

Localization of aurora A and aurora B kinases during interphase: role of the N-terminal domain

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Abstract

Aurora kinases possess a conserved catalytic domain (CD) and a N-terminal domain (ND) that varies in size and sequence. We have previously reported that the N-terminal domain of AuroraA (AurA) participates in the localization of the kinase to the centrosome in interphase. AuroraB (AurB) is a chromosome passenger protein and its N-terminal domain is not necessary for its localization or function during mitosis. Using various combinations of GFP-AurA and AurB protein domains we show that in interphase, AurB N-terminal domain is required for nuclear localization in *Xenopus* XL2 cells. In human cells, however, we found both AurA and AurB kinases in the nucleus, AurA being mainly cytoplasmic and AurB mainly nuclear. Both proteins are actively excluded from the nucleus by a CRM1 dependent pathway. Interestingly, at a functional level, in interphase, every combination of Aurora kinase domains (ND-CD) rescues histone H3 Serine10 phosphorylation defect induced by AurB knockdown. This clearly indicates the presence of a functional AurA in the nucleus. Additionally, the chimera ND-AurA/CD-AurB was much more efficient than the ND-AurB/CD-AurA to rescue multinucleation also induced by AurB knockdown. This indicates that the catalytic domain of AurB is required to fulfill specific functions during mitosis that cannot be fulfilled by the catalytic domain of AurA, probably for localization reasons during mitosis.

MESH Keywords Animals ; Cell Nucleus ; metabolism ; Cells, Cultured ; Centrosome ; metabolism ; Green Fluorescent Proteins ; genetics ; metabolism ; HeLa Cells ; Humans ; Interphase ; physiology ; Protein Structure, Tertiary ; Protein-Serine-Threonine Kinases ; analysis ; chemistry ; metabolism ; Transfection ; *Xenopus*

INTRODUCTION

The Aurora serine/threonine kinases are essential for normal mitosis to proceed. Mammalian cells possess three different Aurora kinases named AurA, -B and -C (AurA, AurB, AurC) 1. AurA is a centrosome kinase while AurB and C are chromosome passenger proteins 2, 3. All three Aurora kinases are overexpressed in numerous cancers 4, 5, 6, but only AurA transforms NIH3T3 or Rat1 cells when overexpressed, revealing an oncogenic potential 7, 8. AurA activity is required for centrosome maturation, and mitotic spindle assembly and stabilization by phosphorylating proteins such as TACC, TPX2 and Eg5 9, 10, 11, 12. The kinase also phosphorylates CDC25B contributing to the G2/M transition 13. AurB activity is required during the metaphase checkpoint to resolve synthetic attachments of chromosome kinetochores through phosphorylation of MCAK 14, 15. The kinase might also be necessary for chromosome condensation by phosphorylating histone H3 16 and for cytokinesis by phosphorylating vimentin, MgcRacGAP and the kinesin Mklp1 17, 18, 19, 20. AurB forms at least two different mitotic protein complexes, one with INCENP and one with INCENP, survivin, and Borealin 21. The function of AurC is still unknown, however the protein overexpressed in HeLa cells behaves like a chromosome passenger protein 22 and rescues AurB deficiency 23. Aurora kinases possess three domains; a large catalytic domain located in the C-terminal half of the protein, a variable N-terminal non-catalytic domain and a very short carboxy-terminal domain 24. Aurora catalytic domains show a high degree of identity, whereas, the N-terminal non-catalytic domains are different in sequence and length (Figure 1A and B). XI-AurA and XI-AurB are 407 and 361 amino acids proteins respectively and they share 52% identity (Figure 1C). Their catalytic domains (CD) are very conserved in length and sequence (69% identity), while their non-catalytic domains (ND) show only 18% identity (Figure 1C). The length of these non-catalytic domains is also different: 138 amino acids in length for XI-AurA and 92 amino acids in length for XI-AurB 25. Interestingly, these two kinases localized differently in interphase cells. AurA begins to localize on duplicated centrosomes in late S-phase then stays associated with the centrosomes until early G1-phase 26. At this cell cycle stage, AurA is targeted by the APC/C (Anaphase Promoting Complex/Cyclosome) and degraded by the proteasome in a Cdh1 dependent manner 27, 28. The protein is then resynthesized during the following S-phase and delocalizes to duplicated centrosomes. AurB is a chromosome passenger protein 29. It appears only in late G2-phase in the nucleus on chromatin condensation foci and the protein is also degraded by the proteasome in a Cdh1 dependent manner 30. In early mitosis, AurB localization is restrained to the kinetochores on condensed chromosomes. At the metaphase anaphase transition AurB moves from kinetochores to the central spindle and decorates the mid-body in telophase cells 31. AurB localization during mitosis depends only on the presence of a short sequence in the C-terminal

domain of the protein. The N-terminal domain of the kinase is not required for the mitotic localization or for its mitotic function 32 . We previously showed that the non-catalytic N-terminal domain of XI-AurA was able to target the GFP (Green Fluorescent protein) to the centrosome mimicking interphase AurA localization 25 . We further demonstrated that this domain participates to the kinase localization to the centrosome using an active mechanism that depends on the presence of microtubules 25 . The catalytic domain can also localize the GFP to the centrosome but with a much lower efficiency and independently of the presence of microtubules. This secondary localization mechanism was proposed to be a passive one due to the interaction between XI-AurA and its substrates already localized on the centrosome. The N-terminal domain of the XI-AurA then plays an essential role in increasing the efficiency of the localization of the kinase, at the centrosome 25 . AurC is the shortest kinase of the family (without N-terminal domain), the kinase is also closely related to AurB, at the sequence level but also at the functional level, AurC can rescue AurB RNAi 23 . AurC is like an AurB without any N-terminal domain. In a previous work we have reported that AurC, in contrast to AurB, does not enter the nucleus during G2 33 . In this report we asked whether the N-term domain of AurB participates to the localization of the kinase during interphase. We found that the non-catalytic N-terminal domain of XI-AurB fused to GFP enters the nucleus in G2 whereas the catalytic domain does not. We also show that by switching the N-terminal domains we were able to localize XI-AurB-ND fused to XI-AurA-CD in the nucleus suggesting that the presence of the N-terminal domain of AurB correlates with an increase efficiency in the nuclear localization of the kinase. Further analysis of Aurora kinases nuclear localization in human cells showed that both AurA and AurB can enter the nucleus. AurA is, however, readily exported in the cytoplasm. We also found that proteins containing the catalytic domain of AurA rescue the histone H3 Ser10 phosphorylation defect due to AurB RNA interference, but they do not rescue the cytokinesis defect.

RESULTS

The N-terminal domain of XI-AurA and both catalytic domains of XI-AurA and XI-AurB localize the GFP to centrosome in interphase cells

In order to check whether the N-terminal of XI-AurB, like for XI-AurA, plays any role in the localization processes of Aurora B protein during interphase we transfected XL2 *Xenopus* cells with various Aurora protein domains tagged with GFP. As a control, GFP protein alone was also expressed. XI-AurA is a centrosome protein and XI-AurB a nuclear protein, therefore, we particularly analyzed the protein localization at these structures.

We started by analyzing the centrosomes localization using γ -tubulin indirect immunofluorescence as control (Figure 2 , panels B1 to B9). When the GFP protein alone was expressed, the whole cell (nucleus and cytoplasm) was fluorescent (Figure 2 , panels A1 and C1) and the centrosomes stained with anti- γ -tubulin were not decorated with GFP (Figure 2 , panels B1 and C1). As we previously reported 25 , the AurA-GFP (Figure 2 , panels A2 to D2) and the ND-AurA-GFP proteins (Figure 2 , panels A3 to D3) localized to the centrosome when expressed in XL2 cells. Eighty-nine \pm 4% of interphase cells transfected with AurA-GFP and 80 \pm 4% transfected with ND-AurA-GFP contained GFP decorated centrosomes (Table 1). Likewise, the CD-AurA-GFP protein localized to centrosomes in XL2 interphase cells (Figure 2 , panels A4 to D4), but with a weaker efficiency, 43 \pm 2% of transfected interphase cells contained GFP stained centrosomes (Table 1). Therefore, as already reported, we confirm that the ND of XI-AurA participates in the centrosome localization of the protein 25 . When the AurB-GFP protein (Figure 2 , panels A5 to D5) or the ND-AurB-GFP protein (Figure 2 , panels A6 to D6) were expressed in XL2 cells, the fusion protein was never observed at the centrosomes in interphase cells. Interestingly, the CD-AurB targeted the GFP to centrosomes in interphase cells (Figure 2 , panels A7 to D7) with efficiency in the same range than CD-AurA. Fifty-six \pm 7% of interphase cells expressing CD-AurB-GFP and 43 \pm 2% for CD-AurA-GFP exhibited GFP-decorated centrosomes (Table 1). In addition, when the ND-AurA/CD-AurB-GFP protein was expressed in XL2 cells, the fusion protein localized to centrosomes in 47 \pm 7% of transfected interphase cells (Figure 2 , panels A8 to D8; table 1). ND-AurB/CD-AurA targeted the GFP on centrosomes with the same efficiency: 46 \pm 5% of transfected cells in interphase (Figure 2 , panels A9 to D9; Table 1). Although ND-AurA is highly efficient to localize the GFP to centrosome, it loses its efficiency when fused to CD-AurB whereas it gains in efficiency when fused to CD-AurA. This suggested that there is cooperation between ND-AurA and CD AurA that does not occur between ND-AurA and CD-AurB, at the contrary. This is also in agreement with the fact that both Aurora-A domains (N-terminal and catalytic-domain) contain sequences involved in centrosome localization of the kinase 34 . To summarize, in interphase all the chimera proteins containing either XI-AurA N-terminal domain or catalytic-domain localized the GFP to the centrosomes while XI-AurB was found in the centrosome only in the absence of its own N-terminal domain.

The N-terminal domain of XI-AurB targets all the fusion proteins in the nucleus

Because the XI-AurA N-terminal domain plays a role in localizing XI-AurA in interphase we asked whether the XI-AurB N-terminal domain would also play a role in the localization of XI-AurB in interphase. All the fusion proteins localized in the cytoplasm, especially AurA-GFP, ND-AurA-GFP and CD-AurA-GFP (data not shown). When the AurB-GFP was expressed, 96 \pm 1% of transfected interphase cells displayed a GFP labeling in the nucleus (Table 1). This localization was consistent with the previous AurB localization described in interphase 20 . Ninety-seven% \pm 2% of interphase cells expressing ND-AurB-GFP exhibited a nuclear GFP staining with the same efficiency than AurB-GFP expressing cells (Table 1). The CD-AurB-GFP never localized in the nucleus (Table 1). These results strongly suggest that without its N-terminal domain, XI-AurB can no longer localize to the nucleus. This implies that the XI-AurB non-catalytic

domain plays a role in the localization of the protein in interphase XL2 cells. Interestingly, none of the AurA domain was able to target the GFP to the nucleus. We then asked whether the XI-AurB non-catalytic domain would be sufficient to target the XI-AurA catalytic domain in the nucleus. When the ND-AurB/CD-AurA-GFP was expressed in XL2 cells, the fusion protein was readily found in the nucleus of $96 \pm 1\%$ of these cells (Table 1). In contrast, the ND-AurA/CD-AurB-GFP was never found in the nucleus. All these data strongly confirm that the XI-AurB N-terminal domain is essential to localize the protein kinase in the nucleus in XL2 cells.

Both human Aurora A and B kinases are found in the nucleus, but the N-terminal domain of Hs-AurB increases the nuclear localization efficiency

Xenopus XL2 cells are known to be resistant to drug and are also difficult to perform RNA interference on, therefore, we decided to study AurA and AurB localization in human HeLa cells during interphase. AurA and AurB are two proteins highly conserved between Xenopus and Human (Figure 1), therefore this study gave us the opportunity to analyze the conservation of localization mechanisms from Xenopus to Human.

We analyzed the nuclear localization of human proteins AurA and AurB tagged with GFP. In Human cells we decided to discriminate three kinds of localization: (1) mainly nuclear, (2) nuclear and cytoplasmic and (3) mainly cytoplasmic (figure 3A). In agreement with our results in XL2 cells, we found that in $74.1 \pm 6.1\%$ of the human HeLa cells Hs-AurB-GFP was mainly nuclear, whereas in $25.6 \pm 6.1\%$ it was both cytoplasm and nuclear, we didn't see any cell with only cytoplasmic AurB-GFP (Figure 3A). Surprisingly in HeLa cells, Hs-AurA-GFP was equally distributed between the cytoplasm and the nucleus in $78.7 \pm 3.8\%$ of the cells. In $18.3 \pm 2.6\%$ of the cells AurA-GFP was nuclear and in only $3\% \pm 1.6\%$ of the cells the kinase was exclusively cytoplasmic.

We then analyzed the localization of ND-AurB, ND-AurA/CD-AurB and ND-AurB/CD-AurA tagged with HA (Figure 3C). We changed the tag for practical reasons; those constructs have been previously used, controlled and tested 32.

We first checked whether the localization of the ND of human AurB in human cells was the same than the localization of the ND of Xenopus AurB in Xenopus cells. We found that in almost 100% of the cells expressing HA-ND-AurB the protein was found in the nucleus, those cells were distributed as followed $13.7\% \pm 1.4\%$ showed a localization mainly nuclear, and $84.9\% \pm 1.2\%$ showed an homogenous distribution nucleus and cytoplasm and only $1.4\% \pm 0.4\%$ a localization mainly cytoplasmic (Figure 3C).

We then analyzed the localization of chimera proteins. The human chimera HA-BA (ND-AurB/CD-AurA tagged with HA) localized in the nucleus ($72.5\% \pm 3.4\%$) like AurB-GFP (Figure 3B). The human chimera HA-AB (ND-AurA/CD-AurB) was also found in the nucleus ($28.8\% \pm 6.2\%$) but with a majority of cells ($51.4\% \pm 5.3\%$) showing a homogeneous staining within the cytoplasm and the nucleus and in $19.8\% \pm 6.3\%$ of them a localization mainly cytoplasmic (Figure 3C). These results suggest that the N-terminal domain of Hs-AurB increases the nuclear localization efficiency. However it is also clear that to do so the N-terminal of AurB must be associated to an Aurora catalytic domain. Indeed AurB is as efficient as HA-BA chimera to localize in the nucleus, whereas HA-AB is 2.5 less efficient with a large part (around 20%) being now mainly cytoplasmic (Figure 3C).

Hs-AurA and Hs-AurB are actively exported from the nucleus

Hs-AurA and Hs-AurB proteins have been found in the nucleus of human cells. We examined whether Hs-AurA and Hs-AurB exited the nucleus in a CRM1 dependent manner. We used Leptomycin B (LMB) to inhibit CRM1 dependent nucleus-to-cytoplasm export. The percentage of cells showing a nuclear GFP-staining restricted to the nucleus was indeed enhanced in cell exposed to LMB compared to control cells. In the presence of LMB almost 100% ($96.4\% \pm 1.7\%$) of cells showed AurB-GFP exclusively in the nucleus whereas in the case of AurA-GFP it was only 50% ($48.4\% \pm 1.6\%$) (Figure 3D). This means that the whole population of AurB proteins goes to the nucleus whereas a subpopulation of AurA never does. The chimera protein HA-BA behaved exactly like the full length AurB in the presence or absence of LMB, almost all the cells show nuclear localization (Figure 3D and E). At the contrary, the chimera protein HA-AB was not as efficient to localize in the nucleus; in this chimera the N-terminal domain of AurB as been replaced by the N-terminal domain AurA (Figure 3E). These data indicated that, although the N-terminal domain of AurB alone does not preferentially localize to the nucleus, when it is associated with an Aurora kinase domain it increases the nuclear localization of the protein (Figure 3C), and plays an important role to keep the protein in the nucleus (Figure 3E).

The ND-AurB is not required to rescue the multinucleated phenotype induced by AurB knock-down

We found that proteins containing the N-terminal domain of AurB were more efficiently localized in the nucleus. We then asked whether the presence of this domain was sufficient to rescue the loss of histone H3 phosphorylation on S10 in interphase cells and the appearance of multinucleated cells due to cytokinesis defects after AurB knock-down by RNA interference (Figure 4). AurB was eliminated using small hairpin RNA interference produced by pSuper-shAurB as described in Scrittore et al. 2004 (Figure 4B) and the rescue was performed by co-transfection of a vector encoding mRNA for either AurA-GFP, AurB-GFP, the HA-tagged chimera HA-AB and HA-BA. All constructs were resistant to RNA interference. AurB is responsible for the mitotic phosphorylation of the serine 10 of histone H3 16, 35. During interphase 8% of the cells were positive for histone H3 on S10 phosphorylation (H3-S10) (Figure 4 A and C).

These cells correspond to late G2 cells containing nuclear AurB. After AurB knockdown by RNA interference the amount of interphase cells showing H3-S10 phosphorylation falls down to 1.6%. Overexpression of AurA, AurB, HA-AB or HA-BA in AurB silenced cells restore H3-S10 phosphorylation during interphase to a level between 3.8 to 4.6%. These data suggest that overexpression of any Aurora kinase is able to phosphorylate H3-S10 in the nucleus during interphase in the absence of endogenous AurB. AurB is also required for cytokinesis 36 , 20 , 37 . As expected, the elimination of AurB induces the appearance of 13.2% of multinucleated cells (Figure 4 D). We found that the expression of AurB and HA-AB rescued cytokinesis to about 5%. On the contrary HA-BA was not efficient to rescue polyploidy since 11.6% of the cells remain multinucleated. This result suggests that the presence of the catalytic domain of AurB is necessary to avoid multinucleated cell formation seen in AurB knockdown cells.

DISCUSSION

Aurora kinases (A, B and C) are critical at multiple stages of mitosis insuring accurate cell division. They regulate centrosome maturation, bipolar spindle assembly and stability, chromosome condensation and segregation, spindle checkpoint and cytokinesis 2 , 6 , 38 . AurA regulates events linked to centrosome/microtubule behavior while AurB and AurC regulate interplay between chromosomes and microtubules and also cytokinesis. Aurora kinases are key mitotic players that fulfill different function and localize differently during mitosis. The main difference between Aurora kinases structures lies in the length and sequence of their N-terminal domains; AurA possesses the longest domain and AurC the shortest. It was then tempting to suggest that this domain could be involved either in the localization and/or function of the kinase during mitosis 25 , however, neither AurA nor AurB really need its N-terminal domain to insure its localization or its function during mitosis 32 . In addition, AurC that possesses only a very short N-terminal domain can rescue AurB deficiency in mitosis 23 . Furthermore a chimera protein associating the N-terminal domain of AurA fused to the C-terminal domain of AurB is able to rescue AurB mitotic function when depleted by RNA interference 23 . All these data, strongly suggest that the N-terminal domain of AurB is not required for the kinase function during mitosis. So why do Aurora kinases possess a different N-terminal domain? What is the function of this N-terminal domain?

We wonder whether the N-terminal domain of AurB could be involved in the localization of the kinase during interphase. We were indeed intrigued by the difference in localization of the two Aurora kinases A and B during interphase. AurA localizes to the centrosome while AurB never does, and AurB is seen in the nucleus at the end of G2 whereas AurA is not. We have also previously reported that the non-catalytic domain of AurA increases the centrosome localization efficiency during interphase 25 . Others have found that a sequence within the AurA catalytic domain also participated to centrosome localization together with a sequence in the N-terminal 34 . So does the non-catalytic domain of AurB play a role in the localization of the kinase during interphase?

We first addressed the question in *Xl2 Xenopus* cells. We repeated the centrosome localization analysis of AurA and included AurB domains and chimera proteins designed with AurA and AurB N-terminal and catalytic domains. As previously reported, we found that the N-terminal domain and the catalytic domain of AurA localized to the centrosome but the presence of ND-AurA increases the efficiency of the centrosome localization. In the case of AurB, the CD-AurB also possesses information for centrosome localization; its efficiency to localize to centrosome is comparable to CD-AurA. In a recent study, we also reported that in human cells GFP-AurC localized to centrosome at the end of G2 33 . AurC is the smallest Aurora kinase, because it carries the smallest N-terminal domain. It seems that every Aurora catalytic domain carries localization information sufficient to target GFP to centrosomes. Only the full length AurB and the N-terminal domain of AurB were never found at the centrosome. We then asked whether AurB N-terminal domain would also play a role in localizing the kinase in the nucleus during G2, while AurA localizes to centrosomes AurB localizes to foci in the nucleus. We decided to analyze the nuclear localization of the same proteins in *XL2* cells. Only the proteins containing the N-terminal domain of AurB were seen in the nucleus. The data obtained in *Xenopus* cell lines were then pretty clear, the N-terminal domain of AurB was required to localize the kinase in the nucleus.

We then extended the study to human cell and analyzed the nuclear localization of Aurora kinases. We found that although the ND of AurB is important for the presence of the kinase in the nucleus, it is not required to enter the nucleus. Indeed, AurB, AurA and all chimera constructs accumulate in the nucleus in the presence of LMB, an inhibitor of nuclear to cytoplasm transport. The AurB full-length protein and the chimera ND-AurB/CD-AurA show exactly the same behavior, about 75% of the cells show nuclear localization of the protein, that increased to about 95% in the presence of LMB indicating that the protein can use CRM1 to out the nucleus. AurA also accumulates in the nucleus in the presence of LMB, but to a much lesser extent indicating that a population of AurA remains exclusively cytoplasmic. These data also clearly indicate that like AurB, AurA can enter the nucleus. Once in the nucleus both kinases are exported back to the cytoplasm by the CRM1 dependent pathway. In the absence of LMB, a large majority of AurB stays in the nucleus presumably because it binds to chromosomes and participates to chromosome passenger complexes 3 . In contrast, AurA has no affinity for chromosomes and is readily translocated to the cytoplasm where it binds to the centrosomes. Finally, in this work, we found that the N-terminal domain of the Aurora kinase contributes to the different behavior of the protein in interphase, the AurA-ND increases the centrosome localization efficiency while the AurB-ND contributes to its nuclear localization. We found slight differences between *Xenopus* and human cells, in *Xenopus* we did not find any construction that enter the nucleus without XI-ND-AurB, while in Human we found that Hs-ND-AurB only increases nuclear localization efficiency. At a functional level, AurA, B and all chimeras can rescue H3 S10 phosphorylation defect induced by

AurB RNAi. However proteins containing the CD of AurA did not rescue multinucleation. Even if NT domains help proper localization of Aurora kinases, specific functions are associated with their catalytic domains, functions that cannot be fulfilled by a different overexpressed Aurora kinase. This is probably a consequence of a localization problem revealed in Scrittore *et al.*, 2005 32, the CD of AurB possesses a small sequence that is not present in the CD of AurA that is required for correct localization during mitosis. This fact has consequences for design of drugs to be used in cancer treatment, Aurora kinases being privileged targets 39.

MATERIALS AND METHODS

Cell culture and transfections

Xenopus XL2 cells line 40 were cultured in Leibovitz medium (L15; Life Technologies, Inc.) containing 5% fetal calf serum (FCS). Cells were incubated at 25°C. For transfection of the various constructs, $5 \cdot 10^5$ *Xenopus* XL2 cells were plated out on glass coverslips in 12-well plate. Cells were transfected with FuGENE 6 transfection reagent (Roche) following the manufacturer's instructions.

Human HeLa cells were maintained in Dulbecco's modified Eagle's medium (DMEM; Invitrogen) supplemented with 10% foetal calf serum (FCS) and penicillin-streptomycin (Invitrogen). For transfection experiments HeLa cells were seeded at $2 \cdot 10^5$ on glass coverslips in 12-well plate. Twenty four hours later cells were transfected with 2µg of DNA construct with Lipofectamine 2000 reagent (Invitrogen) following the manufacturer's instructions.

Both XL2 and HeLa transfected cells were observed 48h after transfection.

DNA constructs

The sequence of the full-length AurB was amplified by PCR using phy22-GST-AurB vector as a template reference (gift from Tim Hunt) and the following primers containing the restriction sites 5'-TTT TAC CGC TAG CAT ATG GAG TAC-3' (*Nhe* I) and 5'-GGA CAG CTA GCA TGT TTT GAT TGG 3' (*Nhe* I). The sequences of the AurB N-terminal domain (ND) and AurB catalytic domain (CD) were also amplified by PCR using vector Phy22-GST-AurB as a template and the following primers containing the restriction sites 5'-TTT TAC CGC TAG CAT ATG GAG TAC-3' (*Nhe* I), 5'-CAA TGG GTA CCG TCA TCG ATG GT-3' (*Kpn* I) and 5'-TTC ACC GGA TCC AAT GGA CTT TGA C-3' (*Bam*H I), 5'GGACAGCTAGCATGTTTGGATTGG3' (*Nhe* I) respectively. The resulting PCR fragments were cloned into pGEM-T Easy vector (Promega). The PCR fragments encoding full-length (*Nhe*I/*Nhe*I fragment) and CD-domain (*Nhe*I/*Bam*HI fragment) of AurB were then subcloned in a modified MCS of pEGFP-N3 (Clontech). The PCR fragment corresponding to the ND-domain of AurB was subcloned in the MCS of the pEGFP-N3 using *Eco*RI and *Kpn*I restriction sites. All fusion proteins have the GFP fused to the carboxy-terminal. All these constructs were checked by sequencing.

Aurora fusion proteins

We used the three *Xenopus* AurA constructs previously prepared (Giet and Prigent 2001) that encoded XI-AurA N-terminal domain (ND-AurA-GFP), XI-AurA catalytic domain (CD-AurA-GFP) and the full length XI-AurA (AurA-GFP). The same three AurB constructs were prepared that encoded XI-AurB N-terminal domain (ND-AurB-GFP), XI-AurB catalytic domain (CD-AurB-GFP) and a full length XI-AurB (AurB-GFP). Two chimera constructs were also used: a XI-AurA N-terminal domain fused to XI-AurB catalytic domain ([ND-AurA/CD-AurB]-GFP) and XI-AurB Nterminal domain fused to XI-AurA catalytic domain ([ND-AurB/CD-AurA]-GFP).

Expression vectors for various human Aurora constructs (HsAurA-GFP, HsAurB-GFP, Hs-HA-ND-AurB, Hs-HA-ND-AurA/CD-AurB and Hs-HA-ND-AurB/CD-AurA) were kindly provided by S. Dimitrov. These constructs have been previously described in Scrittore *et al.*, 2005 32.

ShRNA transfection

HeLa cells were seeded at $2 \cdot 10^5$ on glass coverslips in 12-well plate. Twenty four hours later cells were transfected with 2µg of pSuper-AuroraB construct with Lipofectamine 2000 reagent (Invitrogen) following the manufacturer's instructions. Cells were fixed and stained 48h after transfection for observation.

Inhibition of CRM1 dependant pathways

Twenty four hours after DNA transfection, HeLa cells were treated with Leptomycin B (5 ng/mL; Sigma). Cells were fixed and stained 24h after drug treatment. At the same time, control cells were treated with methanol (0.7 %).

Immunofluorescence

For analysis of XL2 GFP-transfected cells, these were fixed for 10 min at room temperature with 75% methanol, 3.7% formaldehyde in 0.5X PBS and permeabilized for 2 min at RT with 0.1% Triton X-100 in PBS. Regarding HeLa transfected cells, they were fixed for 10 min at room temperature with 1 M PHEM buffer, 3.7% formaldehyde, 0.2% Triton. Immunostaining of centrosomes was performed using

a monoclonal anti- γ -tubulin antibody (1/500 in PBS, 3% BSA; clone GTU-88; Sigma). Immunostaining of microtubules was performed using a monoclonal anti- α -tubulin antibody (1/1000 in PBS, 3% BSA; clone YL1/2; Chemicon). Immunostaining of HA-tag Aurora protein was performed with a monoclonal mouse anti-HA antibody (1/1000 in PBS, 3% BSA; Clone 16B12; Covance).

Samples were observed under a Leica DMIRE2 inverted confocal microscope or Leica DMRXA2 fluorescent microscope with a 63x (N.A. 1.32) lens and equipped with standard fluorescence filters. Images were acquired with a CoolSnapHQ camera (Roper Scientific) using Metamorph software (Universal Imaging) and prepared as single sections or maximum intensity projections before being processed in Photoshop 7.0 (v. 7.0; Adobe).

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ABBREVIATIONS

APC/C : Anaphase Promoting Complex/Cyclosome

GFP : Green Fluorescence Protein

INCENP : INner CENtromeR Protein

MCAK : Mitotic centromere-associated kinesin

TACC : Transforming Acidic Coiled Coil protein

TPX2 : Targetting Protein for Xklp2,

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Fig. 1

Comparison of Aurora A and B primary sequence between *Xenopus* and Human. (A) The N-terminal domain of AurA and AurB of both *Xenopus* and human are weakly conserved whereas (B) their catalytic domains are well conserved. For instance (C), for *Xenopus*, AurA and AurB shared 18% and 69% of homology between N-terminal and C-terminal domains respectively.

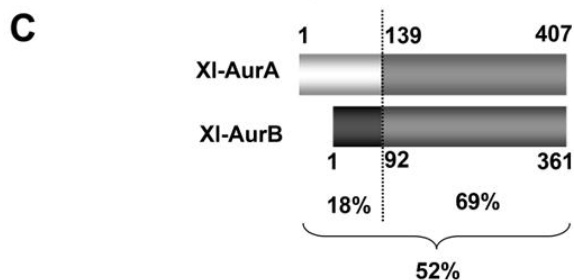
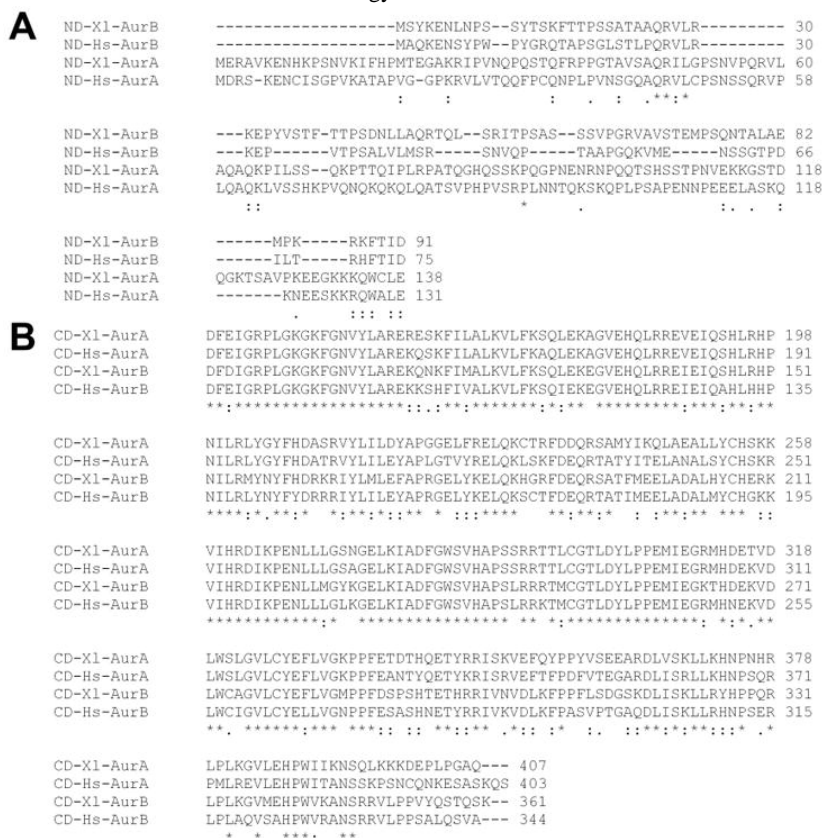


Fig. 2

Centrosomal localization of XI-AurA-GFP and CD-AurB-GFP proteins in interphase X12 cells. This panel shows (column (A): overlay, (B) gamma-tubulin immunofluorescence, (C) GFP and (D) DNA staining with DAPI within X12 cells transfected with the indicated vectors. Original magnification x63, scale bar is 10 μ m.

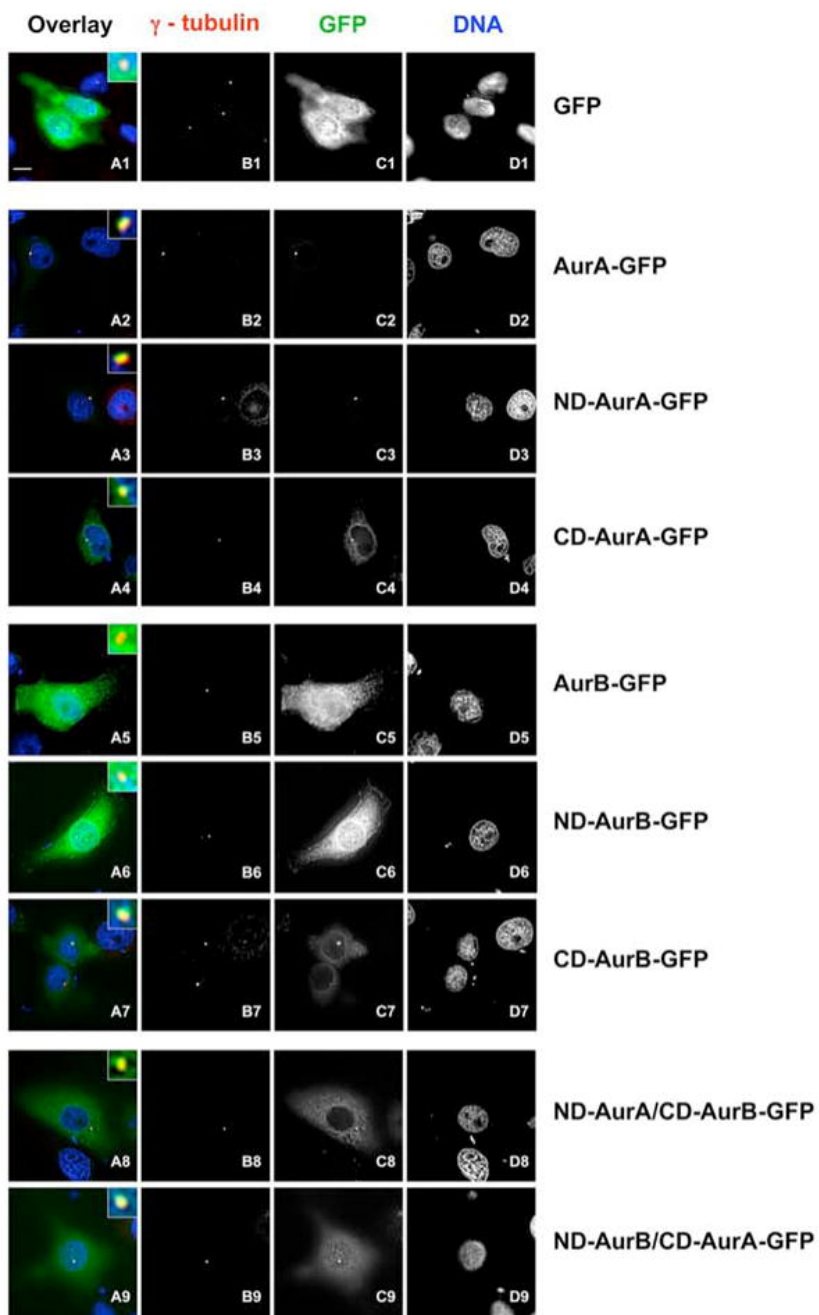


Fig. 3

Localisation of GFP-fusion Hs-AurA and Hs-AurB and chimera AurA/AurB in interphase HeLa cells. (A) Representative images of immunofluorescence used to count cells. Left panel: GFP direct observation or HA indirect immunostaining, Right panel: overlay of nucleus staining (DAPI in blue), GFP or HA in green and alpha-tubulin in red. Bar is 10 μ m, original magnification x63. (B) Percentage of GFP positive cells showing GFP-AurA and GFP-AurB staining localized as indicated (C) Percentage of HA positive cells showing HA-ND-AurB, HA-AB and HA-BA staining localized as indicated (D) Percentage of cells treated with Leptomycin for 24 h and showing GFP-AurA and GFP-AurB staining localized as indicated (E) Percentage of cells treated with Leptomycin for 24 h and showing HA-ND-AurB, HA-AB and HA-BA staining localized as indicated. (B)(C) Statistical tests (Mann-Whitney) were performed, for each vector, by comparison between each localization classes, * $p < 0.05$. (D)(E) Mann-Whitney test was calculated compared to the situation without Leptomycin B * $p < 0.05$, ^{ns} non statistically significant. Black is for mainly nuclear, grey for nuclear and cytoplasmic, and white for mainly cytoplasmic. HA-AB: HAtag-ND-AurA/CD-AurB; HA-BA: HAtag-ND-AurB/CD-AurA.

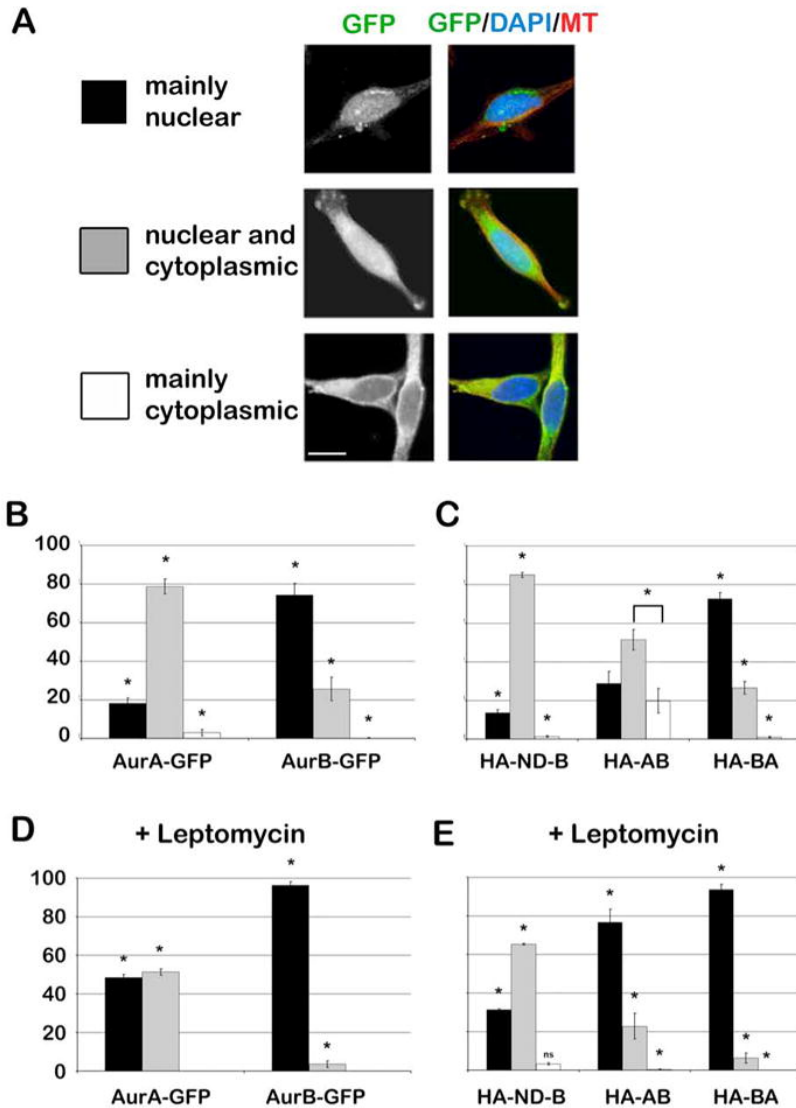


Fig. 4

Functional rescue of Hs-AurB knock-down in HeLa cells. (A) Representative images of H3-phosphoS10 immunofluorescence in interphase cells. Left panel: H3-phosphoS10 staining, right panel: merge with nucleus staining (DAPI) Original magnification x40. (B) Western Blot detecting AurB and β -tubulin in HeLa cells after AurB depletion by shRNA. (C) Count of H3-phosphoS10 positive cells in interphase. (D) Count of multinucleated cells. Mann-Whitney test was calculated compared to pSuper-shAurB transfected cells or as indicated by bracket. * $p < 0.05$, HA-AB: HA-tag-ND-AurA/CD-AurB; HA-BA: HA-tag-ND-AurB/CD-AurA.

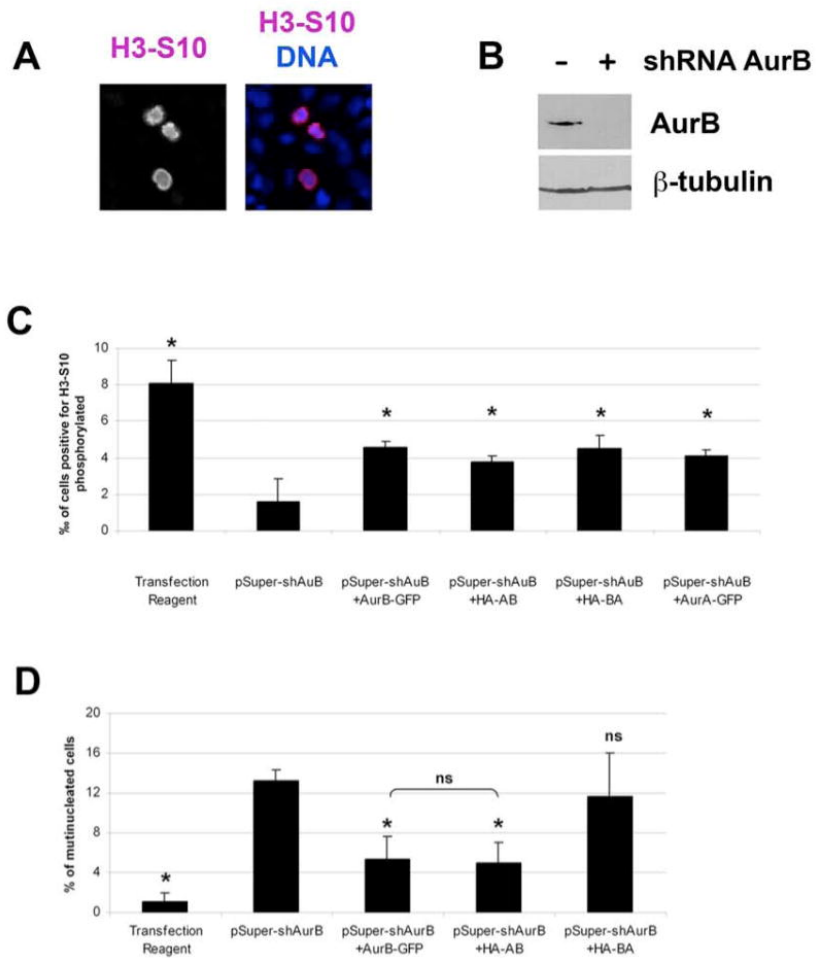


Table 1

Localisation of GFP-fusion proteins in X12 interphase cells.

Fusion protein	Localization	
	centrosomes	nucleus
AurA-GFP	89 ± 4%	0%
ND-AurA-GFP	80 ± 4% *	0%
CD-AurA-GFP	43 ± 2% *	0%
AurB-GFP	0%	96 ± 1%
ND-AurB-GFP	0%	97 ± 2% ^{ns}
CD-AurB-GFP	56 ± 7% #	0%
ND-AurA/CD-AurB-GFP	47 ± 7% * #	0%
ND-AurB/CD-AurA-GFP	46 ± 5% * #	96 ± 1% ^{ns}

* p<0.05 compared to full length AurA-GFP protein,

p<0.05 compared to full length AurB-GFP protein,

^{ns} non statistically significant compared to full length AurB-GFP protein, Mann-Whitney test, n=3.