Human TPX2 is required for targeting Aurora-A kinase to the spindle

Thomas A. Kufer, Herman H.W. Silljé, Roman Körner, Oliver J. Gruss, Patrick Meraldi, and Erich A. Nigg

1Max Planck Institute of Biochemistry, Department of Cell Biology, D-82152 Martinsried, Germany
2European Molecular Biology Laboratory, D-69117 Heidelberg, Germany

A urora-A is a serine-threonine kinase implicated in the assembly and maintenance of the mitotic spindle. Here we show that human Aurora-A binds to TPX2, a prominent component of the spindle apparatus. TPX2 was identified by mass spectrometry as a major protein coimmunoprecipitating specifically with Aurora-A from mitotic HeLa cell extracts. Conversely, Aurora-A could be detected in TPX2 immunoprecipitates. This indicates that subpopulations of these two proteins undergo complex formation in vivo. Binding studies demonstrated that the NH\textsubscript{2} terminus of TPX2 can directly interact with the COOH-terminal catalytic domain of Aurora-A. Although kinase activity was not required for this interaction, TPX2 was readily phosphorylated by Aurora-A. Upon siRNA-mediated elimination of TPX2 from cells, the association of Aurora-A with the spindle microtubules was abolished, although its association with spindle poles was unaffected. Conversely, depletion of Aurora-A by siRNA had no detectable influence on the localization of TPX2. We propose that human TPX2 is required for targeting Aurora-A kinase to the spindle apparatus. In turn, Aurora-A might regulate the function of TPX2 during spindle assembly.

Introduction

One of the most critical steps during cell cycle progression is the correct segregation of sister chromatids during mitosis. This process depends on the reorganization of the interphase microtubules (MTs)* into a highly dynamic bipolar array known as the mitotic spindle. In animal cells, spindle assembly is initiated at the time when centrosomes separate and involves changes in the functional properties of several MT-associated proteins (Karsenti and Vernos, 2001; Wittmann et al., 2001). In many cases, these changes are brought about by reversible phosphorylation, and several protein kinases and phosphatases undergo at least transient association with either centrosomes or spindle MTs (Nigg, 2001). However, little is known about the mechanisms that underlie the recruitment of these enzymes to the spindle apparatus, let alone their exact function and regulation during spindle assembly.

Prominent among the kinases implicated in the regulation of spindle-associated events during early mitosis is Aurora-A, a member of the Aurora family of serine-threonine kinases (Bischoff and Plowman, 1999; Nigg, 2001). Studies in several animal species concur to demonstrate that Aurora-A localizes to centrosomes and the spindle and that protein and activity levels peak at the G2/M transition (Bischoff and Plowman, 1999; Giet and Prigent, 1999). In Drosophila, the disruption of Aurora-A function causes centrosome disorganization and a reduction in the length of astral MTs (Glover et al., 1995; Giet et al., 2002). These phenotypes may relate to the ability of Aurora-A to interact with and phosphorylate D-TACC, a centrosome-associated protein implicated in the regulation of MT dynamics (Giet et al., 2002). Similarly, when Aurora-A (AIR-1) was eliminated by RNA-mediated interferences from Caenorhabditis elegans embryos, spindle assembly failed, and centrosome maturation, a process characterized by the recruitment of \(\gamma\)-tubulin and other components of the pericentriolar material, did not occur (Hannak et al., 2001). Biochemical studies performed in Xenopus egg extracts confirm an important role of Aurora-A in spindle assembly and/or maintenance (Roghi et al., 1998; Giet and Prigent, 2000). In particular, the kinesin-related motor protein Eg5 was identified as a candidate substrate of Aurora-A (Giet et al., 1999). In human cells, overexpression of Aurora-A was found to interfere with mitotic exit, causing tetraploidization and concomitant amplification of centrosomes (Meraldi et al., 2002). Furthermore, overexpression of Aurora-A resulted in neoplastic transformation of NIH-3T3 cells (Zhou et al., 1998). This is intriguing, since Aurora-A is frequently overexpressed in human tumors and the Aurora-A gene maps to a chromosomal locus.

*Abbreviations used in this paper: IVT, in vitro transcription/translation; KD, catalytically inactive; MT, microtubule; WT, wild-type.

Key words: spindle; mitosis; Aurora-A; TPX2; siRNA

Address correspondence to Erich A. Nigg, Max Planck Institute of Biochemistry, Dept. of Cell Biology, Am Klopferspitz 18a, D-82152 Martinsried, Germany. Tel.: 49-89-8578-3100. Fax: 49-89-8578-3102. E-mail: nigg@biochem.mpg.de

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(20q13.2–13.3) that is often amplified in colon, breast, and stomach cancers (Sen et al., 1997).

To better understand the role of Aurora-A in the regulation of spindle assembly and mitotic progression in human cells, we used a biochemical approach to search for proteins that specifically interact with Aurora-A. We report the identification of the human homologue of the spindle component TPX2 as a novel interactor and substrate of Aurora-A.

**Results and discussion**

**Identification of a TPX2–Aurora-A complex in mitotic cells**

To search for proteins interacting with Aurora-A, an antibody raised against a COOH-terminal peptide was used to immunoprecipitate Aurora-A from mitotic HeLa cell extracts. As shown by SDS-PAGE and Coomassie blue staining, the Aurora-A immunoprecipitate contained a protein of the expected size (45 kD) and additional proteins migrating at ~100 kD and >205 kD, respectively (Fig. 1 A, lane 2). None of these proteins were present when immunoprecipitations were performed with beads only (Fig. 1 A, lane 1) or in the presence of excess competing peptide (Fig. 1 A, lane 3). Mass spectrometry confirmed the identity of the 45 kD protein as Aurora-A (unpublished data). More importantly, it identified the 100-kD band as the human homologue of TPX2. By the use of a monoclonal antibody (Ki-S2), this protein had been shown previously to associate with the mitotic spindle (Heidebrecht et al., 1997). Furthermore, *Xenopus* TPX2 has been implicated in targeting the kinesin-related motor XKlp2 to the spindle (Wittmann et al., 1998) and has been shown to be essential for the formation of a robust bipolar spindle (Wittmann et al., 2000). Most recently, TPX2 was also identified as a critical component involved in promoting the RanGTP-regulated nucleation of MTs in the vicinity of chromosomes (Gruss et al., 2001).

To obtain information about the efficiency of complex formation between TPX2 and Aurora-A in mitotic cells, increasing amounts of Aurora-A immunoprecipitates were probed for the presence of TPX2 and vice versa (Fig. 1 B). The two proteins could readily be coimmunoprecipitated, regardless of whether anti–Aurora-A or anti-TPX2 antibodies were used for immunoprecipitation. No spurious precipitations were observed upon blocking the Aurora-A antibody with excess antigenic peptide or when using beads alone for control (Fig. 1 B, lanes 5). The comparison with the Western blot signals seen in total cell lysates (Fig. 1 B, lanes 1) indicates that, under the conditions used here, only a fraction (~5%) of TPX2 is recovered in a complex with Aurora-A and vice versa. What proportions of the two proteins associate in vivo is difficult to estimate, since the recovery of the complex is expected to depend on solubilization conditions. In any event, it appears likely that the in vivo formation of the TPX2–Aurora-A complex is regulated in a dynamic fashion.

**TPX2–Aurora-A interaction is direct and independent of kinase activity**

To determine whether the binding of TPX2 to Aurora-A depends on its kinase activity, GST-tagged constructs of wild-type (WT) and catalytically inactive (KD) recombinant Aurora-A kinases were immobilized on glutathione Sepharose and incubated with extracts prepared from mitotic HeLa cells. Proteins bound to Aurora-A were then analyzed by SDS-PAGE and Western blotting (Fig. 2 A). Coomassie blue staining (Fig. 2 A, top) revealed a prominent band migrating at 100 kD as the major interaction partner of Aurora-A (Fig. 2 A, top, arrowheads). This protein was identified as TPX2 by both Western blotting (Fig. 2 A, bottom)
and mass spectrometry (not depicted). No TPX2 was seen in control experiments using glutathione beads alone (Fig. 2 A, bottom, lanes 3) or in the Aurora-A input (Fig. 2 A, bottom, lanes 4). Most importantly, the extent of binding of TPX2 to WT or KD Aurora-A was virtually identical (Fig. 2 A, compare lanes 1 and 2). Thus, WT and KD Aurora-A have a similar affinity for TPX2.

To establish whether the interaction between Aurora-A and TPX2 was direct or indirect, in vitro binding assays were performed using immobilized recombinant Aurora-A kinases and soluble, recombinant TPX2 tagged with the IgG binding domain of protein A. As shown in Fig. 2 B, TPX2 bound to WT or KD Aurora-A in near stoichiometric amounts, but virtually no TPX2 bound to GST-coated control beads. To map the interacting domains of the two proteins, binding studies were then performed with in vitro transcribed/translated fragments of Aurora-A and TPX2 (Fig. 2 C). The two full-length proteins bound to each other as expected, and no binding occurred to control beads. Binding of full-length TPX2 was also observed with the catalytic, COOH-terminal part of Aurora-A but not with the NH$_2$-terminal domain (Fig. 2 C, top). In a converse type of experiment (Fig. 2 C, bottom), the NH$_2$-terminal 394 amino acids of TPX2 (N1) were able to bind full-length Aurora-A, and weak binding was also observed with the first 149 amino acids of TPX2 (N2). In contrast, no binding occurred with the COOH-terminal part (Fig. 2 C, C; residues 149–747). These data show that the catalytic domain of Aurora-A interacts directly with the NH$_2$-terminal domain of TPX2.

**TPX2 is a substrate of Aurora-A**

To investigate whether TPX2 is a substrate of Aurora-A, in vitro kinase assays were performed. Upon incubation of recombinant, protein A–tagged TPX2 with Aurora-A in the presence of [$\gamma$-32P]ATP, TPX2 was readily phosphorylated by WT Aurora-A but not the KD mutant (Fig. 2 D). No incorporation of 32P into the protein A tag was observed (not depicted). As determined by phosphoamino acid analysis, phosphorylation of TPX2 occurred on serine residues (Fig. 2 D). Human TPX2 has been reported previously to be phosphorylated in intact cells (Heidebrecht et al., 1997), and similarly, Xenopus TPX2 was shown to be phosphorylated specifically in M phase extracts (Wittmann et al., 2000). Although the kinase(s) responsible for these phosphorylations have not been identified previously, our present data identify Aurora-A as a likely regulator of TPX2. At present, we can only spec-
ulate on the physiological significance of TPX2 phosphorylation, but it is attractive to postulate that this modification could regulate the interaction of TPX2 with other spindle-associated proteins. In future studies, it will be important to map the phosphorylation sites within TPX2 and analyze the phosphorylation state of each site through the cell cycle.

**TPX2 and Aurora-A partially colocalize in vivo**

In previous studies, both TPX2 and Aurora-A have been localized independently to the spindle apparatus (Glover et al., 1995; Heidebrecht et al., 1997; Bischoff et al., 1998; Roghi et al., 1998; Schumacher et al., 1998; Wittmann et al., 2000). To compare the subcellular localization of these two proteins more directly, double indirect immunofluorescence microscopy was performed on HeLa and U2OS cells. In both cell types, a substantial colocalization of Aurora-A and TPX2 could be seen on the spindle apparatus. In contrast, spindle poles were strongly positive for Aurora-A but only weakly stained by anti-TPX2 antibodies (Fig. 3, top row). Similarly, centrosomes in G2 cells were positive for Aurora-A but not for TPX2 (Fig. 3, bottom row). Thus, although both TPX2 and Aurora-A localize to spindle MTs, only Aurora-A is prominent at centrosomes and spindle poles.

**TPX2 is required for recruiting Aurora-A to spindle MTs**

To explore the functional significance of the interaction between Aurora-A and TPX2 in HeLa cells, the two corresponding genes were silenced by siRNA (Elbashir et al., 2001). A 72-h treatment with a duplex oligonucleotide specific for Aurora-A resulted in a substantial, albeit not complete, depletion of the kinase (Fig. 4, A and B). As a result, a significant increase in apoptotic events could be seen (not depicted). The remaining Aurora-A–depleted cells did not arrest in the cell cycle and bipolar spindles did form, al-
though tubulin staining revealed that the poles were often broader than usual (not depicted). Of particular interest in the present context, depletion of the bulk of Aurora-A did not detectably interfere with the localization of TPX2 to spindle MTs (Fig. 4 B).

With the duplexes chosen here, the elimination of TPX2 by siRNA was more efficient than that of Aurora-A. The bulk of TPX2 had disappeared already after 36 h (Fig. 5, A and B), and by 48 h, the protein was almost undetectable (Fig. 5 C). Staining of MTs in TPX2-depleted cells showed that spindle formation was progressively impaired, and beginning at ~16 h after TPX2 siRNA treatment, many cells rounded up and arrested in a prometaphase-like stage (unpublished data). Most interestingly, the localization of Aurora-A was profoundly altered in TPX2-depleted cells. By 36 h of TPX2 depletion, Aurora-A was completely absent from MTs, although it could readily be detected at spindle poles (Fig. 5 B, middle row). This result could not be attributed to an absence of MTs, since these could readily be visualized by staining with anti-α-tubulin antibodies (Fig. 5 B, bottom row). By 48 h, spindle poles displayed increasing fragmentation, and again these fragmented poles stained positively for Aurora-A (Fig. 5 C). MT arrays were still present in these cells, but they were highly abnormal and, as observed already at the 36 h time point, devoid of Aurora-A (Fig. 5 C). Together, these results clearly indicate that TPX2 is specifically required for the association of Aurora-A with spindle MTs but not for its localization to spin-
dle poles. Conversely, the spindle association of TPX2 does not depend on the presence of Aurora-A.

In conclusion, we describe the identification of the spindle-associated MT-binding protein TPX2 as a novel interacting partner and candidate substrate of Aurora-A. In particular, we show that the association of Aurora-A with spindle MTs requires TPX2 but not vice versa. Also, Aurora-A is able to localize to spindle poles without TPX2. These findings indicate that TPX2 mediates specifically the dynamic interaction between Aurora-A and spindle MTs. Conversely, they raise the possibility that TPX2 function is regulated by Aurora-A kinase.

Materials and methods

Production of recombinant proteins and antibodies

Aurora-A WT and K162R CDNs (Meraldi et al., 2002) were GST tagged and subcloned into pVL13GST93 (Amersham Biosciences). Recombinant baculoviruses were produced using the BaculoGold kit according to the manufacturer (BD PharMingen). S9 cells were lysed in lysis buffer (LB; 10 mM Hepes, pH 7.7, 150 mM NaCl, 5 mM EGTA, 1% NP-40) containing phosphatase and protease inhibitors as described (Stucke et al., 2002). GST–Aurora-A was subsequently isolated using glutathione-Sepharose™ 4B beads (Amersham Biosciences) and washed with LB containing 300 mM NaCl then with kinase buffer (20 mM Hepes, pH 7.4, 150 mM KCl, 5 mM MnCl2, 5 mM NaF, 1 mM DTT). A rabbit antibody against human Aurora-A was raised using a COOH-terminal peptide (CQNKESASKQS) of human Aurora-A coupled to keyhole limpet hemocyanin as antigen. Antibodies were immunopurified on the antigensic peptide covalently bound to activated thiopropyl Sepharose™ 4B beads (Amersham Biosciences) and washed with LB containing 300 mM NaCl and then with kinase buffer (20 mM Hepes, pH 7.4, 150 mM KCl, 5 mM MnCl2, 5 mM NaF, 1 mM DTT). Power pose aurora-targeted siRNA were affinity purified on the antigen covalently linked to Protein G Sepharose (Bio-Rad Laboratories).

Cell lysates, immunoprecipitations, and immunoblotting

Cell extracts from nocodazole (100 ng/ml) arrested mitotic HeLa S3 cells were prepared as described previously (Stucke et al., 2002). For immunoprecipitations, cell extracts were incubated for 1 h with Aurora-A antibody followed by a 3-h incubation with Anti-Prep™ Protein A beads (Bio-Rad Laboratories). Beads were subsequently washed three times in LS buffer (50 mM Tris, pH 8.0, 150 mM NaCl, 0.1% NP-40) and boiled in SDS-PAGE sample buffer. As a negative control, the antibody was incubated for 0.1 mM ATP for 30 min with a 100-fold excess of ATP before reactions were started by the addition of SDS-PAGE sample buffer. Autoradiograms were made using a PhosphorImager (Fuji Film).

In vitro protein binding and kinase assays

In vitro binding assays were performed by incubating recombinant GST-tagged Aurora-A bound to glutathione-Sepharose with soluble recombinant TPX2 for 1 h at 30°C in kinase buffer containing 10 μM ATP. Subsequently, the beads were washed three times in LS buffer, and proteins were analyzed by SDS-PAGE followed by Coomassie blue staining. For in vitro kinase assays, recombinant Aurora-A WT and KD bound to glutathione-Sepharose were incubated with recombinant TPX2 in kinase buffer including 0.1 μCi [γ-32P]ATP and 10 μM ATP for 30 min at 30°C before reactions were stopped by the addition of SDS-PAGE sample buffer. Autoradiographs were made using a PhosphorImager (Fuji Film).

Phosphoamino acid analysis of in vitro–phosphorylated TPX2 protein was performed by acid hydrolysis and thin layer chromatography as described (Boyle et al., 1991). Fragments of TPX2 and Aurora-A gene were generated by PCR and subcloned into the pcDNA3.1(+) myc3 (Invitrogen) vector. In vitro transcription/translation (IVT) was performed in the presence of [-35S]methionine using TnT-coupled reticulocyte lysate (Promega) and T7 RNA polymerase (Promega). IVT products were diluted three times in PBS and incubated for 3 h at 4°C with an excess of recombinant TPX2 bound to Ni-Sepharose (QIAGEN) or GST–Aurora-A bound to glutathione beads. Beads were washed four times with LS buffer and analyzed by SDS-PAGE followed by autoradiography.

Mass spectrometry

Proteins were in-gel-digested with sequencing-grade porcine trypsin (Promega) essentially as described (Shevchenko et al., 1996). Peptide mass fingerprinting was performed on the extracted peptides using a MALDI-TOF instrument (Reflex III; Bruker) and probability-based database searching (Perkins et al., 1999).

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