RESEARCH ARTICLE

Polo-like kinase phosphorylation determines *Caenorhabditis elegans* centrosome size and density by biasing SPD-5 toward an assembly-competent conformation

Oliver Wueseke1,*, David Zwicker2,*, Anne Schwager3, Yao Liang Wong4, Karen Oegema4, Frank Jülicher5, Anthony A. Hyman3 and Jeffrey B. Woodruff3,‡

**ABSTRACT**

Centrosomes are major microtubule-organizing centers composed of centrioles surrounded by an extensive proteinaceous layer called the pericentriolar material (PCM). In *Caenorhabditis elegans* embryos, the mitotic PCM expands by Polo-like kinase 1 (PLK-1) phosphorylation-accelerated assembly of SPD-5 molecules into supramolecular scaffolds. However, how PLK-1 phosphorylation regulates SPD-5 assembly is not known. We found that a mutant version of SPD-5 that is insensitive to PLK-1 phosphorylation (SPD-5<sup>AA</sup>) could localize to PCM but was unable to rescue the reduction in PCM size and density when wild-type SPD-5 levels were decreased. In *vitro*, purified SPD-5<sup>AA</sup> self-assembled into functional supramolecular scaffolds over long time scales, suggesting that phosphorylation only controls the rate of SPD-5 scaffold assembly. Furthermore, the SPD-5 scaffold, once assembled, remained intact and supported microtubule nucleation in the absence of PLK-1 activity in *vivo*. We conclude that PLK-1 is required for rapid assembly of the PCM scaffold but not for scaffold maintenance or function. Based on this idea, we developed a theoretical model that adequately predicts PCM growth rates in different mutant conditions in *vivo*. We propose that PLK-1 phosphorylation-dependent conversion of SPD-5 into an assembly-competent form underlies PCM formation in *vivo* and that the rate of this conversion determines final PCM size and density.

**KEY WORDS:** *C. elegans*, PCM, Polo-like kinase, SPD-5, Centrosome, Microtubule

**INTRODUCTION**

Centrosomes are the main microtubule-organizing centers of animal cells, consisting of a pair of centrioles that organize a dynamic protein mass called pericentriolar material (PCM). The PCM consists of a structured, small interphase layer (Mennella et al., 2002; Dictenberg et al., 1998; Zimmerman et al., 2004; Buchman et al., 2010; Conduit et al., 2010; Martinez-Campos et al., 2004). The assembly of these proteins is facilitated by SPD-2/Cep192 and Cdk5RAP2/Centrosomin, which resemble SPD-5 in that they consist of a structured, small interphase layer of large proteins such as Pericentrin/D-PLP and Cdk5RAP2/Centrosomin, which resemble SPD-5 in that they contain numerous interspersed coiled-coil domains (Hamill et al., 2002; Dictenberg et al., 1998; Zimmerman et al., 2004; Buchman et al., 2010; Conduit et al., 2010; Martinez-Campos et al., 2004). The assembly of these proteins is facilitated by SPD-2/Cep192 and the phosphorylation activity of the conserved Polo-like kinase Plk1/PLK-1 (Pelletier et al., 2004; Kemp et al., 2004; Decker et al., 2011; Woodruff et al., 2015; Conduit et al., 2014; Gomez-Ferreria et al., 2007; Giancanti et al., 2008; Haren et al., 2009). However, how these molecular interactions lead to PCM assembly and determine final PCM size and density remain outstanding questions.

We previously hypothesized that PCM is nucleated at centrioles and then rapidly expands via autocatalytic incorporation of cytosolic PCM components (Zwicker et al., 2014). In our model, unassembled PCM proteins exist in a soluble form that can transition into an assembly-competent state within the PCM and then become stably incorporated. Once incorporated, PCM proteins will recruit additional PCM components, which is an autocatalytic event. Consequently, in our model the kinetics of PCM assembly depend on the rate by which PCM material, after being recruited to the centrosome, converts from the soluble to the assembly-competent form. The existence of such a conversion is supported by the observations that *C. elegans* PCM proteins are indeed monomeric in cytoplasm prior to assembly, whereas they interact at the centrosome (Wueseke et al., 2014).

We recently reported that purified SPD-5 can form supramolecular PCM-like assemblies *in vitro*, the formation of which is accelerated by PLK-1 phosphorylation of SPD-5 (Woodruff et al., 2015). Mass spectrometry revealed PLK-1 phosphorylation sites on SPD-5 that, when mutated, prevented PCM assembly *in vivo*. These results indicate that PCM formation in *C. elegans* is driven by PLK-1-mediated oligomerization of SPD-5 around centrioles. We also found that only SPD-5 assemblies, and not SPD-5 monomers, recruited other PCM proteins, including PLK-1, leading us to propose that this emergent scaffolding property of SPD-5 could be the basis for
autocatalytic PCM expansion in vivo (Woodruff et al., 2015; Wueseke et al., 2014). Additionally, our in vitro experiments revealed that the stability and scaffolding capacity of SPD-5 assemblies were independent of PLK-1 phosphorylation, suggesting that PLK-1 activity may only regulate the speed of SPD-5 assembly. However, we did not test whether PLK-1 has additional roles in PCM maintenance or function in vivo. Nor did we test if unphosphorylated SPD-5 can be recruited to existing PCM and then be converted to an assembly-competent state as predicted by our previous model (Zwicker et al., 2014).

In this study, we combined in vivo analysis, in vitro reconstitution, and modeling to investigate how PLK-1 regulates SPD-5 assembly to form PCM in C. elegans. Our results indicate that PLK-1 phosphorylation affects the rate of SPD-5 assembly without dramatically affecting SPD-5 recruitment to existing PCM, PCM stability, or PCM function. Additionally, we conclude that a phospho-site binding mechanism cannot explain PCM assembly. Rather, we propose that SPD-5 naturally isomerizes between assembly-incompetent and assembly-competent states, and that PLK-1 phosphorylation biases SPD-5 toward the latter state. Furthermore, our results suggest that the conversion rate of SPD-5 into an assembly competent state is the key determinant of final PCM size and density in vivo.

RESULTS AND DISCUSSION

A SPD-5 phospho-mutant binds to PCM in C. elegans embryos

We first set out to determine if PLK-1 phosphorylation of SPD-5 is required only for PCM expansion or also for SPD-5 binding to PCM. For this purpose we used spinning disk confocal microscopy to observe PCM assembly in C. elegans embryos expressing GFP-tagged versions of SPD-5 (SPD-5WT and SPD-5A) as their sole source of SPD-5. SPD-5A is mutated in the critical sites for PLK-1 mediated centrosome assembly in vivo (Fig. 1A) (Woodruff et al., 2015). As previously shown, GFP::SPD-5A localized to premitotic centrosomes, but, in contrast to GFP::SPD-5WT, failed to expand the PCM (Fig. 1B) (Woodruff et al., 2015). To test if SPD-5A is still capable of binding to existing PCM, we observed PCM assembly in embryos expressing endogenous SPD-5 and GFP::SPD-5A. In such embryos, mitotic PCM assembled and GFP::SPD-5A localized to the PCM (Fig. 1B).

PCM size and density are reduced in embryos ectopically expressing a GFP::SPD-5A transgene

Quantification and comparison of centrosome area from immunostainings against SPD-5 and GFP revealed perfect overlap of total SPD-5 and GFP::SPD-5A signals, showing that GFP::SPD-5A localizes throughout the entire PCM and can be used to determine PCM size in embryos expressing mutant SPD-5 (Fig. 1C). By comparing centrosome sizes determined from GFP signal we found that PCM assembled in the presence of endogenous SPD-5 and GFP::SPD-5A was ~58% smaller in volume (3.4±1.1 µm³; mean±s.d.) at nuclear envelope breakdown (NEBD) than PCM assembled with endogenous SPD-5 and wild-type GFP::SPD-5 (8.0±2.7 µm³, mean±s.d.; Fig. 1D). As reported previously, GFP::SPD-5WT and GFP::SPD-5A, as well as endogenous SPD-5 levels, are similar in these worms (~30% transgenic, ~70% endogenous), suggesting that this difference does not result from altered SPD-5 concentrations (Fig. S1A) (Woodruff et al., 2015). We conclude that SPD-5A binds to PCM and that its expression reduces PCM expansion.

In addition to being smaller, centrosomes assembled in the presence of the SPD-5A mutant were also less dense. Based on the assumption that SPD-5 forms the underlying PCM scaffold (Hamill et al., 2002; Woodruff et al., 2015), we used GFP::SPD-5 fluorescence at the PCM to approximate PCM density from the mean pixel intensity of maximum intensity z-projections. In embryos expressing endogenous SPD-5 and GFP::SPD-5WT, centrosomal GFP signal increased with time after fertilization until the onset of mitosis (Fig. 2A, grey points), indicating an
Fig. 2. The concentration of phosphorylation-receptive SPD-5 determines PCM size and density in vivo. (A) Mean maximum GFP intensity of centrosomes in embryos expressing endogenous SPD-5 and GFP::SPD-5WT (n=10 embryos) or endogenous SPD-5 and GFP::SPD-5AA (n=10 embryos) over time relative to NEBD. Circles represent mean values and shaded areas represent s.e.m. (B) Mean maximum GFP intensity of centrosomes at NEBD as in A showing a 26% difference in intensity of centrosomes assembled in the presence of GFP::SPD-5WT or GFP::SPD-5AA. Error bars indicate mean±s.d.; **P<0.01, two-tailed t-test. (C) Embryos expressing GFP::SPD-5WT and endogenous SPD-5 (n=17) or GFP::SPD-5AA and endogenous SPD-5 (n=19) were fixed and immunostained for SPD-5 and GFP. Insets show close-ups of centrosomes. Scale bar: 10 µm. (D) Quantification of GFP and SPD-5 immunofluorescence signal from centrosomes from C, GFP::SPD-5WT+endogenous SPD-5 (n=17 centrosomes), GFP::SPD-5AA+endogenous SPD-5 (n=19 centrosomes). Wild-type signals were used for normalization. Values represent mean±s.d.; **P<0.01, two-tailed t-test. (E) Embryos expressing endogenous SPD-5 and GFP::SPD-5WT or GFP::SPD-5AA were fixed and stained for SPD-2 and PLK-1. Insets show close-ups of centrosomes. Scale bar: 10 µm. (F) Quantification of (E) using centrosomal SPD-2 and PLK-1 immunofluorescence signal in GFP::SPD-5WT (n=19) or GFP::SPD-5AA (n=25) containing centrosomes. Values represent mean±s.d.; *P<0.05, two-tailed t-test. (G) Western blot showing the compensation of SPD-5 levels upon expression of transgenic SPD-5 or knockdown of endogenous SPD-5. RNAi was carried out for 24 h specifically against endogenous SPD-5. (H) Western blot showing full depletion of endogenous SPD-5 and partial depletion of transgenic SPD-5 after 12 h of mixed RNAi treatment. Quantification of the SPD-5 levels showed that mixed RNAi treatment lowered the transgenic SPD-5 levels to ~63% of the control situation where only endogenous SPD-5 was depleted. The schematic shows the target sequences of RNAi constructs targeting endogenous SPD-5 (endo RNAi) or endogenous and transgenic SPD-5 (total RNAi). (I) Centrosome volumes at NEBD in embryos expressing GFP::SPD-5WT exclusively (100%, n=19), reduced levels of GFP::SPD-5WT (~63%, n=23) or GFP::SPD-5AA plus endogenous SPD-5 (n=23). Values represent mean±s.d.; ***P<0.001, two-tailed t-test. (J) As in H but showing mean maximum centrosomal GFP fluorescence at NEBD. Values represent mean±s.d.; **P=0.001, two-tailed t-test.
increase in PCM density up to mitosis. In embryos expressing endogenous SPD-5 and GFP::SPD-5WT, centrosomal GFP signal started at a similar mean intensity shortly after fertilization but remained constant until mitosis (Fig. 2A, red points). A comparison of GFP fluorescence of centrosomes at NEBD revealed 26% higher intensity for centrosomes assembled with GFP::SPD-5WT (WT=420±99 a.u. vs 4A=332±76 a.u., mean±s.d.; Fig. 2B). We tested if this difference in GFP intensity resulted from hampered binding of GFP::SPD-54A to PCM or generally a lower SPD-5 density at the PCM. Immunostainings against GFP and SPD-5 showed that SPD-5 levels at the PCM were reduced in embryos expressing the 4A mutant (Fig. 2C,D) and that the ratios of transgenic GFP::SPD-5 to total SPD-5 immunostaining signal at wild-type and mutant PCM were very similar (Fig. 2A). These results suggest that the reduction in GFP fluorescence seen in GFP::SPD-54A embryos reflects a general reduction of SPD-5 levels at the PCM. Also, immunostainings revealed a similar difference in SPD-2 and PLK-1 levels at wild type and mutant PCM (Fig. 2E,F), indicating that concentrations of SPD-2 and PLK-1 correlate with SPD-5 concentration at the PCM. Thus, expression of GFP::SPD-54A reduces volume and density of the functional PCM scaffold.

The concentration of phosphorylation-receptive SPD-5 determines PCM size and density in vivo

How can the presence of a mutated transgenic SPD-5 cause a reduction of PCM volume and density? It is possible that GFP::SPD-54A acts as a dominant negative mutant that interferes with accumulation of wild-type SPD-5 at the PCM, possibly by occupying and blocking required SPD-5 binding sites in the PCM scaffold. Alternatively, GFP::SPD-54A may act as a loss-of-function mutant, and, due to protein level compensation, the phenotype seen in embryos expressing mutant SPD-5 could be a consequence of the reduction of available wild-type SPD-5. We previously observed such compensation of the centrosomal protein SPD-2; however, ectopic expression of a codon-adapted version of SPD-5::GFP did not influence the expression of endogenous SPD-5 (Decker et al., 2011). Surprisingly, ectopic expression of transgenic GFP::SPD-5WT in our current strain lead to a reduction in endogenous SPD-5, and selective RNAi against endogenous SPD-5 lead to an upregulation of transgenic SPD-5 (Fig. 2G). These different behaviors could be caused by the sequence differences in the SPD-5 transgenes. The GFP::SPD-5WT transgene used in this study is codon-adapted only at the N-terminus (Woodruff et al., 2015) while the SPD-5::GFP transgene used in Decker et al. (2011) was codon-adapted throughout its sequence. Thus, codon optimization of SPD-5 interferes with regulation of total SPD-5 levels. We conclude that SPD-5 levels are tightly regulated and that worms expressing the transgenic SPD-5 used in this study compensate by down-regulating endogenous wild-type SPD-5.

To test if PCM volume and density respond to wild-type SPD-5 concentration changes, we fully removed endogenous SPD-5 and then reduced the concentration of GFP::SPD-5WT using a double RNAi condition targeting the endogenous and transgenic SPD-5 transcripts with different strengths. Using this method, we reduced GFP::SPD-5WT levels to about 63% compared to the control where only buffer was added (WT+WT versus WT; P<0.007; Fig. 2B). In contrast, total network mass in the sample containing SPD-5WT::GFP and PLK-1, then added either buffer (WT), SPD-54A (WT+4A), or additional SPD-5WT (WT+WT). We warmed the tubes to 23°C to initiate network assembly, then, after 30 min, we squashed a sample under a cover slip for analysis. Under these conditions, small, nascent networks could be seen in the control sample (Fig. 3B), and we verified that growth had not yet plateaued (unpublished data); thus, our experiments should allow detection of any stimulatory or inhibitory effects resulting in an increase or decrease of total network mass.

Total network mass was ~twofold higher in the sample containing unlabeled SPD-5WT compared to the control where only buffer was added (WT+WT versus WT; P<0.007; Fig. 3B). In contrast, total network mass in the sample containing SPD-54A::GFP and PLK-1 was similar to the control sample (P=0.86) indicating that SPD-54A neither promoted nor interfered with network growth (Fig. 3B). These data suggest that during PCM assembly SPD-54A behaves predominantly as a loss-of-function mutant, although we acknowledge that our measurements may not be sensitive enough to detect any minor dominant-negative effects. Our in vitro results corroborate our in vivo findings that PCM assembly rate is largely determined by the amount of phosphorylation-responsive SPD-5 available in the system.

We then used this in vitro assay to test if PLK-1 phosphorylation of SPD-5 is required for proper functioning of the PCM scaffold. As observed previously, SPD-54A assembled into supramolecular networks at a rate similar to unphosphorylated wild-type protein (Woodruff et al., 2015). After one hour of incubation at 23°C, networks exclusively assembled from SPD-5WT::TagRFP or SPD-54A::TagRFP equivalently recruited SPD-2::GFP and PLK-1::GFP (Fig. 3C-E), suggesting that SPD-54A and unphosphorylated SPD-5WT can form functional PCM scaffolds in vitro given sufficient time.

PLK-1 phosphorylation is not required to maintain PCM scaffold stability or function in vivo

Our in vitro results predict that SPD-5 scaffolds, once formed, should function without needing continuous PLK-1 phosphorylation in vivo. To test this idea, we constructed a C. elegans strain expressing GFP::SPD-5WT and an analog-sensitive PLK-1 mutant (PLK-1Δ) that can be inhibited by the drug 1NM-PP1 (plk1Δ; plk-1Rfp gfp::spd-5; Bishop et al., 2000). We permeabilized embryos using partial knockdown of perm-1 via RNAi (Carvalho et al., 2011), then identified pre-mitotic embryos where centrosomes had formed but were not yet full-sized. Addition of 10 µM 1NM-PP1 to these embryos arrested centrosome growth; both centrosome size and GFP::SPD-5 fluorescence remained constant thereafter (Fig. 4A,B; n=10). However, centrosomes continued to grow if DMSO was added instead (Fig. 4C; n=10). Thus, PLK-1 is not required to
maintain SPD-5 at the centrosome; this stands in stark contrast to gamma tubulin, which does require continuous PLK-1 activity for centrosomal localization (Woodruff et al., 2015).

To test the functionality of PCM-localized SPD-5 in the absence of PLK-1 phosphorylation in vivo, we treated permeabilized embryos with 10 μM 1NM-PP1 and the proteasome inhibitor c-lactocystin-lactone for 20 min, then fixed the embryos and visualized microtubules using immunofluorescence. Centrosomes still nucleated microtubules and formed spindles after PLK-1 inhibition, suggesting that SPD-5 retains its functional capacity for scaffolding in the absence of PLK-1 phosphorylation (Fig. 4D; n=8). These in vivo results are in agreement with our in vitro data and suggest that PLK-1 phosphorylation is not required for the maintenance or function of SPD-5 scaffolds but instead only controls the rate of SPD-5 scaffold formation, and, subsequently, PCM assembly.

**A PLK-1-dependent SPD-5 conversion model can explain in vivo PCM assembly**

Our data, combined with previous studies, allow us to propose a simple mechanism for PLK-1-dependent PCM assembly in *C. elegans*. Prior to incorporation into the PCM, SPD-5 is mostly monomeric and does not interact with SPD-2 or PLK-1 (Wueseke et al., 2014). We term this the inactive form of SPD-5, which cannot contribute to PCM assembly itself but can localize to centrioles and contribute to PCM assembly itself but can localize to centrioles and segregate into existing PCM (Fig. 4E). Since GFP::SPD-54A alone is not capable of expanding PCM in vivo (Fig. 1B,D), we assume that SPD-54A as well as unphosphorylated SPD-5WT exist primarily in the inactive form. Secondly, we define an active, assembly-competent form, which can self-assemble into supramolecular structures and contribute to PCM growth (Fig. 4E). Because our in vitro data show that purified SPD-5 can spontaneously self-assemble and that PLK-1 phosphorylation accelerates this assembly process (Woodruff et al., 2015), we propose that SPD-5 can transition into the assembly-competent state spontaneously and that this transition is much more likely if SPD-5 is phosphorylated by PLK-1. Thus, we assume that PLK-1-phosphorylated SPD-5 exists predominately in the assembly-competent state.

Based on this idea we constructed a mathematical model (see Materials and Methods) in which the inactive form of SPD-5 can be converted locally at the centrosome into the assembly-competent form through an active process such as PLK-1 phosphorylation (Zwicker et al., 2014). We used this model to fit the accumulation of SPD-5 in the absence of PLK-1 activity.
rate of total SPD-5 at centrosomes with an exponential function to describe the rate of PCM growth. Total amounts of SPD-5 were estimated from centrosome volumes multiplied by SPD-5 densities (Fig. S3A). We fit the accumulation rate of total SPD-5 from initiation of assembly until NEBD (Fig. 4F). When embryos only expressed SPD-5 WT, the PCM growth rate was 0.48 ± 0.08 min⁻¹. In contrast, when embryos only expressed SPD-5 4A, PCM growth rate was only 0.01 ± 0.05 min⁻¹. We then used these measured rates to predict the PCM growth rate in the mixed scenario where SPD-5 WT is present in a background of endogenous SPD-5 WT. Based on western blot analysis, we estimated that ∼70% of SPD-5 protein is wild-type and ∼30% is mutated in these embryos (Fig. S1A). Using these values, our model predicted that the PCM accumulation rate in these embryos should be 0.34 ± 0.06 min⁻¹ (see Materials and Methods for calculation details). This value is very similar to the accumulation rate we obtained when fitting the data (0.31 ± 0.11 min⁻¹). Taken together, these results suggest that a model based on centrosomal conversion of SPD-5 into an assembly-competent form is adequate to describe the complex process of PCM assembly in C. elegans embryos.

How does PLK-1 change SPD-5 to induce self-assembly? In vitro both unphosphorylated SPD-5 WT and SPD-5 4A assembled into supramolecular networks after a long period of time (Fig. 3) (Woodruff et al., 2015); but, addition of PLK-1 dramatically accelerated SPD-5 WT self-assembly. These results suggest that SPD-5 naturally isomerizes between the inactive form and the assembly-competent form, and that PLK-1 phosphorylation of SPD-5 lowers the energy barrier of this transition (Fig. S3B). The role of PLK-1 in PCM assembly, then, is to bias SPD-5 isomerization towards the assembly-competent state.

Besides PLK-1 phosphorylation, PCM assembly requires SPD-2, a protein known to control centrosome growth rate and thus size in vivo (Decker et al., 2011; Yang and Feldman, 2015). We have shown previously that SPD-2 accelerates SPD-5 assembly in the presence...
and absence of PLK-1 in vitro, demonstrating that multiple mechanisms regulate SPD-5 self-assembly (Woodruff et al., 2015). Whether SPD-2 also enhances SPD-5 self-assembly by affecting its isomerization or by some other process remains to be investigated. We conclude that SPD-5 has the intrinsic capability to assemble functional PCM and that PLK-1 phosphorylation and SPD-2 simply accelerate the rate of assembly.

An unexpected observation from our experiments was that PCM density increased over time from fertilization until mitosis in wild-type embryos. However, when we reduced the speed of PCM assembly by reducing the available pool of phosphorylation-receptive SPD-5, PCM density did not change over time. We do not understand the molecular basis of this phenomenon. One possibility is that this is caused by a buildup of elastic stress as the centrosome grows. If the growth rate is faster than the stress relaxation rate, centrosome density will increase. However, if the growth rate is slowed down, for instance, by reducing the concentration of wild-type SPD-5, then the stress could relax and centrosome density would remain constant. This supports the idea that the PCM is not solid, but rather a viscous, gel-like material.

In Drosophila, PCM assembly is driven by Polo kinase-regulated multimerization of the scaffolding protein Centrosomin (Conduit et al., 2014), suggesting that Centrosomin is the functional homolog of SPD-5. Similar to SPD-5, Centrosomin must be phosphorylated at multiple residues to achieve its full scaffolding potential (Conduit et al., 2014). In vertebrate cells, Polo-like kinase and the Centrosomin homolog CDK5Rap2 are also required for mitotic PCM assembly (Lane and Nigg, 1996; Haren et al., 2009). Thus, a common mechanism for PCM assembly is emerging that centers on Polo-like kinase-mediated phosphorylation of large coiled-coil proteins. It will be of interest to determine the similarities in self-assembly properties and regulation of SPD-5, Centrosomin, and CDK5Rap2.

MATERIALS AND METHODS

Worm strains

Caenorhabditis elegans worm strains were maintained following standard protocols (Stiernagle, 2006). For this study we used previously described worm strains OD847 (gfp::spd-5<sup>4A</sup>) and OD903 (gfp::spd-5<sup>AS</sup>) (Woodruff et al., 2015). Briefly, both strains contain MosSCI single-copy integrants of gfp::spd-5 transgenes on chromosome II rendered RNAi-resistant by re-encoding the sequence between nucleotides 500 to 1079 in the spd-5 genomic sequence. Their genotypes are as follows:

OD847: unc-119(ed9) III; tis202[pVV103/pOD1021]; Pspd-2::GFP; SPD-5 RNAi-resistant; cb-unc-119(+))II

OD903: unc-119(ed9) III; tis228[pPV153/pOD1615]; Pspd-2::GFP; spd-5 sps503a, s627a, s653a, s658a reencoded; cb-unc-119(+))III.

We also used two new lines expressing gfp::spd-5 with plk-1WT (OD2420)/plk-1<sup>AS</sup> (OD2421) in a plk-1 deletion background. The genomic plk-1 locus (plk-1WT) was amplified and the analog sensitive Shokat allele, plk-1<sup>AS</sup>, with the C52V and L115G mutations was generated using site-directed mutagenesis. plk-1WT and plk-1<sup>AS</sup> transgenes were crossed into a plk-1 deletion background. A gfp::spd-5WT transgene was subsequently crossed into each resultant strain to allow direct monitoring of PCM. Their genotypes are as follows:

OD2420: unc-110(ed9) plk-1(ok1787) III; tis654[pOD1021]; pspd-2::GFP::spd-5 RNAi-resistant; cb-unc-119(+))II

OD2421: unc-110(ed9) plk-1(ok1787) III; tis654[pOD1042]; plk-1::PLK-1; cb-unc-119(+))II

RNAi treatments

RNAi against endogenous spd-5 was carried out as previously described (Kamath et al., 2000). Briefly, the following primers were used to amplify nucleotides 501–975 of endogenous spd-5 from cDNA and cloned into Gateway® pDonor<sup>TM</sup>221 vector via BP reaction to create spd-5-pENTR<sup>TM</sup> vector: spd-5-fw (GGGGACAAGTTTGTACAAAAAAGCAGGCTtgctgctagtctg), spd-5-rev (GGGACCCTTTTGTACAGGAACTGCGGTTgtgctagctgctgtc). The amplified sequence was then transferred to L4440_GW (Addgene) destination vector and used to transform HT115 (DE3) bacteria strain for RNA expression. Using this feeding clone, full knockdown of endogenous SPD-5 was achieved typically within 24 h. Simultaneous RNAi against endogenous and transgenic SPD-5 was carried out using the SPD-5 (F56A3.4) clone from the C. elegans RNAi feeding library constructed by the lab of Dr Julie Ahringer, available from Source BioScience. To achieve full knockdown of endogenous and partial depletion of transgenic SPD-5, both clones were grown simultaneously and mixed (30% Ahringer, 70% endogenous) prior to plating. Due to the increased knockdown efficiency of the Ahringer feeding clone, incubation times had to be shortened to 12 h. Quantification of SPD-5 protein knockdown was quantified from western blots using the Gel Analyzer function in Fiji (https://fiji.sc/; Schindelin et al., 2012).

Antibodies and stainings

Stainings were done following standard procedure described before (Hamill et al., 2002). The polyclonal mouse αPLK-1 antibody was generated in house by injecting 1 mg of purified full length PLK-1 into mice, purified from serum, and used in a dilution of 1:300. Endogenous SPD-5 and SPD-2 were detected using the previously described polyclonal rabbit αSPD-2 antibody (anti-spd-2 NT_Acid, 1:4000) as well as αSPD-5 antibody (anti-SPD-5_mid_Acid, 1:7200). Commercially available (Life Technologies) goat anti-mouse-Alexa Fluor 594 conjugates, goat anti-rabbit-Alexa Fluor 594 conjugate and goat anti-rabbit-Alexa Fluor 647 conjugate were used for detection with a 1:1000 dilution. GFP signal was detected directly using 488 nm illumination. Images were recorded using an inverted Olympus IX71 microscope, 40× NA 1.0 Plan Achromat oil objective, CoolSNAP HQ camera (Photometrics), a DeltaVision control unit (AppliedPrecision) and the recording software SoftWoRx 5.5. Centrosome intensity analysis was carried out using Fiji (https://fiji.sc/). Briefly, centrosomes were detected automatically using the auto-threshold function and analyzed subsequently for mean intensity using the analyze particle function. Each identified centrosome was treated as a single sample. For quantification of PCM localized SPD-2 and PLK-1 staining signal the high centriolar signal was excluded for the quantification, see Fig. S2B for detailed procedure. Statistical analyses were carried out using two-tailed Student’s t-test.

Centrosome live imaging

Centrosomes were detected via imaging GFP::SPD-5 on an inverted Nikon TiE microscope with a Yokogawa spinning-disk confocal head (CU-X1), a 60× water 1.2 NA UPlanSApo objective, and a iXon EM+DU-897 BV back illuminated EMCCD (Andor) 63×0.26 µm z-stacks were recorded in 30 s intervals with 15% laser transmission. Images were also taken using an inverted Olympus IX81 microscope with a Yokogawa spinning-disk confocal head (CU-X1), a 60× water 1.2 NA UPlanSApo objective, and a iXon EM+DU-897 BV back illuminated EMCCD (Andor) 63×0.26 µm z-stacks were recorded in 30 s intervals with 15% laser transmission. For experimental comparisons only recordings from the same microscope were used. Image analysis was carried out using Fiji (https://fiji.sc/). Maximum projections were generated from z-stacks and background fluorescence was subtracted from the images. Centrosome area and mean maximum fluorescence intensity were measured throughout development of each embryo by selecting centrosomes using the thresholding and Analyze Particles function in Fiji and were averaged for each embryo to represent a single sample. Centrosome volume was then calculated using the centrosome radius approximated from centrosome area measurements. Total SPD-5 amounts were approximated from centrosome volumes and densities. To do so we multiplied the volumes with concentration corrected intensity values, assuming that the recorded intensities stemmed from the ~30% of the total SPD-5 pool labeled with GFP (as estimated from western blots, see Fig. S1A). Statistical analyses were carried out using two-tailed Student’s t-test.
In vitro SPD-5 scaffold assembly

Proteins were purified and assembled into scaffolds in vitro as previously described (Woodruff et al., 2015). For a detailed protocol please refer to Woodruff and Hyman (2015). In brief, all reactions were carried out in network buffer (25 mM HEPES pH 7.4, 135 mM KCl, 125 mM NaCl, 0.2 mM ATP, 10 mM MgCl₂, 1 mM DTT, 0.02% CHAPS, 0.2% glycerol, 0.025 mg/ml ovalbumin) plus pre-blocked 0.2 µm red fluorescent polystyrene beads (Invitrogen) to aid in finding the focal plane. All proteins and reagents were stored on ice prior to being mixed, aliquoted into multiple tubes and then incubated at 23°C. For analysis of a single reaction, 2 µl of that reaction was spotted onto a non-frosted cover slide and then covered with 18×18 mm pre-cleaned hydrophobic cover slips. Statistical analyses were carried out using two-tailed Student’s t-test.

Cover slips were cleaned and made hydrophobic using the following steps. First, cover slips were placed in a Teflon holder and submerged in a 1:20 dilution of Mucasol detergent (Sigma) for 10 min with sonication. Second, the cover slips were transferred to 100% ethanol and incubated for >30 min, then washed in ethanol, 10 min with sonication. Third, the cover slips were incubated in a 50% solution of Rain-X (diluted in ethanol) for >30 min, then washed in ethanol, then twice in water. Finally, the cover slips were dried using N2 gas and stored in a desiccation chamber.

PLK-1 inhibition in embryos with permeabilized eggshells

PLK-1 inhibition was performed as previously described (Woodruff et al., 2015). Briefly, L4 worms were seeded onto feeding plates containing bacteria expressing perm-1 dsRNA and incubated at 20°C for 14-20 h (Carvalho et al., 2011). Worms containing permeabilized embryos were dissected in an imaging chamber (Microwells) containing osmotic support medium [stock solution: 50 ml ESF 921 Insect Cell Culture Medium (Expression Systems), 5 ml fetal bovine serum+0.77 g sucrose, filter sterilized; this stock solution was then diluted 60/40 in M9 buffer]. To inhibit PLK-1-4A prior to mitotic entry, the buffer was exchanged for buffer containing 10 µM 1-NM-PP1 (Cayman Chemical, 13330). At the end of each experiment, FM-64 (Molecular Probes, T13320) was added to the well to confirm that the imaged embryo was permeable. Imaging was performed as described above, except that 10 s intervals and 8% laser power (4.5 mW) were used.

Analysis of diffusion using fluorescence correlation spectroscopy (FCS)

FCS measurements and diffusion analysis were carried out as described previously (Wueseke et al., 2014). Briefly, FCS measurements were made on a LSM 780 microscope equipped with a 40×1.2 NA water immersion objective and an avalanche photodiode (Zeiss, Jena, Germany) at room temperature using 488 nm excitation. The focal volume was calibrated using Alexa Fluor 488 dye (Life Technologies), resulting in the following parameters: beam diameter (ω₀) = 0.19 µm, structural parameter (S) = 5 and confocal volume (V) = 0.19 fl. Three measurements with a total of 72 s (24 s each) were taken in each embryo at random positions in the cytoplasm (excluding cell membrane, pronuclei and centrosomes) after a 1 s pre-bleach. Autocorrelation curves were calculated from the intensity profiles obtained from the measurements and then averaged for each embryo. To obtain diffusion coefficients, each averaged autocorrelation curve was fitted within a time range of 500 ns to 1 s with a single component three-dimensional anomalous diffusion model including a free triplet component to account for fluorophore blinking (Banks and Fradin, 2005; Kim et al., 2007). Statistical analysis on diffusion coefficients was done using Wilcoxon rank sum test. Autocorrelation analysis and data plotting were carried out using a MATLAB script developed in our lab.

Quantitative model of SPD-5 incorporation

We use a theoretical approach to discuss the effects of the nonphosphorylatable SPD-5*4A mutant on the dynamics of PCM assembly and centrosome growth. We extend the previous physical model of centrosome assembly that is based on the physics of liquid droplets (Zwicker et al., 2014). This model can quantitatively account for the volume growth of centrosomes in vivo. Here, we extend this model to a situation where in addition to the wild-type form SPD-5WT also the mutant form SPD-5*4A is expressed. The biochemical effects of the mutations are not known. By comparing theoretical predictions to experimental data, we aim to identify the biochemical properties of SPD-5*4A during centrosome assembly.

Our original model is based on the idea that SPD-5 molecules exist in two different forms (Zwicker et al., 2014). We distinguish the form A that is soluble in the cytoplasm and the form B that tends to aggregate and phase separate from the cytoplasm. This form B is thus the basis of the PCM phase that forms the centrosome. The two forms of SPD-5 can be converted into each other by chemical processes such as phosphorylation. We showed that the conversion of A to B must be autocatalytic to account for the sigmoidal centrosome growth curves and the reliable initiation of PCM accumulation at the centrioles (Zwicker et al., 2014).

We extend our original model by distinguishing wild-type SPD-5WT from mutant SPD-5*4A. Potentially, both species can exist in the A and the B form and we thus introduce four molecular species: AWT, BWT, A*4A and B*4A. The dynamics of SPD-5WT and SPD-5*4A in the cytoplasm, as revealed by fluorescence correlation spectroscopy (FCS) measurements, are very similar (Fig. S4). We thus consider both A forms to have the same properties, such that they are both soluble in cytoplasm and can also diffuse in the PCM. The PCMs can be formed by aggregation of either BWT or B*4A or by their combined aggregation (Fig. 1B-D, Fig. 3C,D). We thus infer that they tend to phase separate together in one phase. The PCMs volume V is thus given by V = NWT / NWT, where NWT = NWT + NWT is the total number of molecules in form B and NWT is the density of B molecules in the PCM. Our data suggests that the density of SPD-5 in the PCM changes only slightly during centrosome growth (Fig. 2A). For simplicity, we here consider the case where the density NWT is determined by the physics of phase separation and is constant over time. Below we discuss possible causes for the observed small density variations.

The PCM size increases if molecules of form B are generated from their respective A forms. Since PCM growth is reaction-limited (Zwicker et al., 2014), the A molecules can distribute in the PCM more quickly than they get converted to the B form. Consequently, the densities NWT and N*4A of the A forms are approximately homogeneous throughout the PCM. We consider the simple case where the two A forms do not interact with each other, such that we can discuss their densities separately. In the simplest case, the equilibrium of the A form between the inside and the outside is given by an equilibrium constant K, which implies that the density NWT inside the PCM is proportional to the respective density N*4A of the A form in the cytoplasm, NWT = N*4A / K. Here, K can be interpreted as an affinity of the PCM toward molecules of species A.

Chemical reactions lead to the creation and removal of molecules of form B inside the PCM, which is described by (Zwicker et al., 2014).

\[
\frac{dN_B(t)}{dt} = k^2N_TN_J - k_BN_B(t) = \left(\frac{N_T}{N_J} - 1\right)N_B(t)
\]
Here,
\[
\lambda = k^\text{WT} \xi^\text{WT} c^\text{WT} + k^\text{4A} \xi^\text{4A} c^\text{4A} - k_B^A
\]
(3)
is the PCM growth rate. If we include the depletion of the \( A \) form in the cytoplasm, \( N^A_B(t) \) exhibits sigmoidal growth (Zwicker et al., 2014). Since we do not observe a saturation of \( N^A_B(t) \) in our experimental data, we focus on the early growth phase where depletion can be neglected.

We compared the predictions of our model to our experimental measurements. In our experiments, we label one of the SPD-5 species with GFP, such that the measured total centrosome fluorescent intensity is a proxy for the total number \( N' = N^A + N^B \) of molecules of species \( i \), where \( N^i = n_i V \), and \( V \) is the PCM volume. For the case \( k_B^A \ll k \), the time evolution of \( V \) can be approximated by
\[
V(t) \approx \frac{N_0}{n_B} (e^{\lambda t} - 1).
\]
(4)

Consequently, the total number of molecules is given by
\[
N^i(t) \approx \frac{N_0}{n_B} \left( 1 + \frac{k^i_B}{\lambda} \right) (e^{\lambda t} - 1).
\]
(5)

We use this functional form to measure the growth rate \( \lambda \) by fitting the function \( f(t)=C(e^{\lambda t} - 1) \) to our measured intensities multiplied by the centrosome volume as a function of time (Fig. 4F). Here, the prefactor \( C \) sets the intensity scale. The measured growth rates were \( \lambda^\text{WT}=0.48\pm0.08\text{ min}^{-1} \) and \( \lambda^\text{4A}=0.01\pm0.05\text{ min}^{-1} \) in the experiments with only SPD-5\text{WT} and only SPD-5\text{4A}, respectively. Since \( \lambda^\text{WT} \ll \lambda^\text{4A} \), the mutant does not lead to significant PCM growth.

Why does the mutant SPD-5\text{4A} not contribute to PCM growth? According to Eqn 3, there are three parameters that could be responsible for this: the cytoplasmic concentration could be reduced \( (c^\text{4A} \ll c^\text{WT}) \), binding to pre-existing PCM could be less efficient \( (\xi^\text{4A} \ll \xi^\text{WT}) \), or the transition to the \( B \) form could be hindered \( (k_B^A \ll k_B^\text{WT}) \).

We measured the total amount of SPD-5 in all experiments (Fig. 2G-H; Fig. S1). The associated concentrations approximate the cytoplasmic ones in the early growth phase where centrosomes are small. Even though the concentration in the experiment with only SPD-5\text{4A} is only half of that of the wild-type, this cannot explain that the growth rates differ by more than an order of magnitude. Consequently, differences in the cytoplasmic concentration cannot explain the observed difference in growth.

We will next show using our fluorescent intensity measurements that the binding coefficients \( \xi^\text{4A} \) and \( \xi^\text{WT} \) are also not significantly different. Here, we consider the experiments where GFP-SPD-5 in either the wild-type or the mutant form is expressed in a background of unlabeled wild-type SPD-5 (Fig. 2C,D). Our measurements (Fig. S1A) show that the relative GFP fluorophore intensities in the PCM are similar, which implies similar densities \( n^i = n^\text{WT} + n^\text{4A} \) of fluorescent SPD-5 in the PCM \( (\approx n^\text{WT}) \). Since the mutant does not contribute to PCM growth, the density of its \( B \) form is negligible \( (n^B^\text{4A} \ll n^B^\text{WT}) \). This implies that the density of the mutant \( A \) form is larger or equal to that of the wild-type \( (n^A^\text{4A} \approx n^A^\text{WT}) \). Since the cytoplasmic concentrations \( c^i \) of the fluorescent SPD-5s are similar (Fig. S1) we conclude that the binding coefficients \( \xi = n_i c_i \) are also similar. In fact, \( \xi^\text{4A} \) might even be larger than \( \xi^\text{WT} \). Consequently, a reduced binding efficiency of the mutant is not consistent with our data.

The only possible explanation for the mutant’s reduced contribution to PCM growth is that the conversion rate of the mutant from form \( A \) to form \( B \) must be much smaller than that of the wild-type \( (k_B^\text{4A} \ll k_B^\text{WT}) \). Since the mutant cannot be phosphorylated by PLK-1, this furthermore suggests that phosphorylation by PLK-1 plays an important role in this conversion.

Our model implies that the PCM growth rate is proportional to the concentration of SPD-5\text{WT}, since \( k_B^\text{4A} \ll k_B^\text{WT} \). We tested this prediction with two additional experiments. First, we quantified centrosome growth in an experiment where both mutant and wild-type SPD-5 were expressed. Using Eqn 3, we express the growth rate \( \lambda^\text{both} \) in terms of the already measured growth rate \( \lambda^\text{WT} \) as \( \lambda^\text{both} \approx \frac{\lambda^\text{WT}}{\xi^\text{WT} + \xi^\text{4A}} \). In our experiment, 71% of the SPD-5 molecules are wild-type (Fig. S1), which implies \( \lambda^\text{both}=0.71 \lambda^\text{WT}=0.34\pm0.06\text{ min}^{-1} \). This value agrees well with the measured rate 0.31±0.11 min\(^{-1}\). Second, we reduced the concentration of SPD-5\text{WT} to a fraction of the wild-type concentration without introducing SPD-5\text{4A} and found that the PCM volume is reduced by a similar fraction (Fig. 2H-J). In summary, our model can capture the growth behavior in all our experiments when the only effect of the mutation of SPD-5 is that it cannot transition from form \( A \) to form \( B \).

In addition to the growth behavior discussed above, we also observed a slight increase in the density of wild-type SPD-5 over time in the experiment without the mutant (Fig. 2A). Our current model does not explain this behavior, since it considers phase separation with a constant density \( n_B \) of SPD-5 in its \( B \) form. However, the PCM is not a simple incompressible fluid but a complex polymeric material. Therefore, the incorporation of SPD-5 can lead to a transient buildup of elastic stresses in the PCM, which then relax, e.g., by internal rearrangement of SPD-5 molecules. If this relaxation is slow compared to the SPD-5 incorporation rate \( \lambda \), we expect increased SPD-5 densities over time. Conversely, if the relaxation rate is larger than or comparable to \( \lambda \), the density would be rather constant. We indeed observe these two cases in our experiments (Fig. 2A). Our data thus suggests that if only wild-type SPD-5 is present, PCM grows faster than stresses can relax, while they relax during the slower growth in the presence of SPD-5\text{4A}. Note however that the presence of GFP-SPD-5\text{4A} not only affects the growth rate \( \lambda \), but might also have an effect on the relaxation rate, which we cannot measure directly. We therefore did not analyze this further. Nevertheless, these arguments imply a slow stress relaxation rate of less than 0.5 min\(^{-1}\), which suggests that the PCM is a rather viscous, gel-like material.

Video abstract
A 2-min video abstract of this paper is available at https://youtu.be/KQsupW6h7Cc.

Acknowledgements
We thank the Protein Expression & Purification and Light Microscopy facilities of MPI-CBG (Dresden).

Competing interests
The authors declare no competing or financial interests.

Author contributions
O.W., J.B.W., and D.Z designed the experiments and wrote the manuscript. O.W. performed the in vivo experiments and quantifications of centrosome size and density as well as protein levels from western blots and stainings. D.Z. developed and tested the model with help from F.J. J.B.W. performed the in vitro experiments and in vivo analysis of centrosome size in the plk-1as embryos. Y.L.W and K.O. created the plk-1as gfp::spd-5 strain. A.A.H. assisted with experimental design.

Funding
This project was funded by the Max-Planck-Gesellschaft (Max Planck Society) and the European Commission’s Seventh Framework Programme [grant number FP7-HEALTH-2009-241548/MitoSys] and a Max Planck Research Network in Synthetic Biology (MaxSynBio) grant to A.A.H and F.J. J.B.W. was supported by an EMBO fellowship [no. ALTF 759-2012] and MaxSynBio.

Supplementary information
Supplementary information available online at http://bio.biologists.org/lookup/doi/10.1242/bio.020990.supplemental

References


Fig. S1. Protein levels in the used transgenic *C. elegans* strains

(A) Western blot analysis of transgenic and endogenous levels of SPD-5 in GFP::SPD-5\(^{WT}\) and GFP::SPD-5\(^{4A}\) expressing worms as shown previously in Woodruff et al. (2015).

Quantification of protein levels:

<table>
<thead>
<tr>
<th></th>
<th>WT</th>
<th>4A</th>
</tr>
</thead>
<tbody>
<tr>
<td>GFP::SPD-5</td>
<td>30%</td>
<td>29%</td>
</tr>
<tr>
<td>endog. SPD-5</td>
<td>70%</td>
<td>71%</td>
</tr>
</tbody>
</table>

Taken from Woodruff et al. (2015), Science
Fig. S2. Estimation of protein levels at the centrosome from immunostainings

(A) Ratio of transgenic GFP vs. total SPD-5 immunostaining signal at centrosomes based on quantification from Figure 2D.

(B) Demonstration of the workflow used to quantify PLK-1 and SPD-2 levels at the PCM of GFP::SPD-5WT and GFP::SPD-54A containing centrosomes (Figure 2F). Top panel shows intensity profiles of PLK-1 and SPD-2 staining signal depicting the strong centriolar localization of the two proteins, which was excluded for the analysis of PLK-1 and SPD-2 levels at the PCM. Bottom panel shows exemplary centrosomes with excluded centriolar signal. Yellow dotted lines indicate the boundary of the centrosome detected through automatic thresholding using Fiji.
Fig. S3. Data and concept used to generate and test the theoretical model

(A) Total SPD-5 amount at PCM approximated as the product of centrosome volume (Figure 1D) and mean maximum centrosome intensity (Figure 2A) corrected for protein concentrations.

(B) Energy diagram of possible conformational states of unphosphorylated and phosphorylated SPD-5.
Fig. S4. Analysis of cytoplasmic diffusion dynamics of transgenic SPD-5 molecules

(A) Normalized autocorrelation curves from fluorescence correlation spectroscopy measurements of GFP::SPD-5<sup>WT</sup> and GFP::SPD-5<sup>4A</sup> in the presence or absence of endogenous SPD-5. Lines represent means, shaded areas represent SEM. n = 8 for every experiment.

(B) Diffusion coefficients obtained from fitting the autocorrelation curves from measurements represented in (A) using a single component 3D anomalous diffusion model as previously described (Wueseke et al., 2014). Diffusion of GFP::SPD-5<sup>WT</sup> in the presence of endogenous SPD-5 (D = 1.2 ± 0.2 µm<sup>2</sup>/s), and GFP::SPD-5<sup>4A</sup> in the presence of endogenous SPD-5 (D = 1.1 ± 0.2 µm<sup>2</sup>/s), and GFP::SPD-5<sup>4A</sup> only (D = 1.0 ± 0.3 µm<sup>2</sup>/s).