

Canoe binds RanGTP to promote Pins^{TPR}/Mud-mediated spindle orientation

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Regulated spindle orientation maintains epithelial tissue integrity and stem cell asymmetric cell division. In *Drosophila melanogaster* neural stem cells (neuroblasts), the scaffolding protein Canoe (Afadin/Af-6 in mammals) regulates spindle orientation, but its protein interaction partners and mechanism of action are unknown. In this paper, we use our recently developed induced cell polarity system to dissect the molecular mechanism of Canoe-mediated spindle orientation. We show that a previously uncharacterized portion of Canoe

directly binds the Partner of Inscuteable (Pins) tetratricopeptide repeat (TPR) domain. The Canoe–Pins^{TPR} interaction recruits Canoe to the cell cortex and is required for activation of the Pins^{TPR}–Mud (nuclear mitotic apparatus in mammals) spindle orientation pathway. We show that the Canoe Ras-association (RA) domains directly bind RanGTP and that both the Canoe^{RA} domains and RanGTP are required to recruit Mud to the cortex and activate the Pins/Mud/dynein spindle orientation pathway.

Introduction

Spindle orientation is essential to maintain epithelial integrity; planar spindle orientation results in both daughter cells maintaining apical junctions and remaining part of the epithelium, whereas apical/basal spindle orientation can lead to the loss of the basal daughter cell from the epithelium (Lu et al., 2001; Egger et al., 2007). Spindle orientation is also important during asymmetric cell division of stem, progenitor, and embryonic cells; when the spindle orients along an axis of intrinsic or extrinsic polarity, it will generate two different daughter cells, but, when the spindle aligns perpendicular to the axis of polarity, it will generate two identical daughter cells (Cabernard and Doe, 2009; Siller and Doe, 2009). Proper spindle orientation may even be necessary to prevent tumorigenesis (Gonzalez, 2007; Fleming et al., 2009; Quyn et al., 2010). Thus, it is essential to understand the molecular mechanisms that regulate spindle orientation, particularly those that use evolutionarily conserved proteins and pathways, to help direct stem cell lineages and potentially treat pathological conditions caused by aberrant spindle orientation.

Drosophila melanogaster neural stem cells (neuroblasts) provide an excellent system for studying spindle orientation

during asymmetric cell division. Neuroblasts have an apical/basal polarity and orient their mitotic spindle along this cortical polarity axis to generate distinct apical and basal daughter cells. The apical neuroblast inherits fate determinants responsible for neuroblast self-renewal, whereas the basal daughter cell inherits fate determinants responsible for neuronal/glial differentiation (Doe, 2008). Genetic studies have identified proteins that regulate spindle orientation during asymmetric cell division, including the apically localized proteins Inscuteable, Partner of Inscuteable (Pins; LGN/AGS-3 in mammals), Mushroom body defect (Mud; nuclear mitotic apparatus [NuMA] in mammals), Discs large (Dlg), and Gα_i (Doe, 2008). In addition, many proteins that are not asymmetrically localized are required for spindle orientation, including the dynein complex and the Aurora A and Polo kinases (Siller and Doe, 2009).

We have recently developed an induced cell polarity/spindle orientation system using the normally apolar S2 cell line to biochemically dissect *Drosophila* and vertebrate spindle orientation (Johnston et al., 2009; Ségalen et al., 2010). Using this system to characterize *Drosophila* spindle orientation, we showed that cortical Pins nucleates two spindle orientation pathways: (1) the Pins^{LINKER} domain is phosphorylated

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Abbreviations used in this paper: NuMA, nuclear mitotic apparatus; PBD, Pins-binding domain; Pins, Partner of Inscuteable; RA, Ras-association; TIR, TPR-interacting peptide; TPR, tetratricopeptide repeat; UTR, untranslated region.

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A Canoe protein structure: RA (blue), RA (blue), FHA (light blue), DIL (green), PDZ (green), F-actin (grey).

B Pins protein structure: TPR (red), LINKER (orange), GoLocos (yellow, numbered 1, 2, 3).

C-H Fluorescence microscopy images of ommatidia. C: Canoe^{FL} (green). D: Pins^{FL} (red). E: Pins^{FL} (green). F: Pins^{FL}TPR+LINKER (green). G: Pins^{FL}TPR (green). H: Pins^{FL}LINKER+G (green). White arrowheads in E-H point to the ommatidial core.

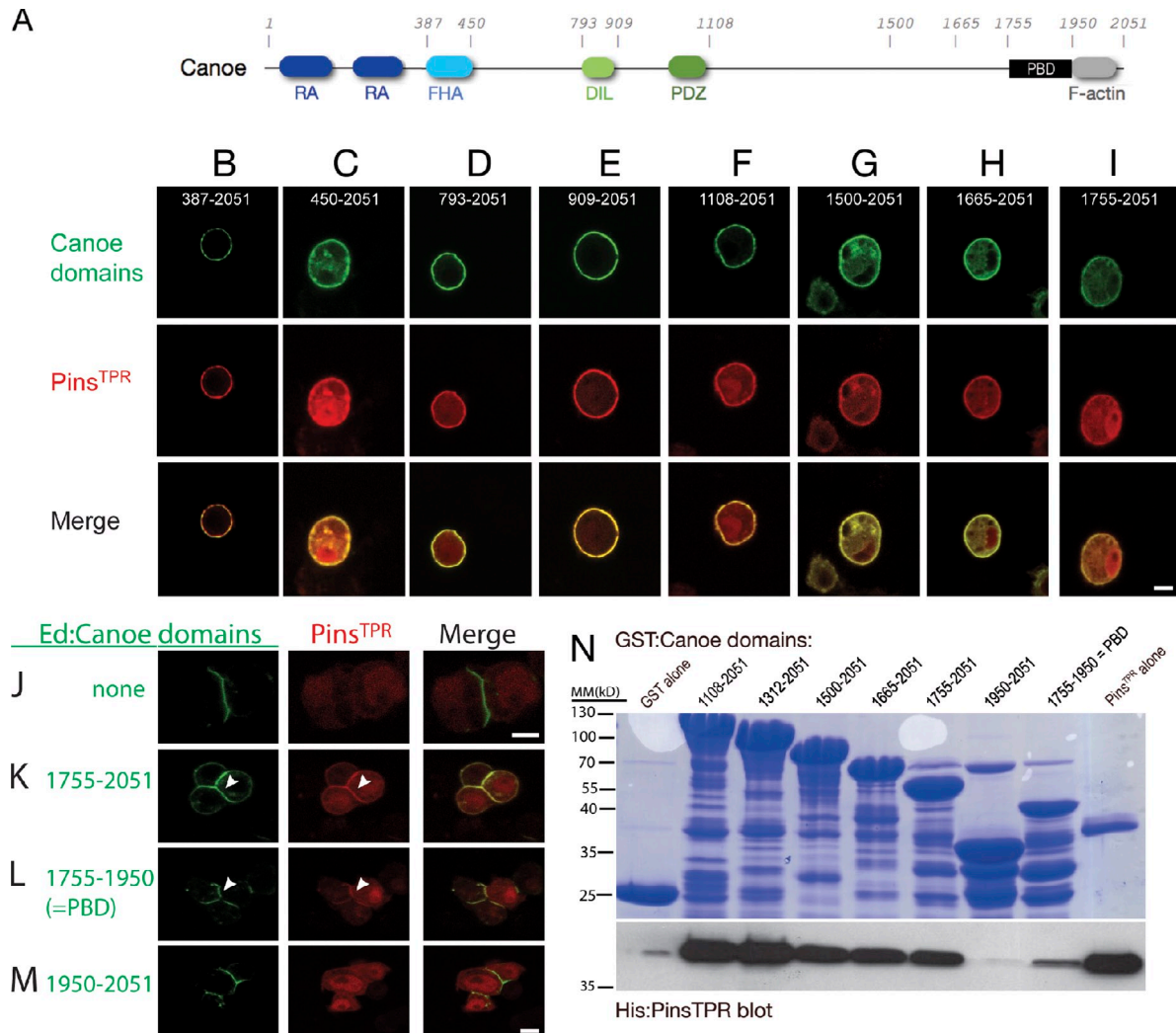


Figure 2. Canoe¹⁷⁵⁵⁻¹⁹⁵⁰ is necessary and sufficient for Pins^{TPR} binding. (A) Domain architecture of full-length Canoe protein. Amino acids are shown in gray. DIL, Dilute; FHA, Forkhead. (B–I) Coexpression of Canoe and Pins in S2 cells. All tested GFP:Canoe N-terminal-truncated proteins (numbers represent amino acids present in protein) recruit Cherry:Pins^{TPR} to the cortex. (J–M) Coexpression of Ed:GFP:Canoe domains with Cherry:Pins^{TPR} in S2 cells. Only Canoe proteins containing the 1,755–1,950 domain recruited Pins^{TPR} to the cortex (arrowheads). (N) Canoe^{1,755–1,950} directly binds the Pins^{TPR} domain. GST:Canoe fragments were incubated with His-tagged Pins^{TPR} protein and probed for Canoe-dependent binding of Pins^{TPR}. (top) Coomassie stain of purified GST:Canoe protein fragments or His-tagged Pins^{TPR} protein (rightmost lane). (bottom) Western blot to detect bound Pins^{TPR}. Bars, 5 μ m.

In contrast, all proteins containing the Canoe^{PBD} were able to bind Pins^{TPR}, as was the Canoe^{PBD} alone (Fig. 2 N). We conclude that the Canoe^{PBD} directly binds the Pins^{TPR} domain and suggest that this interaction is responsible for the cortical Pins–Canoe interaction in S2 cells (Figs. 1 and 2) and mitotic neuroblasts (Speicher et al., 2008).

Canoe is required for Pins^{TPR}/Mud-mediated spindle orientation

Based on the observed binding of Canoe to the Pins^{TPR} domain, we next tested whether Canoe is part of the Pins^{TPR}/Mud/dynein spindle orientation pathway. To assay spindle orientation in S2 cells, we need to create a localized cortical domain of protein so we can determine whether the spindle aligns with this domain. To do this, we used our recently developed induced cell polarity/spindle orientation assay (Johnston et al., 2009). In this assay, expression of the Ed transmembrane cell adhesion

molecule in S2 cells results in clustering of the Ed protein to the site of cell contact as a result of homophilic adhesion of the extracellular Ed domain, creating a polarized distribution of Ed at the cell cortex. Fusion of any test protein or protein domain to the C terminus of Ed allows us to create a cortical crescent of the test protein and assay for its function in spindle orientation during mitosis. For example, Ed:Pins^{TPR+LINKER} gives excellent spindle orientation of $<15^\circ$; Ed:Pins^{LINKER} only gives partial spindle orientation of $\sim 30^\circ$ as a result of the absence of the TPR part of the pathway, and the Ed:GFP control gives random spindle orientation of $\sim 45^\circ$ (Johnston et al., 2009).

Here, we use this assay to test the role of Canoe in Pins-mediated spindle orientation. We confirm that Ed:GFP alone had no spindle orientation activity ($49 \pm 30^\circ$; quantified in Fig. 3 H; Fig. 3 A), whereas Ed:Pins^{TPR+LINKER} showed excellent spindle orientation ($13 \pm 8^\circ$; quantified in Fig. 3 H; Fig. 3 B). RNAi knockdown of endogenous Canoe in S2 cells

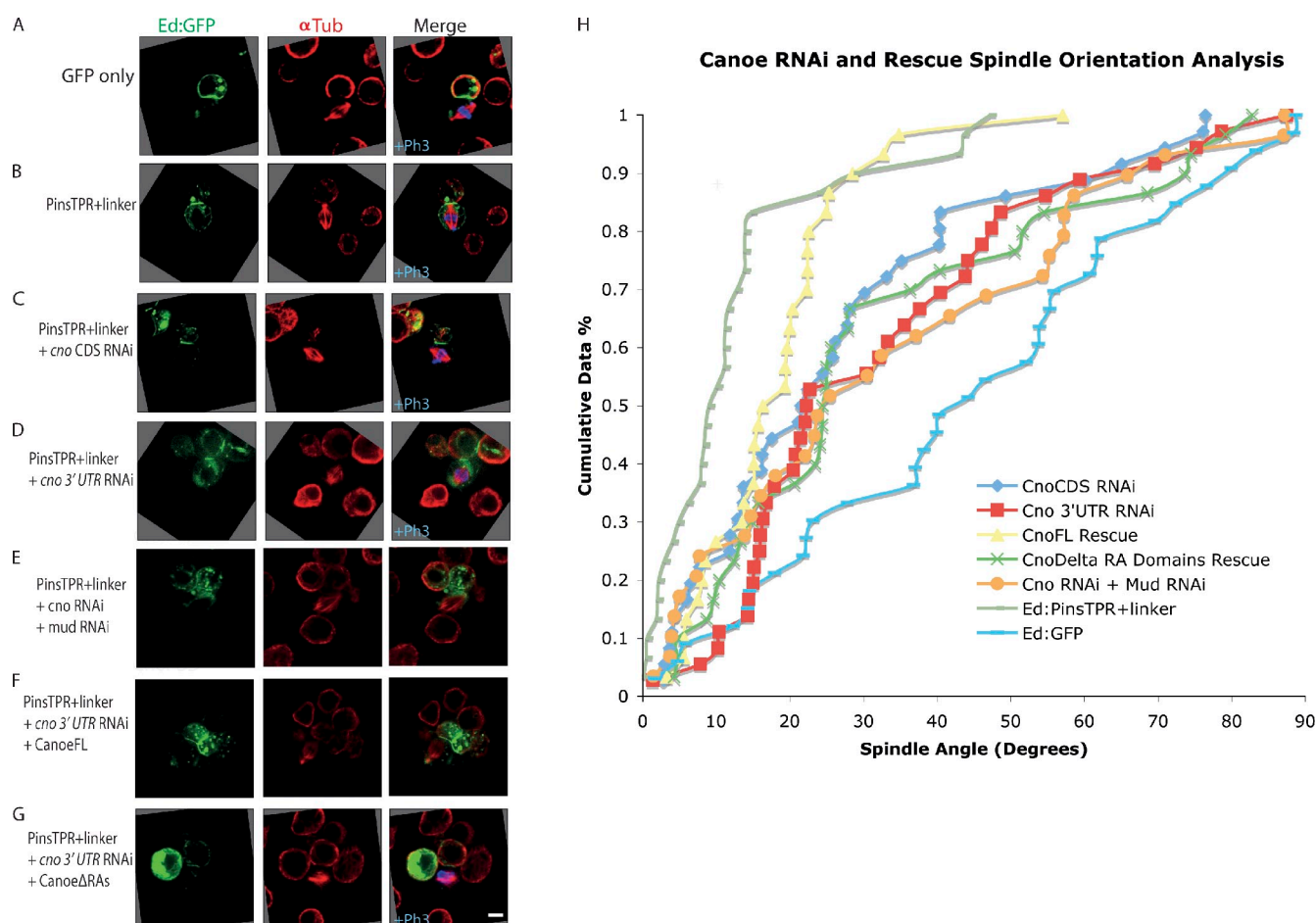


Figure 3. Canoe regulates Pins-mediated spindle orientation. (A–G) S2 cell spindle orientation assay. Representative images are shown, and the quantification of each experiment is shown in H. Ed:GFP or Ed:GFP:Pins proteins were induced to form cortical crescents by cell aggregation, and the angle of the mitotic spindle was measured relative to the center of the cortical crescent. Pins cortical localization (green), mitotic spindle (α -tubulin [α Tub]), and merge (in some cases also showing the mitotic DNA marker phospho-histone H3 [PH3]) are shown. CDS, coding sequence. Bar, 5 μ m. (H) Quantification of experiments shown in A–G depicted as a cumulative plot. Random spindle orientation is a diagonal line (e.g., Ed:GFP); optimal spindle orientation is reflected in a leftward shift in the plot (e.g., Ed:Pins^{TPR+LINKER}), and partial spindle orientation falls in between. The key is an abbreviated version of the experiments shown on the left in A–G. CnoCDS RNAi, $n = 36$; Cno 3' UTR RNAi, $n = 36$; CnoFL Rescue, $n = 30$; CnoDelta RA Domains Rescue, $n = 30$; Cno RNAi + Mud RNAi, $n = 29$; Ed:PinsTPR+linker, $n = 30$; Ed:GFP, $n = 33$.

expressing Ed:Pins^{TPR+LINKER} resulted in partial spindle orientation ($27 \pm 21^\circ$; quantified in Fig. 3 H; Fig. 3, C and D), as expected for a functional Pins^{LINKER} pathway in the absence of the Pins^{TPR}/Mud/dynein pathway (Johnston et al., 2009). *canoe* RNAi reduced endogenous protein levels (Fig. S2) and did not result in mitotic spindle abnormalities (Fig. S1), suggesting that the spindle orientation phenotypes were not caused by a decrease in astral microtubules or spindle microtubules. Importantly, double RNAi knockdown of *canoe* and *mud* together did not significantly enhance the *canoe* single RNAi phenotype ($33 \pm 25^\circ$; quantified in Fig. 3 H; Fig. 3 E), consistent with both proteins acting in the same pathway. We conclude that Canoe is part of the Pins^{TPR}/Mud/dynein spindle orientation pathway.

Canoe^{RA} domains are required for spindle orientation

To assess what protein domains of Canoe are necessary and sufficient for it to stimulate Pins/Mud-mediated spindle

orientation, we performed spindle orientation rescue assays with Canoe deletion constructs. In this assay, Ed:Pins^{TPR+LINKER} and a Canoe deletion allele were coexpressed in S2 cells while endogenous Canoe levels were reduced using RNAi targeted to the *canoe* 3' untranslated region (UTR). The *canoe* 3' UTR RNAi probe reduced Pins-mediated spindle orientation similar to the *canoe* coding sequence RNAi probe ($32 \pm 22^\circ$; quantified in Fig. 3 H; Fig. 3, C and D). Expression of a full-length Canoe protein in this background rescued spindle orientation to near wild-type levels ($18 \pm 11^\circ$; quantified in Fig. 3 H; Fig. 3 F). We then coexpressed Ed:Pins^{TPR+LINKER} with Canoe deletion alleles in a *canoe* 3' UTR RNAi background. We reasoned that the truncation of the necessary domains responsible for mediating spindle orientation would fail to rescue Pins-mediated spindle orientation. Interestingly, deletion of both RA domains failed to rescue Pins-mediated spindle orientation ($32 \pm 24^\circ$; quantified in Fig. 3 H; Fig. 3 G). We conclude that the Canoe^{RA} domains are required for spindle orientation.

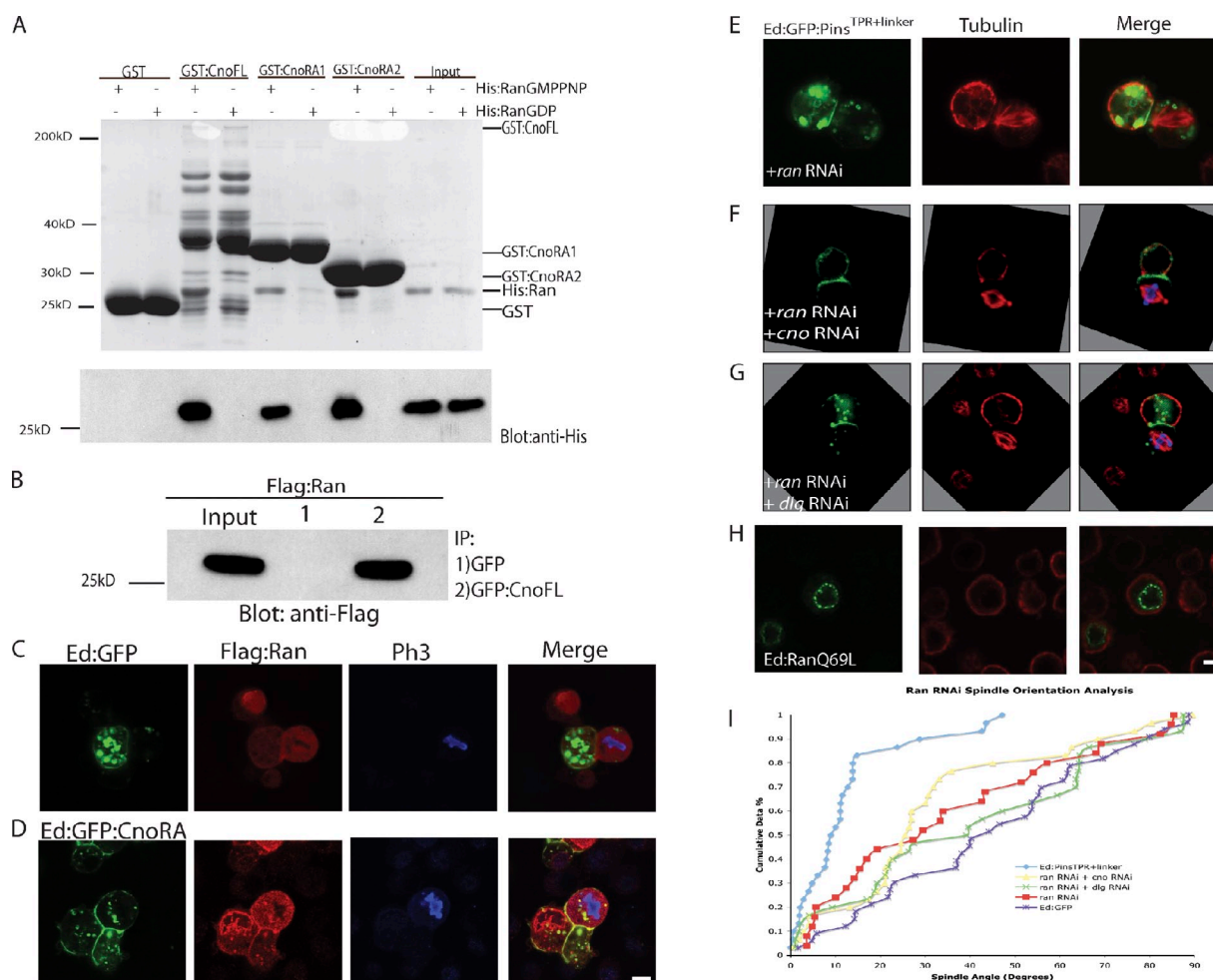


Figure 4. RanGTP binds Canoe^{RA} domains and is required for Pins^{TPR}/Mud-mediated spindle orientation. (A) GST:Canoe domains incubated with His-tagged Ran protein loaded with GMPNP or GDP probed for Ran binding. Ran directly binds the Canoe^{RA} domains in a GTP-dependent manner. (top) Coomassie stain of purified GST:Canoe protein fragments or His-tagged Ran protein (rightmost lane). (bottom) Western blot to detect bound Ran. (B) Ran immunoprecipitates (IP) with Canoe. S2 lysates expressing GFP or GFP:Canoe^{FL} and Flag:Ran were incubated with an anti-GFP antibody and blotted with anti-Flag antibody. (C and D) Canoe^{RA}-dependent cortical localization of Ran. Ed:GFP or Ed:GFP:Cno^{RA} was used to form cortical crescents by cell aggregation, and the localization of Flag:Ran was visualized in mitotic cells. Ed cortical crescents (green), Ran (anti-Flag; red), mitosis marker (Ph3; blue), and merge are shown. *n* = 20 cell interfaces. Bar, 5 μ m. (E–H) S2 cell spindle orientation assay. Ed:GFP:Pins protein was induced to form a cortical crescent by cell aggregation, and the angle of the mitotic spindle was measured relative to the center of the cortical crescent. Ed:Ran or Pins cortical localization (green), mitotic spindle (α -tubulin; red), and merge (in some cases also showing the mitotic DNA marker phospho-histone H3 [PH3]) are shown. Bar, 5 μ m. (I) Quantification of a negative control (Ed:GFP; Fig. 3 A) and a positive control (Ed:Pins^{TPR+LINKER}; Fig. 3 B) and experiments shown in Fig. 4 (E–H) shown as a cumulative plot (see Fig. 3 legend for details). Ed:Pins^{TPR+linker}, *n* = 30; ran RNAi + cno RNAi, *n* = 30; ran RNAi + dlg RNAi, *n* = 30; ran RNAi, *n* = 25; Ed:GFP, *n* = 33.

RanGTP binds Canoe^{RA} domains and is required for Pins^{TPR}/Mud-mediated spindle orientation

RA domains are known to bind small monomeric GTPases such as Ran, Ras, and Rap1 (Kuriyama et al., 1996; Boettner et al., 2003; Dallol et al., 2009). Because Ran is the small GTPase most closely linked to the mitotic spindle assembly and function (Kalab and Heald, 2008), we tested whether Ran binds Canoe RA domains and, if so, whether it regulates spindle orientation. We made GST fusions with full-length Canoe or the individual RA1 and RA2 domains and tested whether they could interact with purified Ran loaded with the GTP analogue GMPNP or GDP. We found that RanGTP preferentially bound Canoe full-length (Canoe^{FL}), RA1, or RA2 proteins (Fig. 4 A, third, fifth, and seventh lanes) compared with RanGDP (Fig. 4 A, fourth,

sixth, and eighth lanes). The negative control GST alone did not bind appreciable RanGTP nor RanGDP (Fig. 4, first and second lanes). Furthermore, Ran coimmunoprecipitated with Canoe from S2 cells and also localized to Ed:Canoe^{RA} crescents (Fig. 4, B–D). We conclude that the Canoe RA domains can interact directly with GTP-loaded Ran.

Next, we asked whether Ran is necessary for Pins-mediated spindle orientation. To address this question, we performed RNAi knockdown of endogenous Ran in S2 cells expressing Ed:Pins^{TPR+LINKER} and found that spindle orientation was reduced to $34 \pm 27^\circ$ (quantified in Fig. 4 I; Fig. 4 E). *ran* RNAi reduced endogenous protein levels without affecting centrosome number or spindle morphology (Figs. S1 and S2). The effect of *ran* RNAi on spindle orientation is similar to the *canoe* RNAi phenotype as well as to the amount of spindle orientation

provided by the Pins^{LINKER} pathway alone after elimination of the Pins^{TPR} pathway components Mud, dynein, or Lis1 (Johnston et al., 2009). To test whether the effects of Ran on spindle orientation are specific to the Pins^{TPR}/Mud pathway, we performed double RNAi knockdowns of *canoe* and *ran* in S2 cells expressing Ed:Pins^{TPR+LINKER} and found that spindle orientation was reduced similar to *canoe* RNAi alone ($31 \pm 23^\circ$; quantified in Fig. 4 I; Fig. 4 F), consistent with Ran and Canoe acting in the same pathway. In contrast, double RNAi knockdowns of *ran* and the Pins^{LINKER} pathway component *dlg* led to a more severe spindle orientation phenotype than *ran* RNAi alone ($40 \pm 28^\circ$; quantified in Fig. 4 I; Fig. 4 G), consistent with each gene acting in different pathways. To see whether Ran is sufficient to orient the mitotic spindle, we expressed Ed:Ran^{Q69L} (a RanGTP mimic) in S2 cells but were unable to assay its function in spindle orientation because the transmembrane-tethered Ed:Ran protein was trapped in vesicles around the nucleus (Fig. 4 H). We conclude that RanGTP directly binds the Canoe^{RA} domains and is required in a Pins^{TPR}/Canoe/Mud spindle orientation pathway.

Canoe and RanGTP are required for Mud recruitment to Pins cortical crescents

How does Canoe/RanGTP promote activity of the Pins^{TPR}/Mud spindle orientation pathway? A prior study showed that *canoe* mutants lack Mud localization to the Pins cortical crescent (Speicher et al., 2008), so we tested whether Canoe is required for Pins/Mud colocalization in our S2 cell assay. We confirm that endogenous Mud is recruited to Ed:Pins^{TPR+LINKER} crescents (Fig. 5 A; Johnston et al., 2009) but that Mud failed to localize with Ed:Pins^{TPR+LINKER} crescents after *canoe* RNAi (Fig. 5 B). Similarly, Mud failed to localize to Ed:Pins^{TPR+LINKER} crescents after *ran* RNAi (Fig. 5 C). To assess whether the Canoe–Ran interaction is necessary for Mud recruitment to Pins crescents, we performed rescue assays with full-length Canoe and RA domain deletion constructs. The full-length Canoe construct rescued endogenous Mud recruitment to Pins crescents, whereas deletion of both RA domains failed to recruit endogenous Mud (Fig. 5, D and E). The requirement for Canoe/RanGTP is specific to the Pins^{TPR} pathway because *canoe* RNAi does not affect endogenous Dlg recruitment to the Pins^{LINKER} (Fig. 5, F–H). We conclude that the Canoe RA domains/RanGTP are required for recruitment of endogenous Mud to cortical Pins^{TPR} crescents and the activation of the Pins^{TPR}/Mud spindle orientation pathway.

How might Canoe/RanGTP promote Mud recruitment to the Pins cortical domain? One model is that Ran sequesters importin- α/β away from the Mud NLS, thereby allowing Mud to interact with Pins. This model is based on the observation that RanGTP inhibits binding of importin- β to the NLS of NuMA (the mammalian orthologue of Mud), increasing the pool of NuMA available to promote spindle formation (Nachury et al., 2001; Wiese et al., 2001). The model predicts that Mud can bind importin- α/β and that this binding prevents Mud/Pins association. Consistent with the model, importin- β /Mud were coimmunoprecipitated from S2 cell lysates (Fig. 5 K), and a GST:Mud fragment containing the adjacent Mud TPR-interacting

peptide (TIP)–NLS domains (GST:Mud^{TIP-NLS}) could bind purified importin- β in the presence of importin- α (Fig. 5 K). However, we found that increasing the concentration of purified importin- α/β did not effect the amount of Pins pulled down with GST:Mud^{TIP-NLS} (Fig. 5 K, first through third and fifth through ninth lanes), which does not support a model in which Ran must sequester importin- α/β to allow Pins/Mud binding. Furthermore, a GFP-tagged Mud^{TIP-NLS} fragment localized to Ed:Pins^{TPR+LINKER} crescents independently of the Canoe/Ran pathway (Fig. 5, I and J), showing that the Mud NLS is not involved in the Canoe/Ran-regulated localization mechanism. Interestingly, Canoe/RanGTP regulation is required for recruitment of full-length endogenous Mud (Fig. 5 B) but not for the recruitment of the smaller Mud^{TIP-NLS} fragment (Fig. 5, I and J); this indicates that Canoe/RanGTP normally functions by blocking an unknown inhibitor of the Mud–Pins^{TPR} interaction.

In conclusion, we have characterized the molecular mechanism by which Canoe regulates spindle orientation. We identified a region of Canoe (amino acids 1,755–1,950) that directly interacted with the Pins^{TPR} domain and showed that these domains are necessary and sufficient for Canoe–Pins association. We showed that the Canoe RA domains bind directly to RanGTP, that both the Canoe RA domains and Ran are necessary for the Pins^{TPR}/Mud spindle orientation pathway, and that Canoe/RanGTP acts by promoting Mud recruitment to the cortical Pins domain. All of the proteins in the Pins/Canoe/Ran/Mud pathway are conserved from flies to mammals, suggesting that this pathway could be widely used to regulate spindle orientation.

Materials and methods

Construction of transgenes and S2 expression

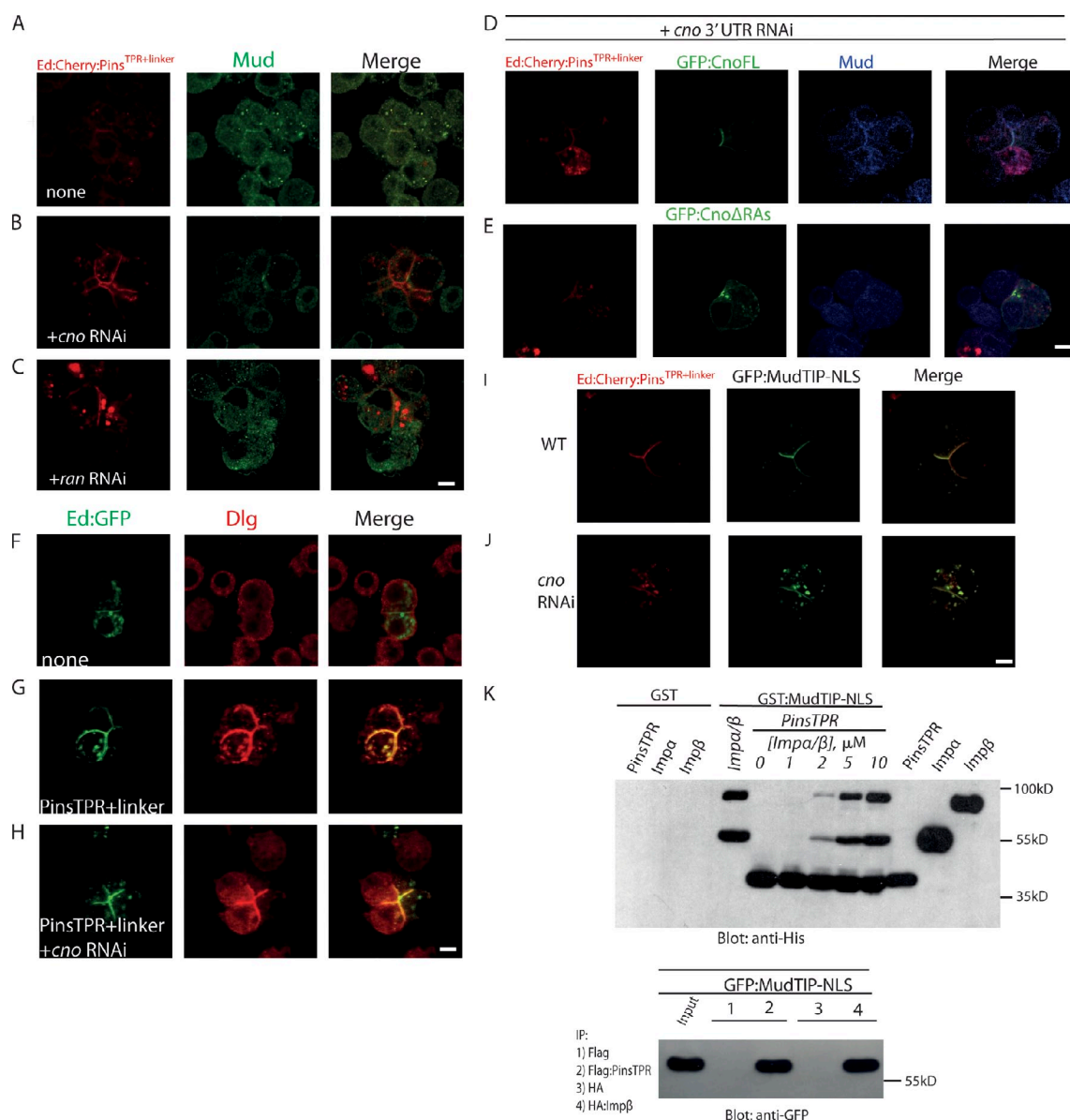
Echinoid:GFP transgenes were generated within the pMT expression vector as previously described (Johnston et al., 2009; Ségalen et al., 2010); *canoe* coding sequences were cloned downstream of GFP using 5' NheI and 3' NotI restriction sites. Pins^{TPR+LINKER} and Ran coding sequences were cloned downstream of GFP using 5' BglII and 3' SalI restriction sites. GFP: Canoe, Cherry:Pins, Flag:Ran, HA:importin- β , and GFP:Mud were cloned into pMT expression vector alone. *Drosophila* Schneider (S2) cells were maintained in Schneider's medium with 10% FBS at room temperature. Approximately 3×10^6 cells were seeded per well in a 6-well plate and transfected with 0.5–0.8 μ g total DNA per well using the Effectene manufacturer's protocol and incubated overnight, and gene expression was induced by adding 0.5 mM CuSO₄ for 24 h. Cells were then collected, resuspended in fresh media, and placed in a 6-well plate, and cell clustering was induced by shaking at ~ 175 rpm for 2–3 h.

RNAi design and treatment

RNAi primers were designed using T7 promoter tags and used to PCR amplify ~ 300 –500 bp of *canoe* or *ran* coding sequence. Transcription was performed using the Megascript T7 kit (Invitrogen) according to the manufacturer's protocol. Transfected S2 cells were seeded in 1 ml of serum-free Schneider's media in a 6-well dish at 10^6 cells per well, and 120 μ l RNA was incubated for 1 h, 2 ml of serum-containing growth media was added, and, 3 d later, expression was induced with CuSO₄.

Immunohistochemistry, imaging, and spindle angle measurements

200 μ l of clustered cells was seeded on 12-mm-diameter glass coverslips in a 24-well plate, allowed to adhere for 1 h, and encouraged to enter mitosis by addition of 300 μ l of fresh growth media for 3–4 h. Adherent cells were fixed for 20 min with 4% formaldehyde in PBS followed by three rinses of wash buffer (0.1% saponin in PBS) and two rinses of block buffer (0.1% saponin and 1% BSA in PBS). The primary antibodies used were mouse anti-tubulin (1:2,000; Sigma-Aldrich), rabbit anti-phosphohistone-3 (1:1,000; Millipore), mouse anti-Dlg (1:250; Developmental Studies Hybridoma Bank),



mouse anti-FLAG (1:500; Sigma-Aldrich), rabbit anti-Mud (1:500; a gift from Y. Bellaiche, Institut Curie, Paris, France), and mouse anti-γ-tubulin (1:1,000, Sigma-Aldrich). Coverslips were incubated with primary antibodies at 4°C overnight, rinsed three times in block buffer, incubated with species-specific fluorochrome-conjugated secondary antibodies (Invitrogen) diluted in 1:200 in block buffer at room temperature for 2 h, rinsed three times with washing buffer, mounted in antifade reagent (Bio-Rad Laboratories), and assembled in Illustrator and Photoshop (Adobe). Raw images with a maximum pixel intensity of <100 were adjusted using the Photoshop Levels command to use the entire 1–256-pixel intensity range; in all cases, the entire panel was subjected to the same processing. Images

were taken with a confocal microscope (SP2; Leica) using an oil immersion 60× 1.4 NA objective. Spindle angles were defined as the angle between a line drawn perpendicular to the center of the Ed crescent and a line connecting the spindle poles.

Biochemistry

GST:Canoe and GST:Mud fusions were generated by cloning Canoe into the pGEX-4T1 vector using the 5' EcoRI and 3' NotI restriction sites and 5' BamHI and 3' SalI sites, respectively. Purified 6×His-tagged Pins and Ran proteins were generated by cloning Pins and Ran into the pBH vector using the 5' BglII and 3' SalI restriction sites. Nucleotide exchange of

purified Ran proteins was performed as previously described (Peterson et al., 2004). In brief, GMPPNP or GDP was added to purified Ran protein at a threefold molar excess in 1 mM EDTA at room temperature for 30 min. Nucleotide exchange was quenched by addition of 10 mM MgCl₂. Purified 6x-His-tagged importin- α and - β proteins were generated by cloning importin- α and - β into the pET28b vector using the 5' NheI and 3' NotI restriction sites. All proteins were expressed in *Escherichia coli* BL21(DE3). For pull-down assays, GST fusions were added to glutathione agarose and rotated at 4°C for 30 min, washed three times in binding buffer (20 mM Hepes, 100 mM NaCl, 5 mM MgCl₂, 1 mM DTT, and 0.5% Tween 80), incubated with 50 μ g of ligands in binding buffer, and rotated at 4°C for 1 h followed by washing, elution, and analysis by SDS-PAGE. For Western blots, His-tagged proteins were detected with a mouse penta-His antibody (1:1,000; Santa Cruz Biotechnology, Inc.).

For immunoprecipitations, S2 cells were lysed with NP-40 buffer (150 mM NaCl, 1% NP-40, 50 mM Tris, pH 8.0, and 1 mM PMSF) and passed through a 21-gauge needle. 5 μ g of mouse anti-GFP antibody (Invitrogen), mouse anti-FLAG (Sigma-Aldrich), or mouse anti-HA (Roche) was added to lysates and gently mixed for 1 h at 4°C. 50 μ l protein G-Sepharose (Invitrogen) was added and gently mixed for 1 h at 4°C followed by washing, elution, and analysis by SDS-PAGE. For Western blots, the following antibodies were used: mouse anti-Flag (1:500; Sigma-Aldrich), mouse anti-Dlg (1:500; Developmental Studies Hybridoma Bank), rabbit anti-Canoe (1:200; Speicher et al., 2008), mouse anti-GFP (1:500; Invitrogen), and rabbit anti-Ran (1:1,000; Cell Signaling Technology).

Online supplemental material

Fig. S1 shows that RNAi depletion of Ran or Canoe does not significantly alter spindle morphology, centrosome number, or spindle length in S2 cells. Fig. S2 demonstrates the reduction in Dlg, Canoe, and Ran protein levels by Western blotting after *dlg*, *canoe*, or *ran* RNAi in S2 cells. Online supplemental material is available at <http://www.jcb.org/cgi/content/full/jcb.201102130/DC1>.

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