was essentially identical for all the conditions (0.27–0.32 s). However, cells depleted of Lam (9.6±0.9 s) or Nup98 (6.7±0.5 s) (mean±s.d.) both displayed significantly faster half times for the second phase of recovery, and thus higher mobility of GFP–actin than cells treated with control GFP dsRNA (12.2±1.0). In this assay, Capt-depleted cells (11.7±1.05) did not show significant differences compared to the control cells. Taken together, these results show that depletion of Lam and Nup98 increases actin mobility within the nucleus.

Table 1. Specific regulators of nuclear actin identified from the screen, their mouse orthologs and putative mechanism by which they regulate nuclear actin

<table>
<thead>
<tr>
<th>Fly symbol</th>
<th>Flybase ID</th>
<th>Predicted function</th>
<th>Mouse symbol</th>
<th>Predicted from</th>
<th>Putative mechanism</th>
</tr>
</thead>
<tbody>
<tr>
<td>Capt</td>
<td>FBgn0261458</td>
<td>Actin-binding</td>
<td>Cap1, Cap2</td>
<td>Homologene, Isobase, OrthoDB</td>
<td>Polymerization of nuclear actin?</td>
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<tr>
<td>CG40042</td>
<td>FBgn0058042</td>
<td>Mitochondrial transporter</td>
<td>Timm23</td>
<td>Homologene, Isobase, OrthoDB</td>
<td>Phosphorylation of cofilin?</td>
</tr>
<tr>
<td>Chinmo</td>
<td>FBgn0086758</td>
<td>Transcription</td>
<td>Bach2</td>
<td>Isobase</td>
<td>Phosphorylation of cofilin</td>
</tr>
<tr>
<td>Cpa</td>
<td>FBgn0034577</td>
<td>Actin-binding</td>
<td>Capza1, Capza2, Capza3</td>
<td>Homologene, OrthoDB, Isobase</td>
<td>Phosphorylation of cofilin</td>
</tr>
<tr>
<td>Cpb</td>
<td>FBgn0011570</td>
<td>Actin-binding</td>
<td>Capzb</td>
<td>Homologene, Isobase, OrthoDB</td>
<td>Phosphorylation of cofilin</td>
</tr>
<tr>
<td>CtrlA</td>
<td>FBgn0062413</td>
<td>Copper ion transporter</td>
<td>Slc31a1, Slc31a2</td>
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<td>Modulation of RanBP9/Importin 9</td>
</tr>
<tr>
<td>Dco</td>
<td>FBgn0002413</td>
<td>kinase</td>
<td>Csnk</td>
<td>Homologene, OrthoDB, Isobase</td>
<td>Phosphorylation of cofilin?</td>
</tr>
<tr>
<td>Kay</td>
<td>FBgn0001297</td>
<td>Transcription</td>
<td>FOSL2</td>
<td>Compara, Phylome</td>
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<td>Lam</td>
<td>FBgn0002525</td>
<td>Nuclear envelope</td>
<td>Lmnb1, Lmnb2, Lmna</td>
<td>Homologene, Isobase, OrthoDB</td>
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<tr>
<td>Marf</td>
<td>FBgn0029870</td>
<td>GTPase</td>
<td>Mfn2, Mfn1</td>
<td>Homologene, Isobase, OrthoDB</td>
<td>Modulation of RanBP9/Importin 9</td>
</tr>
<tr>
<td>Nup358</td>
<td>FBgn0039302</td>
<td>Nucleocytoplas-mic transport</td>
<td>RANBP2</td>
<td>Homologene,</td>
<td>Polymerization of nuclear actin</td>
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<tr>
<td>Nup98</td>
<td>FBgn0039120</td>
<td>Nucleocytoplas-mic transport</td>
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<td>Pak3</td>
<td>FBgn0044826</td>
<td>kinase</td>
<td>Pak1, Pak3, Pak7, Pak4</td>
<td>Isobase, OrthoDB</td>
<td></td>
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<td>Rab18</td>
<td>FBgn0015794</td>
<td>Membrane trafficking</td>
<td>Rab18</td>
<td>Homologene, Isobase</td>
<td>Phosphorylation of cofilin</td>
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<td>Rack1</td>
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<td>Kinase</td>
<td>Gnb21</td>
<td>Homologene, OrthoDB</td>
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<tr>
<td>Shi</td>
<td>FBgn0003392</td>
<td>Motor</td>
<td>Dnm1, Dnm2, Dnm3</td>
<td>Homologene, Isobase, OrthoDB</td>
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<td>SNF4γ</td>
<td>FBgn0025803</td>
<td>Kinase</td>
<td>Prkag1, Prkag2</td>
<td>Homologene, Isobase</td>
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<td>Transcription</td>
<td>Srp1</td>
<td>Homologene, Isobase, OrthoDB</td>
<td>Phosphorylation of cofilin?</td>
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<td>FBgn0040512</td>
<td>Membrane trafficking</td>
<td>Copz1, Copz2</td>
<td>Homologene, Isobase, OrthoDB</td>
<td></td>
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</tbody>
</table>
New regulators of cofilin phosphorylation

We previously showed that the nuclear localization of actin is governed by the transport factor importin 9 and dephosphorylated Tsr (the Drosophila cofilin) (Dopie et al., 2012). Cells could therefore regulate the levels of nuclear actin by modulating the abundance and/or activity of these import mediators. We used quantitative RT-PCR (qRT-PCR) analysis to study RanBP9 (Drosophila importin 9) mRNA levels. Of the hits, depletion of only the copper ion transporter Ctr1A and mitochondrial protein Marf affected RanBP9 expression (supplementary material Fig. S4A). However, the mechanism by which these proteins operate here is not obvious.

Cofilins are actin filament-disassembling proteins (Bugyi and Carlier, 2010) and their actin-binding activity is regulated by phosphorylation on serine 3 (Agnew et al., 1995). Dephosphorylation of cofilins is essential for their role in the nuclear import of actin, and thus RNAi-mediated silencing of Ssh, the phosphatase of Tsr, results in the nuclear exclusion of actin (Dopie et al., 2012). Ssh also scored as a hit in our screen (supplementary material Fig. S4A). However, the mechanism by which these proteins operate here is not obvious.

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phosphorylation, we performed a co-depletion experiment and

determined the levels of p-Tsr. Interestingly, depletion of either
Limk or Cdi was sufficient to abolish the increased p-Tsr levels
induced by CG40042, Cpb, Dco, Rack1, Shi and Ssrp depletion
(Fig. 5B). However, p-Tsr remained in cells after Chinmo was
co-silenced with Limk, and was lost only upon Cdi silencing
(Fig. 5B,C). This indicates that Chinmo might specifically regulate
cofilin phosphorylation through Tesk.

As Chinmo (Chronologically inappropriate morphogenesis) is a
transcriptional repressor that contains a Bric-a-brac, Tramtrack,
Broad Complex (BTB) domain (Zhu et al., 2006), we wondered
whether it could regulate the expression of Cdi. Strikingly, the
expression of Cdi was significantly upregulated in Chinmo-depleted
cells as measured by qRT-PCR (Fig. 5D). This suggests that under
normal conditions, Chinmo represses Cdi expression to maintain
Tsr in an unphosphorylated, and thus active, state.

**Chinmo regulates nuclear actin levels in vivo**

Although the nuclear actin bar represents an excellent model
for robust scoring of nuclear actin phenotypes, it is, nevertheless, a
non-native structure that is formed only upon depletion of specific
factors. To confirm that our assay was capable of identifying factors
that would regulate actin also in vivo in the context of whole
organism, we investigated actin distribution within the pouch of
the Drosophila wing imaginal disc, which we have found to be
amenable for staining nuclear actin in vivo. We used the UAS-
GAL4 system (Brand and Perrimon, 1993) to drive Chinmo or
exportin 6 RNAi in the wing disc, and analyzed the nuclear and
cytoplasmic actin distribution (Fig. 6A,B). Strikingly, both RNAi
strains for Chinmo displayed decreased nuclear actin levels as
compared to wild-type flies. As expected, exportin 6 silencing
resulted in increased nuclear actin (Fig. 6A,B), but did not lead
to formation of a similar nuclear actin bar as observed in cultured
S2R+ cells (Fig. 1A). This could be because the silencing efficiency
was lower in vivo, or, alternatively, the cultured cells could be
lacking some regulatory mechanisms that prevent ectopic actin
polymerization in tissues. Our results therefore uncover Chinmo as a
factor capable of regulating nuclear actin levels in model organisms,
and highlight that the appropriate regulation of cofilin activity is
important in maintaining nuclear actin in vivo.
Nuclear actin import regulators are evolutionary conserved
To address the evolutionary implications of our findings, we examined whether silencing the mammalian orthologues of the identified Drosophila genes would affect nuclear import of actin. We selected a subset of hits including Chinmo (Bach2), Rab18, Rack1 (Gnb2l1) and SNF4Aγ (Prkag1) and analyzed the specific siRNAs targeting these proteins for their ability to prevent the nuclear accumulation of endogenous actin after exportin 6 silencing in mouse NIH 3T3 cell line. Silencing of Bach2, Prkag1 and Rab18 efficiently suppressed the nuclear accumulation of actin induced by exportin-6 depletion (Fig. 7A; supplementary material Fig. S4B).

However, we failed to reproduce the phenotype of Rack1 in mammalian cells. Moreover, depletion of either Bach2 or Rab18 significantly decreased the nuclear import rate of actin (Fig. 7B), as measured with a fluorescence recovery after photobleaching assay (Dopie et al., 2012; Skarp and Vartiainen, 2013), demonstrating that these proteins are indeed involved in nuclear entry of actin. Finally, silencing of Bach2 in NIH 3T3 cells resulted in increased levels of phosphorylated cofilin (Fig. 7C,D), similar to what is observed upon Chinmo depletion in S2R+ cells (Fig. 4). These results suggest that, like nuclear export regulators (Rohn et al., 2011), nuclear import regulators of actin are also evolutionary conserved, underscoring the importance of nuclear actin level control in different organisms.

DISCUSSION
Actin has been linked to processes spanning the whole gene expression cascade (Grosse and Vartiainen, 2013), and active nuclear import of actin is required to sustain maximal transcriptional activity of the cell (Dopie et al., 2012). Given that altered nuclear actin levels have been linked to cell quiescence (Spencer et al., 2011) and differentiation (Xu et al., 2010), which are very fundamental biological processes, it is fair to assume that the nucleo-cytoplasmic shuttling of actin is very tightly regulated, and perhaps the target of several cellular signaling pathways. The fact that actin uses an active transport mechanism for both nuclear import (Dopie et al., 2012) and export (Stuven et al., 2003), despite being at the limit for passive diffusion through the nuclear pore, already supports this hypothesis. Polymerization of actin into helical filaments is fundamental for its functions in the cytoplasm, and one of the most tightly regulated processes in the cell. Understanding the mechanisms that regulate nuclear actin polymerization is one key to deciphering the exact nature of nuclear actin polymers. Our genome-wide RNAi screen uncovered 19 new regulators of nuclear actin import and export.

Fig. 5. Chinmo regulates cofilin phosphorylation through the expression of Cdi/Tesk. (A) Quantification of the relative levels of Slingshot (Ssh) mRNA in cells treated with indicated dsRNAs. Data are mean±s.d. of two independent experiments. *P<0.05 (Student’s t-test). (B,C) Representative western blots showing the levels of Twinstar (Tsr) and phosphorylated Tsr (p-Tsr) in cells treated with indicated dsRNAs. Tubulin was detected as a loading control. (D) Quantification of Tesk and Limk mRNA expression as measured by qRT-PCR in cells treated with either Chinmo or GFP dsRNA. Data are the mean±s.d. of at least two independent experiments.
actin polymerization and import (Table 1), thus expanding the cellular processes impinging on nuclear actin (Fig. 7E).

Our assay was based on ‘rescuing’ the formation of a phalloidin-stainable nuclear actin bar caused by exportin 6 depletion. The identified proteins are then candidates for regulating either nuclear import of actin or the actual formation of the nuclear actin bar. Our actin antibody staining demonstrates that we identified both types of proteins in our screen. Depletion of Capt, Lam, or Nup98 together with exportin 6 resulted in clear nuclear accumulation of actin in the absence of the actin bar, indicating that these proteins are candidates for regulating nuclear actin polymerization. Moreover, depletion of Lam and Nup98 also increased nuclear mobility of actin in a FRAP assay (Fig. 3C). Of interest, Lam is the Drosophila lamin, a component of the nuclear lamina underlying the nuclear envelope. Loss of or mutations in LMNA in mammalian cells result in impaired nuclear actin polymerization due to mislocalization of emerin, an ABP of the inner nuclear membrane (Ho et al., 2013). Moreover, a recent study has demonstrated that there is transient actin polymerization, which is dependent on the linker of cytoskeleton and nucleoskeleton complex (LINC) and emerin, upon cell spreading (Plessner et al., 2015). Whether Lam operates through similar mechanisms in Drosophila cells remains to be determined; however, emerin is perhaps not involved here because it did not score as a hit in our screen.

Loss of or mutations in LMNA in mammalian cells result in impaired nuclear actin polymerization due to mislocalization of emerin, an ABP of the inner nuclear membrane (Ho et al., 2013). Moreover, a recent study has demonstrated that there is transient actin polymerization, which is dependent on the linker of cytoskeleton and nucleoskeleton complex (LINC) and emerin, upon cell spreading (Plessner et al., 2015). Whether Lam operates through similar mechanisms in Drosophila cells remains to be determined; however, emerin is perhaps not involved here because it did not score as a hit in our screen. Nevertheless, our study reinforces the notion that the nuclear lamina might play a pivotal role in regulating nuclear actin dynamics. In addition to nucleo-cytoplasmic transport, Nup98 has been implicated in gene expression, and chromosomal rearrangements affecting its gene are associated with a wide range of malignancies (Gough et al., 2011). In our experimental system, neither depletion of Nup98 nor the other nucleoporin hit from our screen, Nup358, caused a general block in nuclear import (supplementary material Fig. S3B). It is therefore possible that these factors are involved in nuclear trafficking of some specific actin regulators. Alternatively, Nup98 could regulate the expression of some key nuclear actin polymerization factors. Somewhat surprisingly, our assay did not reveal any canonical actin polymerization promoters, such as Arp2/3 complex or formins, that have been linked to nuclear actin and gene expression processes (Yoo et al., 2007; Baarlink et al., 2013). This could be due to the fact that these proteins also have important roles in the cytoplasm that will dominate their RNAi phenotypes. Alternatively, there might be functional redundancy among actin nucleators in the nucleus.

Finally, one limitation of our assay is that once the exportin 6 bar is fully formed, we have noticed that it is rather stable. Hence proteins that are stable, and thus depleted by RNAi slower than exportin 6, will likely be missed with our assay.

Our present study strengthens the notion that appropriate regulation of nuclear actin levels through controlled nucleo-cytoplasmic shuttling is an evolutionary conserved phenomenon, because both nuclear import regulators (this study) and export regulators (Rohn et al., 2011) have been conserved from fly to mammals. Receptor for activated C kinase 1 (Rack1, also known as Gnb2l1 in mammals) was the only protein of the four that we tested that failed to prevent the nuclear accumulation of actin induced by exportin 6 depletion in mouse cells. Rack1 is involved in many signaling complexes (Mamidipudi et al., 2004; Doan and
Huttenlocher, 2007; Jia et al., 2013), and it is therefore possible that in mammals there is more redundancy in the signaling pathways utilizing this protein than in the fly.

Nuclear actin levels can be regulated at several different steps (Dopie et al., 2012; Huet et al., 2013), and thus the import hits from our screen could act at any of these points. Of the identified hits, only Ctr1A and Marf affected the levels of RanBP9/importin 9 (supplementary material Fig. S4A). Ctr1A is the primary copper transporter in Drosophila, responsible for copper uptake across the plasma membrane and required for fly development (Turski and Thiele, 2007). Marf, by contrast, is an essential transmembrane GTPase that mediates mitochondrial fusion (Dorn et al., 2011). The mechanism by which these proteins could regulate RanBP9/importin 9 expression is therefore not very obvious. How the activity of importin 9 might be regulated is not known, and therefore some of the hits could operate this way.

Several identified hits affected the cofilin protein Tsr, either by reducing its protein levels (supplementary material Fig. S2A,B) or by modulating its activity through phosphorylation (Fig. 4). Cofilin proteins have a dual role in nuclear import of actin: as the main actin filament disassembly and severing protein (Lappalainen and Drubin, 1997), it maintains the transport competent monomer pool, and at the same time, it mediates the interaction between importin 9 and actin (Dopie et al., 2012). Of our cofilin regulators, to our knowledge only Rack1 has been linked to cofilin phosphorylation previously (Cao et al., 2011). Although expression of the constitutively active Tsr-S3A mutant restored the actin bar formation induced by exportin 6 depletion in Chinmo-, Rack1-, Shi- and Cpb-depleted cells, it failed to do so in Ssrp-, CG40042- and Dco-depleted cells. This suggests that although Ssrp, CG40042 and Dco prevent activation of cofilin, whereas Cpb promotes the expression of Ssrp, in a process that might be sensitive to the polymerization status of actin. Nup98 and Lam are candidates for regulating polymerization of nuclear actin.
that caps the barbed ends of growing actin filaments and prevents filament elongation (Amatruda et al., 1990). The Cpb-depleted cells displayed decreased levels of the cofilin phosphatase Ssh (Fig. 5A), which likely explains the accumulation of phosphorylated cofilin in these cells. Actin filaments seem to regulate the activity of Ssh (Soosairajah et al., 2005). Given that capping protein regulates the growth of actin filaments, it is possible that there is an indirect feedback mechanism through the actin cytoskeleton to Ssh expression. Of note, the other subunit of capping protein, Cpa, was also identified as a hit in our screen (Table 1), but failed to elicit accumulation of p-Tsr (Fig. 4). Interestingly, with the exception of Chinmo, we could prevent the accumulation of p-Tsr by co-depleting either Link or Tesk (Fig. 5B,C). This indicates that in S2R+ cells, the activities of these two kinases are interdependent. Many upstream signaling pathways are known to regulate Link, but the signaling pathways leading to Tesk activation are less characterized (Mizuno, 2013). It is possible that one of our newly characterized Tsr/cofilin regulators could act to bridge the signaling to these two kinases.

Chinmo, which modulates cofilin activity by regulating Cdi/Tesk expression (Fig 4; Fig.5C,D), is a transcriptional repressor that characterizes Tsr/cofilin regulators could act to bridge the signaling pathways leading to Tesk activation are less characterized (Mizuno, 2013). It is possible that one of our newly characterized Tsr/cofilin regulators could act to bridge the signaling to these two kinases.

It is rather intriguing that out of the 19 ‘specific’ hits, three (zetaCOP/Copz1, Rab18 and Shi/dynamin) are all connected to membrane trafficking. How this relates to nuclear transport of actin remains to be investigated, but especially the role of the small GTPase Rab18, which has been linked to ER–Golgi trafficking (Dejgaard et al., 2008), is intriguing, given that its function seems to be also conserved in mammalian cells (Fig. 7). Another protein with a conserved role in nuclear localization of actin is the regulatory subunit of the AMP-activated protein kinase (AMPK), SNF4A/Prkag1 (Fig. 7), which is part of the central AMPK enzyme that monitors cellular energy status. AMPK is activated in response to decreased ATP levels, promoting energy-producing pathways and inhibiting energy-consuming processes (Hardie, 2007). AMPK has also been linked to actin cytoskeleton remodeling (Miranda et al., 2010). The mechanism by which AMPK impinges on nuclear import of actin needs to be clarified, but it is intriguing that nuclear accumulation of actin has been reported upon ATP depletion (Pendleton et al., 2003) as well as upon many other types of cellular stresses (Nishida et al., 1987; Iida et al., 1992). It is tempting to speculate that activation of AMPK in these conditions ‘pushes’ actin to the nucleus to somehow modulate gene expression.

Taken together, our genome-wide RNAi screen has identified 19 new regulators of nuclear actin. Four of these factors, Chinmo/Bach2, Rack1, Shi/dynamin and Cpb operate by regulating the phosphorylation status of Tsr/cofilin, whereas Ctr1A and Marf, through an unknown mechanism, control RanBP9/importin 9 levels. Lam and Nup98, by contrast, are new candidates for regulating nuclear actin polymerization (Fig. 7E). How the remaining hits impinge on nuclear actin remains to be investigated. However, the hits have been linked to a wide variety of processes ranging from membrane trafficking (e.g. Rab18) to cellular energy metabolism (SNF4A/Prkag1). This suggests that regulation of nuclear actin is linked to many different cell biological processes.

**MATERIALS AND METHODS**

**Primary genome-wide RNAi screening**

The Drosophila RNAi Screening Center (Harvard Medical School) library 2.0 (http://www.flyrnai.org/DRSC-DRS.html) was used for the primary screen. This library contained about 13,900 genes that cover over 95% of the entire *Drosophila* genome and the screen was performed in duplicate in 384-well black thin-bottomed screening plates (PerkinElmer). In total, 128 pre- aliquoted screening plates were used. Before cells were seeded in plates, water in the designated ‘empty wells’ was replaced with 25 ng of dsRNA against Tsr. S2R+ cell suspension, in serum-free medium, was mixed with exportin 6 dsRNA to a final concentration of 0.025 µg/ml. About 10 µl of dsRNA-containing cell suspension was quickly seeded (8000 cells/well) in the screening plates and incubated at 25°C. After 30 min, 35 µl of complete Schneider’s medium was added and cells were incubated in a humidified chamber at 25°C. After 5 days of dsRNA treatment, 50 µl of 8% paraformaldehyde (PFA) was added to wells and fixed for 20 min. Cells were washed with PBS and permeabilized using 0.2% Triton X-100 (Sigma). Cells were stained with Alexa-Fluor-488-labeled phalloidin (Molecular Probes) and DAPI (Sigma) for 30 min and washed three times with PBS. Approximately 50 µl of PBS was left on each well to prevent cells from drying out during imaging. Four fields were imaged per well using the 20×/0.7 NA water immersion objective of the Perkin Elmer Evotec Opera confocal microscope (Perkin Elmer). A script in the Acapella script collection was used to export FLEX file images into TIFF files for image processing and analysis.

**Image processing, data analysis and hit identification of the RNAi screen**

Images were processed and analyzed using a customized automated MatLab algorithm, and data was scored as the ratio of cells with nuclear actin bars per well (Fig. 2A,B; supplementary material Fig. 5B). For the data analysis, individual plates were median centered by dividing the well data by the plate median to correct for drifts. Then the median and the median absolute deviation (MAD) was determined for the entire dataset and absolute deviations from the median were calculated for individual plates. ‘Wells of interest’ were defined as dsRNAs with replicate well values greater than 2MAD (2MAD) (Zhang et al., 2006). We chose 2MAD because this covered over 95% of all positive controls in the screen (Fig. 2B). About 1000 wells of interest were selected for further consideration, and the targeted protein provided by DRSC (supplementary material Table S1). Images were visually inspected and dsRNAs that affected cell viability were eliminated.

**Retesting and secondary validations**

Hits were manually annotated based on function, using the publicly available Flybase (http://flybase.org/) and DRSC databases (www.flyrnai.org). About 200 dsRNAs were retested (supplementary material Table S2), out of which 113 also had an effect in this second screen and were retained for secondary screening (supplementary material Table S3). dsRNA against different amplicons of the hits were provided by the DRSC and their effect on the nuclear localization of actin was tested in 96-well black clear-bottomed plates (Perkin Elmer). Images for secondary screening were acquired using the 20×/0.7 NA water immersion objective of the Perkin Elmer Evotec Opera confocal microscope (Perkin Elmer). A script in the Acapella script collection was used to export FLEX file images into TIFF files for image processing and analysis.

**Antibodies and DNA constructs**

The antibodies used in this study include: rabbit polyclonal anti-actin (A2103; Sigma), mouse anti-α-tubulin (Sigma), rabbit anti-p-Tsr (Signalway Antibody) and rabbit anti-Tsr (kind gift from James Bamberg, Department of Biochemistry & Molecular Biology, Colorado State University, USA) as well as secondary horseradish peroxidase (HRP)-conjugated anti-mouse-IgG and anti-rabbit-IgG antibodies (Sigma); Alexa-Fluor-conjugated
anti-mouse-IgG and anti-rabbit-IgG antibodies (Molecular probes). pAW-NLS-GFP-PK was generated by PCR from a pEGFP-C1 plasmid containing NLS–GFP–pyruvate-kinase and cloned into the pAW gateway destination vector (Invitrogen). pAGW-actin (encoding GFP-actin) was created by cloning Drosophila actin-5C sequence to a Gateway-entry vector, and then to pAGW. The Twinstar S3A mutant (Tsr-S3A), was generated using primers (forward, 5’-ATGGCTGCTGGTAACTGGTGCTGTC-3’ and reverse, 5’-GACAAGACACAGATTTACACCAGG-3’) carrying the serine 3 to alanine mutation (bold nucleotides) in an in vitro mutagenesis reaction using a wild-type Tsr construct cloned into the pAWH destination vector (Invitrogen) as a template.

Cell culture and RNAi
Drosophila S2R+ cells were maintained in a humidified chamber at 25°C, in Schneider’s medium supplemented with 10% heat-inactivated fetal bovine serum (FBS) and penicillin-streptomycin (GBBCO). NIH 3T3 cells were cultured in Dulbecco’s modified Eagle’s medium (DMEM; Sigma) containing 10% FBS and penicillin-streptomycin (GBBCO) and maintained at 37°C and 5% CO2 until needed for experiments. dsRNAs were synthesized and purified using the MEGAscript® T7 Kit and NucAwayTM Spin columns (Applied Biosystems), respectively. Exportin 6 and importin 9 siRNAs have been described previously (Dopie et al., 2012). The other siRNAs were from Sigma, and the targeted sequences were: BACH2, 5’-GCAUUUGACCAUGUCUCUAUA-3’; PRKAG1, 5’-CCUAGAGUUGUCUGGAC-3’; RAB18, 5’-GCCAAGAUUCAUGUGU-3’; and RACK1, 5’-GUUAUGGAAACUCUGUUG-3’. RNAi experiments and immunostainings were carried out as described previously (Dopie et al., 2012). Cells were imaged using 63×1.4 NA objective of Axio Imager M2 equipped with AxioCam HRm camera and AxioVision software (Zeiss) or TCS SP5 II HCS A confocal microscope using FRAPbooster. Laser power and Cytoplasmic fluorescence intensities were measured using ImageJ (NIH).

Nuclear import rates of GFP were measured as described previously (Dopie et al., 2012; Skarp and Vartiainen, 2013). FRAP assays were performed on 11–18 cells from two independent experiments.

Flat-embedding for electron microscopy was performed as described previously (Seemann et al., 2000; Jokitalo et al., 2001) with the exception of fixed the cells with 2% glutaraldehyde, 2% paraformaldehyde in 0.1 M sodium cacodylate buffer, pH 7.4, and performing staining with 1% uranyl acetate, 0.3 M sucrose in distilled water en-block at -4°C for 1 h prior to dehydration. Sections (90-nm thick) were cut parallel to the coverslip, post-stained with uranyl acetate and lead citrate, and imaged with a Jeol JEM-1400 (Tokyo, Japan) microscope, equipped with a Gatan Orius SC 1000B bottom mounted CCD-camera (Gatan Inc., USA), operating at 80 kV.

For western blotting, proteins were separated in 12% SDS-PAGE gels and transferred onto nitrocellulose membranes. The following primary antibodies and respective dilutions were used: mouse anti-a-tubulin (Sigma, dilution 1:10,000), rabbit anti-p-Tsr/cofilin (Signalway Antibody, dilution 1:1000), rabbit anti-Tsr (kind gift from James Hamburg, dilution 1:15,000), rabbit anti-cofilin (dilution, 1:1000). Secondary antibodies include: anti-mouse-IgG and anti-rabbit-IgG HRP-conjugated antibodies (Sigma, dilution 1:10,000). Immunoblots were developed using the LAS 3000 (FujiFilm) and where necessary, bands were quantified using ImageJ. For analysis of Tsr and actin levels (supplementary material Fig. S2), the experiment was performed at least four times, and due to the variability in the assay, the two most complete sets of blots were quantified. The trend was, nevertheless, the same in all experiments.

Real-time quantitative PCR
RNAi was performed as described above and after 5 days, total mRNA was extracted using the Nucleospin RNA II kit according to the manufacturer’s protocol (Macherey-Nagel). 500 ng of total mRNA was used for reverse transcription PCR using the Thermo Scientific RT-PCR kit and random primers (Thermo Scientific). Quantitative PCR was carried out using the Bio-Rad CFX machine (Bio-Rad) and SYBR green qPCR reagent (Thermo Scientific). The following primers were used: Gapdh_forward, 5’-AAGGGTGCCTCCTATGATGA-3’; Gapdh_reverse, 5’-GCCAAACTCGTGGTCTGACC-3’; Tesk_forward, 5’-TGCACATCCTGACACCCGG-3’; Tesk_reverse, 5’-GCTTATATTTGCTCCGCG-3’; Limk_forward, 5’-GGCCGTAGAATCTCTACAGA-3’; Limk_reverse, 5’-TGTCGGCGTCAACTACTGC-3’; Shh_forward, 5’-CGTACCACAATCAGCTGTA-3’; Shh_reverse, 5’-TGTGGCTTCGAATTTGTGCT-3’; RP49 forward, 5’-AGGGATGCAACACAGAGTG-3’; and RP49 reverse, 5’-CACCAAGAATCTTTGAAT-3’. Relative expression levels were calculated by the comparative Ct method, normalizing to Gapdh or RP49 cDNA with the equation 2^(-ΔΔCt) (target/ΔCt).
the Integrative Life Science program of University of Helsinki. Deposited in PMC for immediate release.

Supplementary material
Supplementary material available online at http://jcs.biologists.org/lookup/suppl/doi:10.1242/jcs.169441/-/DC1

References


(A) Electron microscopy image showing exportin 6 dsRNA treated Drosophila S2R+ cell. Actin bar (A) protruding from the nucleus (N) and pushing the nuclear envelope (NE) to the cytoplasm (C) are indicated. Boxed area is shown with higher magnification on the right.

(B) A workflow diagram of the image analysis process for the identification of rod-shaped nuclear actin bars. (1) Original image with DAPI label for nuclei in blue and actin label in green. (2) Overlay of nuclear segmentation mask in blue and whole cell segmentation mask in green. (3) Overlay of nuclear actin bar mask in red on top of nuclear and whole cell masks. (4) Skeletonization of nuclear actin bar mask. (5) Cleaned up skeleton of nuclear actin bar after removing all the side branches. (6) Overlay of the skeleton of nuclear actin bar on top of the original image.
Supplemental material Figure S2

Actin and tsr levels upon depletion of the hits from the screen.

(A) Representative Western blot from whole cell lysates treated with indicated dsRNAs. GFP dsRNA was included as non-targeting control. Tubulin was detected as a sample loading control. Quantification of the levels of twinstar (B) and actin (C) from blots depicted in A. Western blot bands were quantified using NIH ImageJ and the values for actin and Tsr were normalized to the respective values of tubulin. Data is normalized to GFP, and is mean of two independent experiments, with error bars SD and statistical significance (*) with Students t-test (p< 0.05).
Supplementary Figure S3

(A) Representative fluorescent microscopy images of S2R+ cells expressing NLS-pyruvate kinase-GFP (NLS-PK-GFP) (green) co-stained with phalloidin (red) and DAPI (blue). Ketel/importin ß dsRNA treated cells were included as a positive control.

(B) Quantification of the percentage of cells with nuclear NLS-PK-GFP in cells treated with the indicated dsRNAs. Data is the mean of two independent experiments (50 cells each), with error bars SD, statistical significance (*) with Students t-test (p< 0.05).

(C) Confocal microscopy images of Exportin 6 depleted S2R+ cells showing co-localization (merged, right panel) of actin antibody staining (left panel) and phalloidin staining (middle panel). Scale bar = 20 μm.
(A) RanBP9 mRNA levels in cells depleted of candidate hits. Quantification of the mRNA levels of RanBP9 in cells treated with the indicated dsRNAs. RanBP9 dsRNA was used as a control. Data is the mean of two independent experiments, with error bars SD, statistical significance (*) with Students t-test (p< 0.05).

(B) A subset of hits prevent exportin 6 induced nuclear accumulation of actin also in mouse cells. Representative anti-actin immunofluorescence images of NIH 3T3 cells co-transfected with siRNA against exportin 6 (EXP6) and control (Cont) or gene-specific siRNAs as indicated. Scale bar = 10 µm. Quantification in figure 7A.