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Membrane affinity difference between MinD monomer and dimer is not crucial for MinD gradient formation in *Bacillus subtilis*

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eLife Assessment

In the gram-positive model organism *Bacillus subtilis*, the membrane associated ParA family member MinD, concentrates the division inhibitor MinC at cell poles where it prevents aberrant division events. This **important** study presents **compelling** data suggesting that polar localization of MinCD is largely due to differences in diffusion rates between monomeric and dimeric MinD. This finding is exciting as it negates the necessity for a third, localization determinant, in this system as has been proposed by previous investigations.

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Abstract

Proteins can diffuse micrometers in seconds, yet bacterial cells are able to maintain stable protein gradients. The best studied bacterial protein gradient is the Min system of *Escherichia coli*. In rod-shaped bacteria the MinCD proteins prevent formation of minicells by inhibiting FtsZ polymerization close to the cell poles. In *E. coli* these proteins oscillate between cell poles within a minute, resulting in an increased MinCD concentration at the poles. This oscillation is caused by the interaction between MinD and the protein MinE, which form an ATP-driven reaction-diffusion system, whereby the ATPase MinD cycles between a monomeric cytosolic and a dimeric membrane attached states. *Bacillus subtilis* also has MinCD, but lacks MinE. In this case MinCD form a static gradient that requires the transmembrane protein MinJ, located at cell poles and cell division sites. A recent reaction-diffusion model was successful in *recreating* the MinD gradient in *B. subtilis*, assuming that MinD cycles between cytosol and membrane, like in *E. coli*. Here we show that the monomeric and dimeric states of *B. subtilis* MinD have comparable membrane affinities, that MinD interacts with MinJ as a dimer, and that MinJ is not required for membrane localization of MinD. Based on these new findings we tested different models, using kinetic Monte Carlo simulations, and found that a difference in diffusion rate between the monomer and dimer, rather than a difference in membrane affinity, is important for *B. subtilis* MinCD gradient formation.

Introduction

Bacterial cells are capable of positioning proteins at midcell and cell poles, and can form protein gradients without the support of specific membrane compartments or guidance by cytoskeleton elements, as found in eukaryotic cells. A well-known example is the formation of a MinCD protein

gradient along the cell axis of rod-shaped *E. coli* and *B. subtilis* cells. These proteins ensure that cell division occurs at midcell and not close to nascent division sites or cell poles (1). The formation of these protein gradients is remarkable considering that the diffusion of proteins in cells is in the order of μm^2 per second, whereas these bacteria are only a few μm in length (2).

The Min system of *E. coli* is the best studied gradient system, and comprises the membrane associated MinD and MinE proteins that form a reaction-diffusion couple (3-5), resulting in a MinCD gradient that oscillates between cell poles in a matter of seconds (6, 7). This system has been reconstructed on artificial membranes resulting in dynamic wave patterns (8), and extensively simulated to understand the reaction parameters (e.g. (3-5, 9-12)). *B. subtilis* also forms a MinD gradient that decreases in concentration from cell poles and nascent cell division sites towards the middle of the cell. However, unlike *E. coli*, this gradient does not oscillate (13-15). In this study, we investigated how the MinCD gradient is formed in *B. subtilis*.

The core of the Min system consists of the protein couple MinC and MinD that prevent aberrant polymerization of the key cell division protein FtsZ close to newly formed septa or cell poles (15-17). MinC inhibits polymerization of FtsZ by direct protein-protein interactions and needs to bind to the Walker A-type ATPase MinD for its recruitment to septa or the polar regions of the cell (18-21). Binding of ATP leads to MinD dimerization (22, 23), and subsequent association with the cell membrane, whereby its C-terminal amphipathic helix functions as membrane anchor (23, 24). MinC is recruited to the cell membrane by association with MinD dimers (23, 25, 26). The *E. coli* Min system comprises a third protein, the peripheral membrane protein MinE, that interacts with MinD, thereby displacing MinC and stimulating the ATPase activity of MinD, which ultimately triggers the release of MinD from the membrane (25, 27-30). The interaction with MinD causes a conformational change in MinE that stimulates its membrane affinity (27). These reciprocal interactions of MinD and MinE represent a natural reaction-diffusion system, resulting in the oscillation of MinCD proteins between cell poles with a periodicity of approximately 50 seconds (6-8). Through this oscillation, the average concentration of MinC is higher close to cell poles and lower at midcell, thereby inhibiting polymerization of FtsZ close to cell poles and favoring Z-ring formation at midcell (31).

The MinCD proteins of *E. coli* and *B. subtilis* are highly conserved. However, *B. subtilis* does not encode a MinE homologue and instead requires the proteins DivIVA and MinJ for the proper polar and septal localization of MinCD (32, 33). DivIVA is a general scaffold protein conserved in Gram-positive bacteria that associates with strong negatively curved membrane areas at the base of division septa, resulting in polarly located DivIVA clusters after division is completed (34, 35). The integral membrane protein MinJ interacts with DivIVA and shows the same localization pattern. MinJ also interacts with MinD, and inactivation of MinJ eliminates a MinCD gradient, resulting in filamentous cells and minicell formation due to uncontrolled activity of MinC (32, 33). Since DivIVA is recruited to midcell in the early stages of septum synthesis when a strong concave membrane area is formed (34), the Min proteins are already present when septum synthesis is ongoing, and their primary activity is to inhibit Z-ring formation next to nascent division sites (15).

The ATP-driven cycle between membrane association and dissociation of MinD is critical to the formation of the oscillating MinD gradient in *E. coli*. Mathematical modelling has shown that such an ATP-driven reversible membrane attachment cycle can also explain the formation of a MinD gradient in *B. subtilis* (36, 37). However, the C-terminal amphipathic α helix of *B. subtilis* MinD has a much stronger affinity for the cell membrane compared to its *E. coli* counterpart, and when fused to GFP can recruit this protein to the cell membrane, which the *E. coli* MinD C-terminal membrane anchor is not capable of (24). In fact, a MinD point mutant that prevents binding of ATP and maintains the protein in its monomeric state is still recruited to the *B. subtilis* cell membrane (38). It is therefore unclear whether dimerization-dependent changes in the membrane affinity of MinD are crucial for the formation of a *B. subtilis* MinCD gradient.

In this study, we analyzed and manipulated the membrane affinity of *B. subtilis* MinD, and combined *in vivo* experiments with *in silico* Monte Carlo simulations to assess the role of membrane affinity in the formation of a MinCD gradient. The main difference between our kinetic

Monte Carlo model and previous mathematic models based on reaction-diffusion equation is that our treatment is particle-based, rather than continuum field-based, and naturally includes the effect of stochastic fluctuations, i.e. noise of the system. The experiments demonstrated that, unlike in *E. coli*, a difference in membrane affinity between MinD monomer and dimer is not critical for the creation of a MinCD gradient. In addition, we examined how differences in MinD membrane affinity affect the recruitment of MinC to the membrane, a process that is critical for the FtsZ-regulating activity of the Min-system.

Results

Effect of dimerization on the localization of *B. subtilis* MinD

We began by examining how much the membrane affinity of monomeric *B. subtilis* MinD differs from the dimeric form by constructing MinD variants that are fixed in one of these conformations. Dimerization of MinD and other members of the MinD/ParA protein family requires binding of ATP. The conserved lysine in the Walker A-type ATPase domain, amino acid position 16 in the protein (Fig. S1), forms hydrogen bonds with the phosphate groups of the nucleotide, as revealed in the crystal structure of *Pyrococcus furiosus* MinD (39). Exchanging this residue into an alanine (K16A, apo monomer) prevents ATP binding and formation of dimers in several Walker motif-containing proteins, including *E. coli* MinD and RecA, and *B. subtilis* ParA/Soj (40–42). The conserved glycine at position 12 makes contacts with the γ -phosphate of ATP across the dimer interface (40). It has been shown that changing this residue into a valine in *B. subtilis* ParA causes a steric clash in the active site (G12V, ATP-bound monomer), thereby preventing dimerization while retaining ATP binding (40, 42). These two monomer-forcing amino acid exchanges (K16A and G12V) were introduced into *B. subtilis* MinD, which was fused at the N-terminus with GFP to follow its localization in the cell. It has been shown that a GFP-MinD fusion retains its biological activity (14), and the fusion protein was expressed at levels that resulted in normal sized cells and the absence of minicells (Fig. 1A). To prevent possible localization artefacts due to the weak dimerization characteristics of GFP (43), we used a monomeric GFP (mGFP) variant. The different MinD fusion proteins were expressed from the ectopic *amyE* locus, under control of the xylose-inducible *Pxyl* promoter (44), in a strain lacking wild type *minD* ($\Delta minD$), as well as in a strain lacking *minD* and *minC* ($\Delta minCD$). Western blot analysis showed that the different MinD-variants were stable and expressed at levels comparable to that of wild type MinD (Fig. S2). Induction of mGFP-MinD with 0.1 % xylose reduced minicell formation in a $\Delta minD$ background to wild type levels (from 14.7 % to 0.07 %, $n > 300$). However, the mGFP-MinD-K16A and -G12V variants were unable to prevent formation of minicells (11.2 % and 9.5 %, respectively, $n > 600$).

Fig. 1B shows the effect of the K16A exchange on mGFP-MinD localization. In line with previous results (38), preventing the binding of ATP abolishes the mGFP-MinD concentration gradient, which becomes clearer in longitudinal fluorescence intensity profiles (Fig. 1, right panels). The fluorescence peaks visible at midcell are caused by the presence of two septal cell membranes layers, as indicated by the fluorescence intensity profiles of a wild type cell stained with the fluorescent membrane dye FM 5-95 (Fig. 1G).

The monomeric ATP binding G12V variant shows the same absence of a protein gradient as the K16A variant (Fig. 1C). In contrast to *E. coli* MinD (29), both monomeric *B. subtilis* MinD mutants still bind to the cell membrane. To measure the membrane association *in vivo*, transverse fluorescence intensity profiles were collected (Fig. 1, middle panels), and the membrane affinities were estimated based on the ratio between valley (cytoplasmic) and peak (membrane) signals. This confirmed that the different monomeric mutants have a comparable membrane affinity as wild type MinD (Fig. 1F). As controls we used the fluorescence membrane dye FM5-95 and cells expressing cytosolic GFP (Fig. 1E).

It has been shown that exchanging a conserved aspartic acid residue in the ATPase domains of *B. subtilis* ParA and *E. coli* MinD blocks ATP hydrolysis and traps the proteins in a dimeric state (40, 42). When this aspartic acid residue, located at amino acid position 40 in the *B. subtilis* MinD sequence (Fig. S1), was replaced by an alanine (D40A, ATP-bound dimer, ATP hydrolysis deficient)

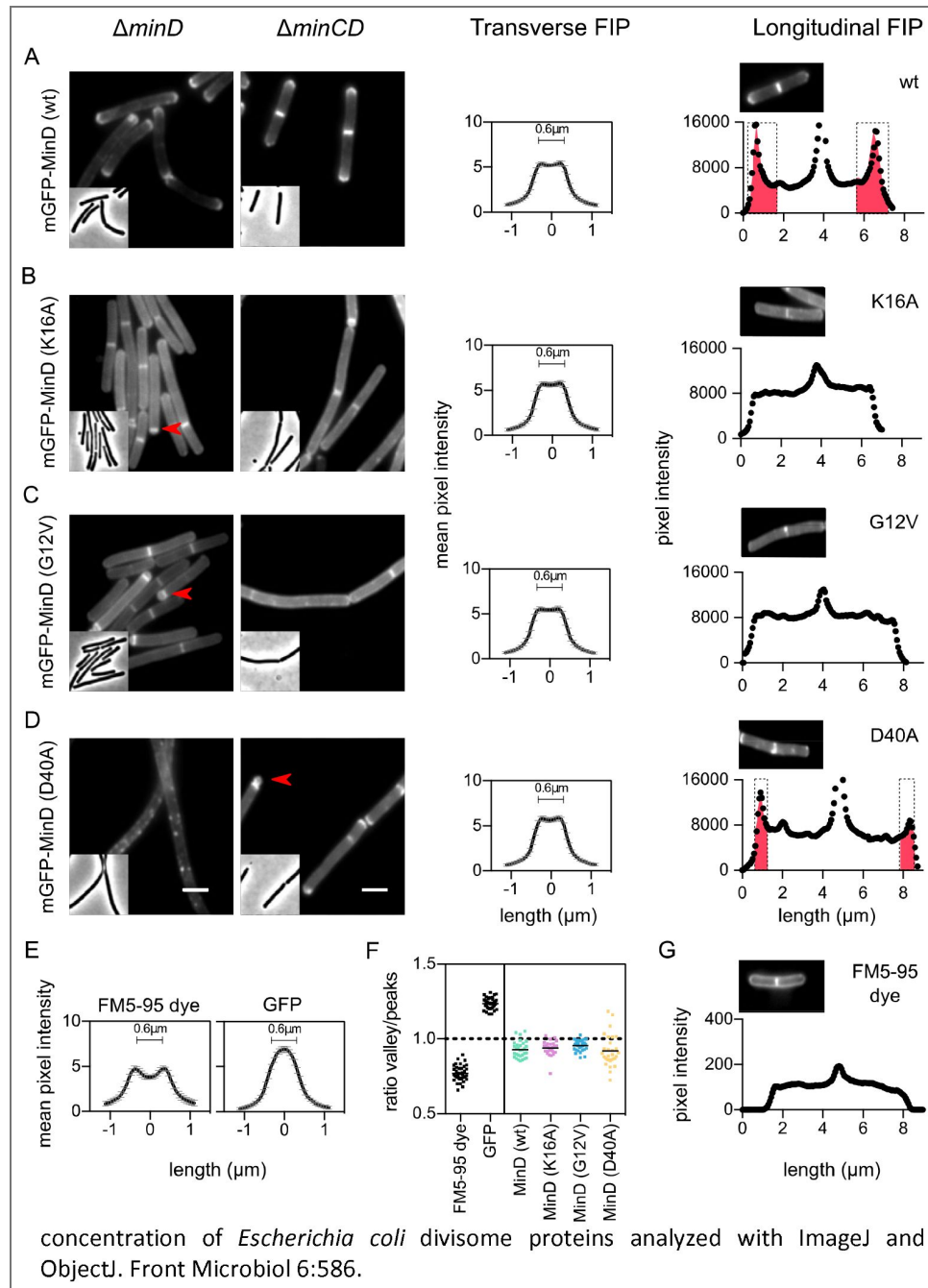


Fig. 1. Localization of monomeric and dimeric MinD variants

Cellular localization of (A) wild type MinD, (B) MinD K16A, (C) MinD G12V, and (D) MinD D40A. Localization was monitored by an N-terminal mGFP fusion. Fusion proteins were expressed in either a $\Delta minD$ or $\Delta minCD$ background. Fluorescence images (left panels) and corresponding phase contrast images (inset) are shown in the left panels. Some minicells are indicated with red arrows. Scale bar is 2 μm . Middle panels show the transverse fluorescence intensity profiles (FIP) with standard deviations calculated using an average of at least 30 cells ($\Delta minCD$ background) per data set. Right panels depict the longitudinal fluorescence intensity profiles (FIP) using the $\Delta minCD$ background. The manually shaded red areas highlight the polar gradients. Additional examples for wild type MinD and the D40A variants are shown in Fig. S3. (E) Transversal fluorescence intensity profile (FIP) with standard deviations of exponentially growing wild-type cells stained with fluorescence membrane dye FM5-95, and wild-type cells expressing GFP are shown as controls. (F) Membrane affinities, with median values, estimated from the valley/peak ratios shown in the middle panels of (A-D) and controls (E). (G) Longitudinal fluorescence intensity profile (FIP) along the exponentially growing wild-type cells stained with the fluorescence membrane dye FM5-95. Strains used in (A): LB249 and LB305, (B): LB250 and LB306, (C): LB251 and LB307, (D): LB252 and LB308, (E): LB609 and (G) 168.

in the mGFP-MinD fusion, expression of this variant in a $\Delta minD$ strain resulted in highly filamentous cells with clusters of mGFP-MinD-D40A formed along the membrane (**Fig. 1D** [↗](#), left picture). Introduction of a *minC* deletion restored cell division (**Fig. 1D** [↗](#), right picture), indicating that the locked MinD dimer causes hyper activation of MinC. Interestingly, in this $\Delta minCD$ background the clusters disappeared and mGFP-MinD-D40A showed a clear polar and septal accumulation, although the polar and septal signal intensities were approximately 60-70 % compared to that of wild type cells (Fig. S3B), and the longitudinal protein gradient was clearly reduced (**Fig. 1D** [↗](#) and S3A). Quantification of the membrane affinity showed that the membrane affinity of the D40A variant is only slightly higher compared to the monomeric mutants (**Fig. 1F** [↗](#)).

Localization of trapped MinD dimer depends on MinJ

The polar and septal localization of the D40A trapped dimer-variant of MinD presumably relies on the interaction with MinJ. It has been reported that the absence of MinJ results in detachment of MinD from the membrane (32, 37). However, when we introduced the $\Delta minJ$ in our $\Delta minCD$ deletion strain background we found that all MinD-GFP variants remained attached to the membrane, and the septal and polar localization of wild type and the trapped dimer MinD disappeared (**Fig. 2** [↗](#)). These results show that, while MinJ is not required for membrane attachment of MinD *per se*, it is required for polar and septal localization of MinD through interactions specifically with the dimeric form of MinD.

Recruitment of MinC by the different MinD mutants

Several biochemical studies with different bacterial species, including *B. subtilis*, have shown that MinC and MinD dimers can assemble into long polymers (45–48). However, the assembly of large MinCD multimers has not been observed *in vivo*, and a genetic study indicated that the formation of such polymers are not necessary for the function of the Min system in *E. coli* (49). The D40A MinD variant showed a clustered membrane localization pattern that resolved into a smooth membrane pattern when *minC* was deleted (**Fig. 1D** [↗](#)). This change in localization pattern might be related to the formation of higher-order MinCD assemblies. To confirm this, we introduced an active mCherry-MinC fusion to see whether mGFP-MinD and mCherry-MinC would colocalize when the former is fixed in a dimeric state. First, we examined the localization of MinC in the presence of monomeric K16A and G12V MinD variants. As shown in **Fig. 3B** [↗](#) and **C** [↗](#), the mCherry-MinC signal was dispersed throughout the cytosol in these strains, indicating a lack of interaction with monomeric MinD variants, in line with a previous report (38). In case of the mGFP-MinD-D40A variant, the mCherry-MinC expression was only induced for 1 h to prevent excessive filamentation. As shown in **Fig. 3D** [↗](#), the mCherry-MinC signal showed foci along the membrane that often colocalized with mGFP-MinD-D40A foci, confirming that MinD dimerization is crucial for MinC interaction, and that both proteins can indeed form large assemblies in the cell, presumably in the form of MinCD copolymers.

The colocalization of the MinD-D40A and MinC fluorescent fusion proteins enabled us to investigate whether MinD dimerization is sufficient for MinC activity or whether localization at the cell membrane is also required. To test this, the membrane binding capacity of MinD was impaired by replacing isoleucine 260, located in the C-terminal membrane targeting amphipathic alpha helix, with a glutamate residue (**Fig. 3E** [↗](#)) (50). Next, we introduced this mutation in the mGFP-MinD-D40A mutant to create a trapped MinD dimer that was no longer able to bind to the membrane. Expression of this cytosolic MinD variant did not result in cell filamentation (**Fig. 3F** [↗](#)), indicating that interaction with MinD dimers alone is not sufficient to inhibit FtsZ polymerization. Rather, MinC needs to be localized and enriched to the membrane surface to be effective, which is not surprising since Z-ring formation occurs at the membrane periphery.

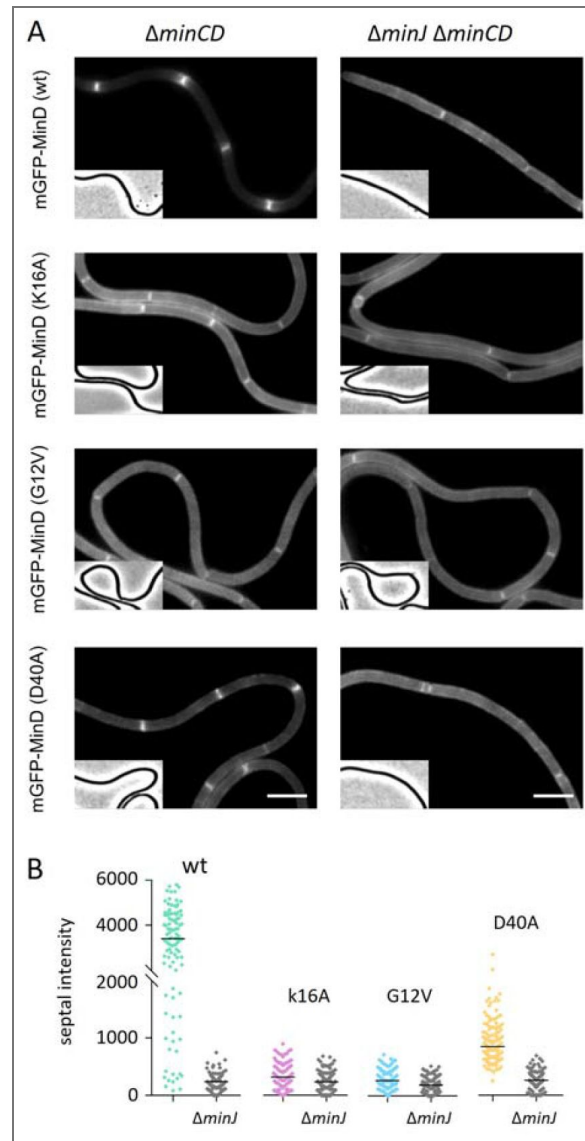


Fig. 2. Effect of a *minJ* deletion on MinD-GFP localization

(A) Fluorescence microscopy images of $\Delta minCD$ and $\Delta minJ \Delta minCD$ mutant cells expressing different mGFP-MinD variants. Corresponding phase contrast images are shown in the insets. (B) Quantification of related septal fluorescence intensities, with median values, at septa ($n > 100$). Since the strongly filamentous $\Delta minJ$ strain is delicate to handle, cells were grown on agarose patches on microscopy slides. Scale bar is 5 μm . Strains used for wt: LB405 and LB409, K16A: LB406 and LB410, G12V: LB407 and LB411, and D40A: LB408 and LB412.

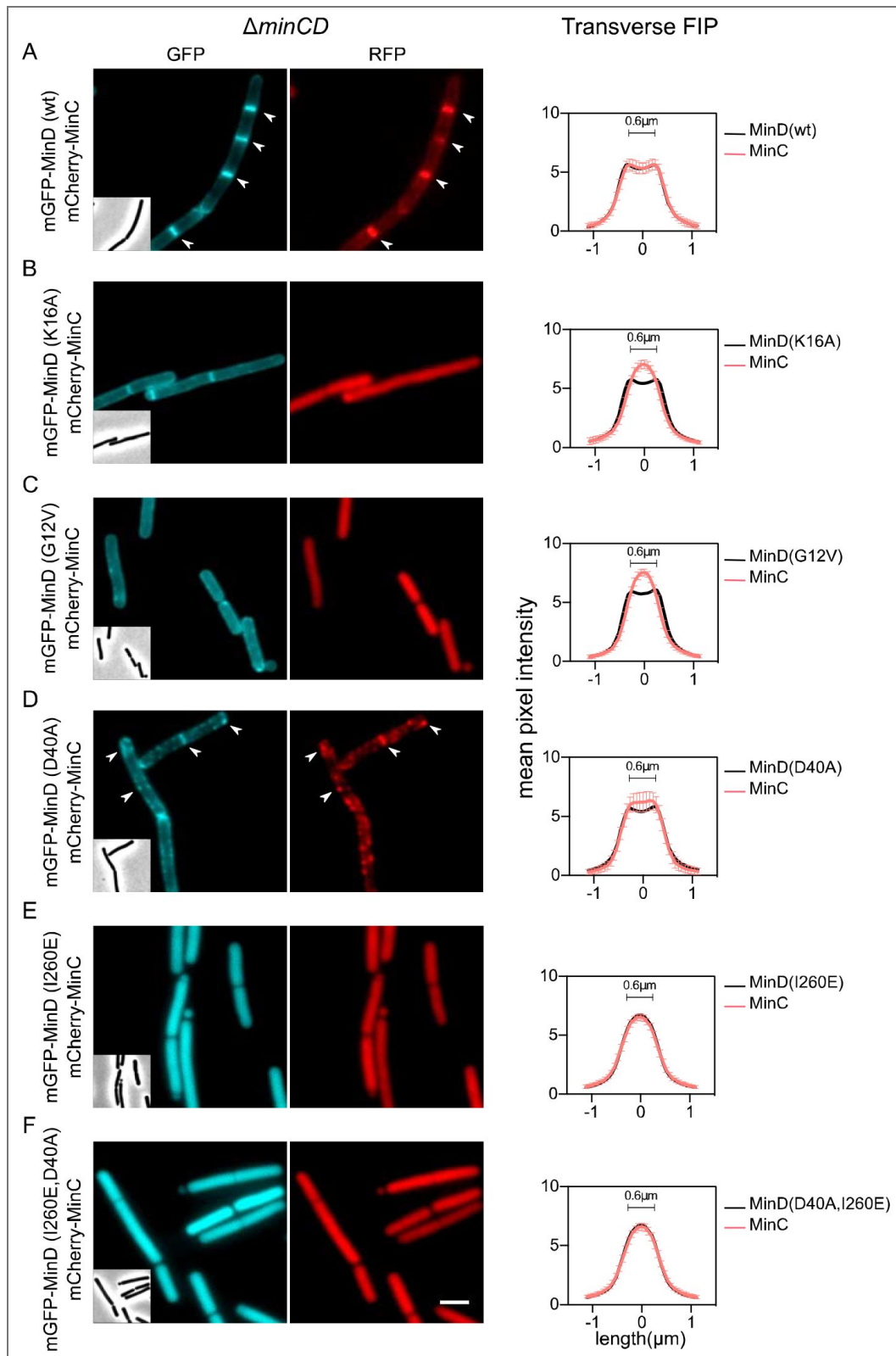


Fig. 3. Membrane recruitment of MinC by MinD variants

Fluorescence microscopy images of cells expressing different mGFP-MinD variants (cyan) and mCherry-MinC (red). Corresponding phase contrast images shown in the insets. (A) Wild type MinD, (B) MinD K16A, (C) MinD G12V, (D) MinD D40A, (E) MinD I260E, (F) MinD D40A, I260E. Right panels show the transverse fluorescence intensity profiles (FIP) with standard deviations averaged over at least 30 cells. White arrows in (D) highlights colocalization. Scale bar is 2 μ m. mGFP-MinD variants and mCherry-MinC were expressed in a Δ minCD background strain. Strains used: (A) LB318, (B) LB319, (C) LB320, (D) LB321, (E) LB643 and (F) LB644.

Weak membrane interaction is important for MinD gradient formation

The absence of a clear difference in membrane affinity between monomeric and dimeric MinD raised the question whether a reversible membrane binding is important for the formation a protein gradient. To examine this, we tried to increase the membrane affinity of MinD by adding an extra copy of its C-terminal membrane targeting amphipathic helix. The extra amphipathic helix was connected to the original helix by a short 11 amino acid long flexible linker (**Fig. 4A**). First, we tested whether such tandem amphipathic helix (2xAH) increases the membrane affinity by fusing it to mGFP. As shown in **Fig. 4B**, fusion of this tandem helix to mGFP increased the membrane association of the latter considerably when compared to a single MinD amphipathic helix.

Next, we replaced the membrane targeting amphipathic helix of mGFP-MinD by the tandem amphipathic helix. Western blot analysis showed that this new C-terminus did not affect the protein levels to a significant degree (**Fig. S2**). As shown in **Fig. 5B** and **D**, the tandem helix notably increased the fluorescent membrane signal all along the cell membrane, thereby reducing the longitudinal fluorescence gradients.

To confirm that the tandem amphipathic helix increased the membrane affinity of MinD, we tested its sensitivity to membrane depolarization. Previously, it has been shown that binding of the MinD amphipathic helix to the cell membrane requires the presence of the membrane potential (50). Dissipation of the proton motive force by the specific proton-ionophore carbonyl cyanide *m*-chlorophenylhydrazine (CCCP) did not affect the membrane localization of the tandem amphipathic helix fusion, whereas CCCP quickly disturbed the membrane attachment of wild type MinD (**Fig. S5**).

We also tested what happens with the MinD gradient when its membrane affinity is reduced. For this, the well-studied membrane binding amphipathic helix 2 from the Hepatitis C virus protein NS4B was chosen (51, 52), which is hardly able to attach mGFP to the cell membrane (**Fig. 4B**). Replacing the wild type membrane targeting helix of MinD by the weak NS4B amphipathic helix reduced the membrane association of mGFP-MinD (**Fig. 5D**), as well as its septal and polar localization (**Fig. 5C** and **Fig. S4**). Interestingly, this mutant still displayed a longitudinal protein gradient. Together these data suggests that a reversible membrane association is important for the formation of a MinD gradient along the cell axis.

Effect of MinD membrane affinity on MinC recruitment and activity

The results shown in **Fig. 3B** indicated that the attachment of the MinD dimer to the membrane is essential for the activity of MinC. When this attachment was strengthened by using the tandem amphipathic helix, the respective strain regularly featured additional septa resulting in minicells (**Fig. 5B**, red arrows), although the frequency was lower compared to a $\Delta minD$ mutant (**Fig. 6A**). The strain also exhibited an elongated cell phenotype that was comparable to that of the *minD* deletion strain (**Fig. 6B**). As shown in **Fig. 7B**, the mGFP-MinD(2xAH) variant is capable of recruiting mCherry-MinC along the whole cell membrane, which likely explains the elongated cell phenotype.

Weakening the membrane affinity of mGFP-MinD, by replacing the wild type amphipathic helix with the NS4B amphipathic helix, also resulted in occasional minicell formation, but again not as numerous as in a *minD* deletion strain (**Fig. 6A**). The cell length distribution of the strain expressing the mGFP-MinD(NS4B-AH) variant was closer the wild type strain (**Fig. 6B**). When mCherry-MinC was co-expressed in this strain background, also the MinC fusion protein showed a clear fluorescent gradient along the cell axis (**Fig. 7C**). Thus, a reversible association of MinD with the cell membrane seems to be critical to prevent misplacing the FtsZ inhibiting activity of

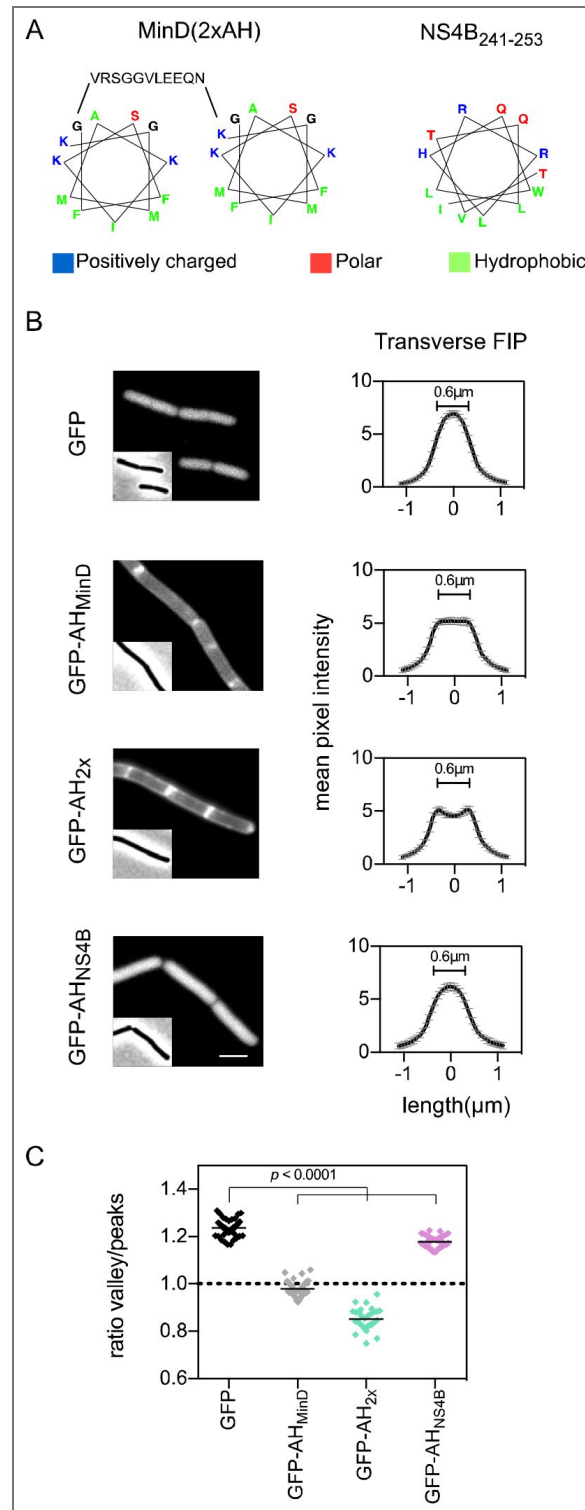


Fig. 4. Membrane association of different amphipathic helices

(A) Schematic presentation of the tandem amphipathic helix and the weak amphipathic helix from Hepatitis C virus protein NS4B₂₄₁₋₂₅₃. (B) Fluorescence microscopy images and transverse fluorescence intensity profiles (FIP) with standard deviations of cells expressing the different amphipathic helix sequences fused to the C-terminus of GFP. A strain expressing cytoplasmic GFP was included for comparison. Scale bar is 2 μm. Strains used: FBB043 (GFP-AH_{MinD}), FBB05 (GFP-AH_{2x}), FBB046 (GFP-AH_{NS4B}), LB609 (GFP). (C) Average membrane affinities calculated from the transverse fluorescence intensity profiles ($n > 30$). Significance of difference was confirmed using t-test.

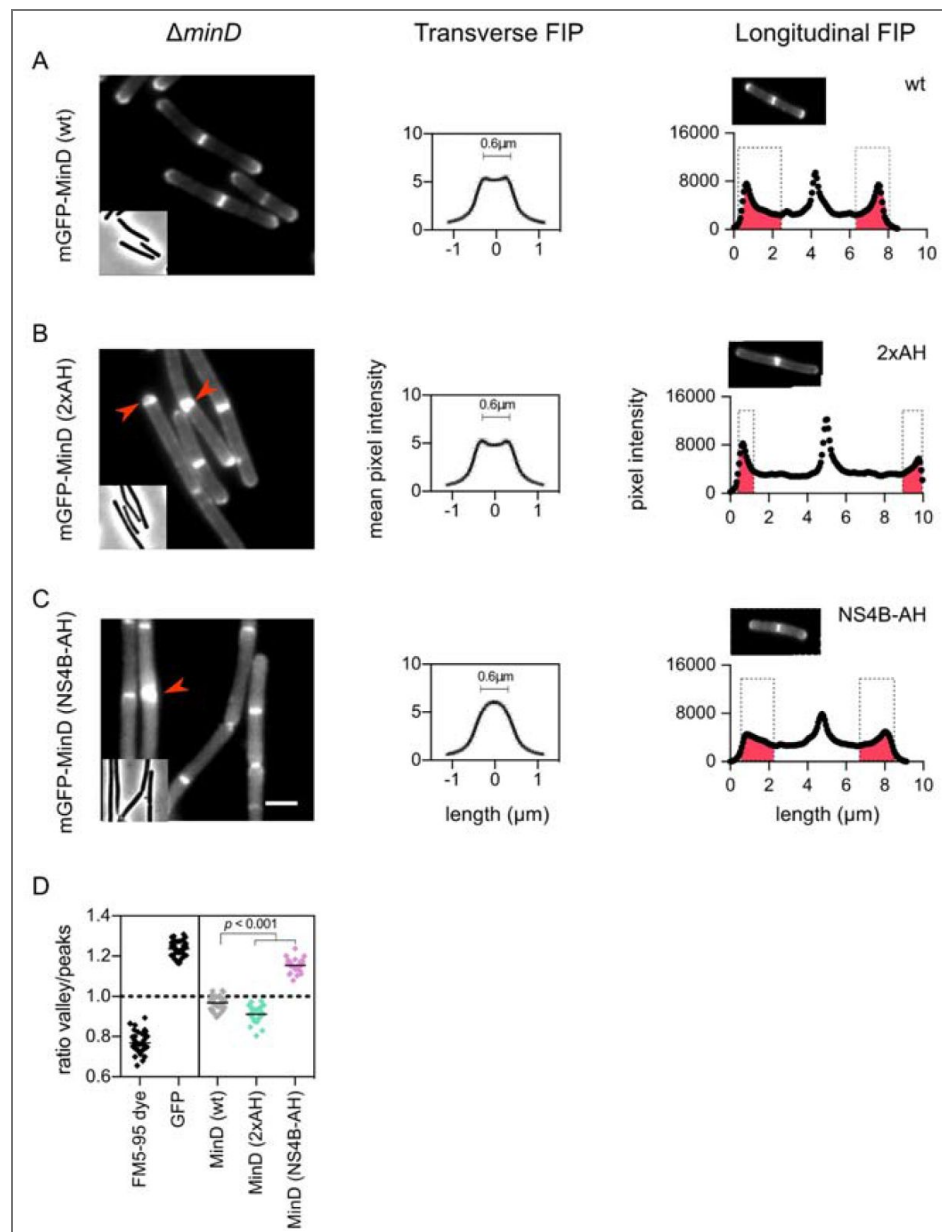


Fig. 5. Membrane affinity affects MinD gradient

Fluorescence microscopy and fluorescence intensity profiles (FIP) with standard deviations of cells expressing mGFP-MinD containing either the native amphipathic helix (wt) (A), the tandem MinD amphipathic helix (2xAH) (B) or the weak Hepatitis C virus protein NS4B amphipathic helix (NS4B-AH) (C). The manually shaded red areas highlight the polar gradients. Additional examples are shown in Fig. S4. (D) Relative membrane affinities with median values of the different mGFP-MinD variants calculated from transverse fluorescence intensity profiles ($n > 30$). Significance of difference was confirmed using t-test. The MinD variants were expressed in a $\Delta minD$ background. Phase contrast images are shown as insets. Some double septa are indicated with red arrows. Scale bar is 2 μm . Red areas in the intensity profiles highlight the polar gradients. Strains used in (A) LB249, in (B) LB507, in (C) LB508.

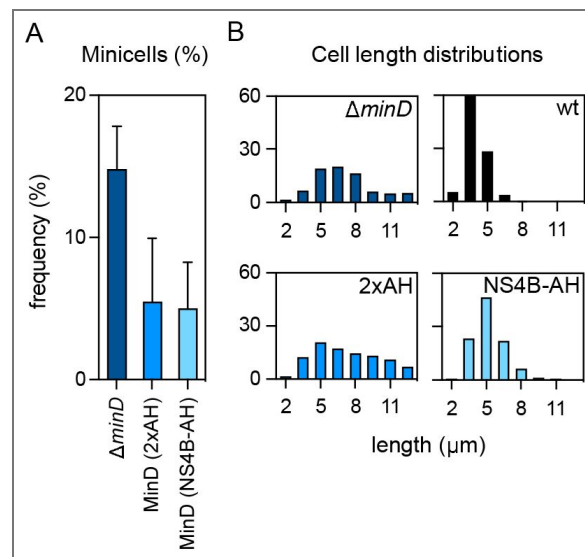


Fig. 6. Functionality of MinD with different membrane affinities

(A) Minicell formation in cells expressing mGFP-MinD with different membrane affinities. The MinD variants were expressed in a $\Delta minD$ background ($n > 300$). Standard deviations are indicated. (B) Cell length distributions of the different strains ($n > 300$). Strains used: 1901 ($\Delta minD$), LB249 (wild type MinD), LB507 (2xAH) and LB508 (NS4B-AH).

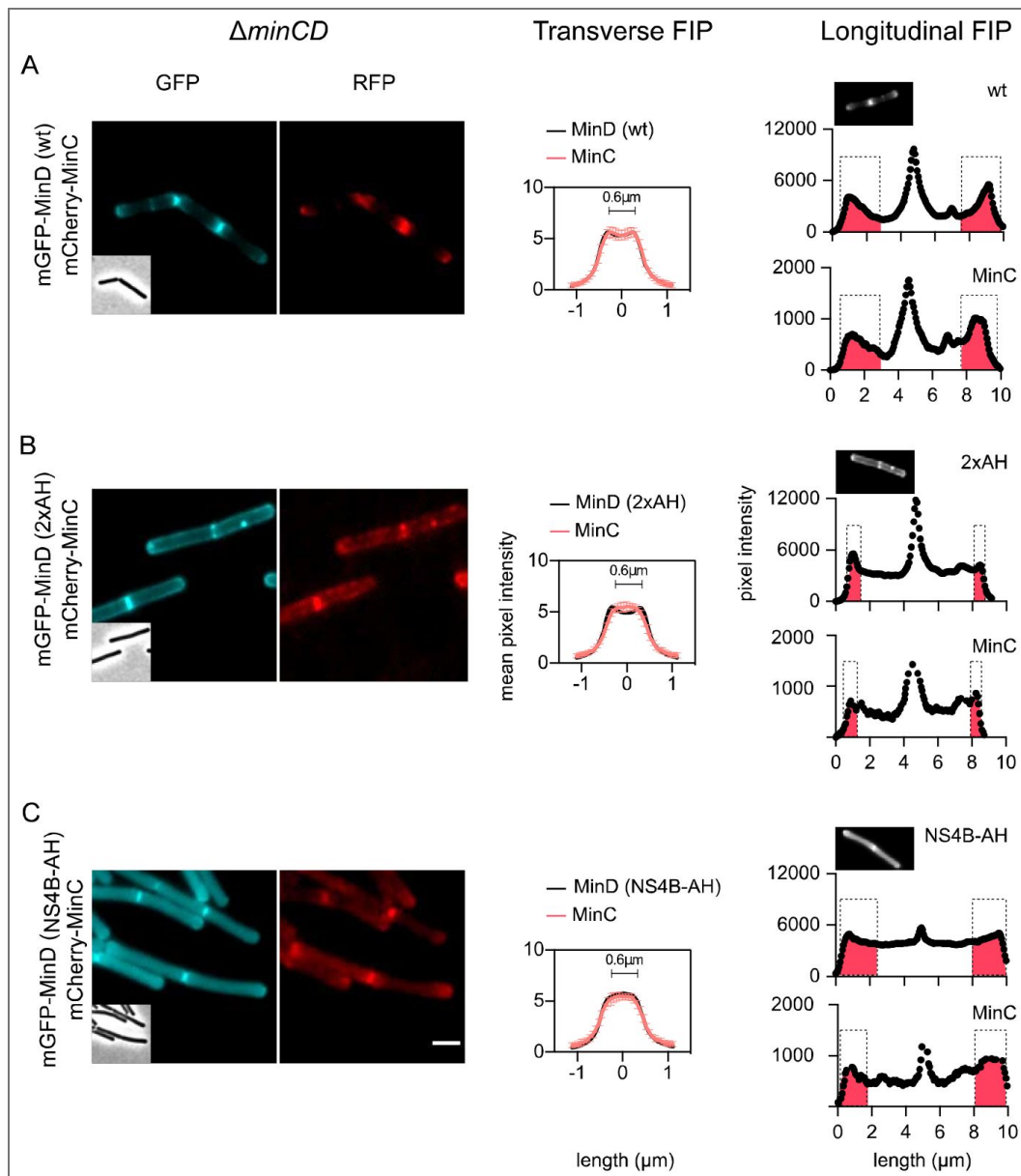


Fig. 7. Increased MinD membrane affinity affects MinC recruitment

Fluorescence microscopy images of cells expressing mGFP-MinD (cyan) and mCherry-MinC (red), with either the native membrane anchor (A), the tandem amphipathic helix (B), or the weak Hepatitis C virus protein NS4B derived amphipathic helix (C). Corresponding phase contrast images are shown in insets. Scale bar is 2 μm . Transverse fluorescence intensity profiles (FIP) with standard deviations are shown in the right panels ($n > 30$). Right panels depict the longitudinal fluorescence intensity profiles (FIP) with manually shaded red areas to highlight the polar gradients. Additional examples are shown in Fig. S6. The mGFP-MinD variants and mCherry-MinC were expressed in a ΔminCD background strain. Strains used: (A) LB318, (B) LB584, (C) LB559.

MinC along the cell axis. Both the mGFP-MinD(2xAH) and mGFP-MinD(NS4B-AH) variants were, at least partially, able to prevent minicell formation, presumably because they are still recruited to cell poles and cell division sites through interaction with MinJ.

Membrane gradient formation in kinetic Monte Carlo simulations

The different experiments indicated that the formation of a MinCD gradient requires the dynamic switching between monomer and dimer states of MinD (Fig. 1), and a reversible MinD membrane interaction (Fig. 5). So far, *in silico* simulations of the *B. subtilis* Min gradient have assumed a strong difference in membrane interaction between the monomeric and dimeric state of MinD, which is based on properties of the *E. coli* Min system (36, 37). However, our data suggests that for *B. subtilis* these affinities do not differ much (Fig. 1). To investigate more closely whether a difference in membrane affinity between monomer and dimer is required for the formation of a MinD gradient in *B. subtilis*, we resorted to kinetic Monte Carlo simulations (see Methods for more details). The Monte Carlo algorithm attempts to move one molecule at a time by a small amount in a three-dimensional space. The new interaction energy experienced by the particle is then calculated and compared with its old energy, and the move is subsequently accepted or rejected according to the standard Metropolis test (53, 54). This procedure is used to guide the system to the correct Boltzmann distribution in equilibrium. It has been shown that this Monte Carlo dynamics corresponds well with Brownian or molecular dynamics (55, 56), and can be used to examine mechanisms underlying spatiotemporal protein gradients in cells (34), provided that the moves are small enough and that the acceptance probability remains high (55).

MinD monomers were presented as spheres (hydrodynamic radius 2.5 nm) that diffuse within and along a spherocylindrical cell geometry. The following rules were implemented: (i) Diffusion along the membrane is 10-fold slower than through the cytoplasm, and (ii) the dimer, due to its larger diameter, diffuses 2-fold slower compared to the monomer in both environments, emanating from Stokes-Einstein law and a hydrodynamic radius for the dimer which is double that of the monomer. (iii) Based on the data from Fig. 3, we started out with a 10 % stronger membrane affinity for the dimer. (iv) The membrane dwell time of monomers and dimers is 0.01 - 0.5 sec and during the simulations approximately 70 % of MinD molecules reside at the membrane, approaching the valley to peak values observed experimentally (Fig. 1F). (v) Dimerization and monomerization are modelled as chemical reactions between a monomer and a dimer state. Baseline rates are set such that the two states are in a 1:1 ratio, based on the longitudinal fluorescence intensity profile in Fig. 1A, and the assumption that dimers are located at the polar regions and monomers along the lateral wall. In our baseline model, dimerization at the pole, membrane and in the cytoplasm is equally likely, and is modelled in a simple way as a reaction turning a monomeric to a dimeric MinD at constant rate. (vi) The transition from dimer to monomer, stimulated by ATP hydrolysis, occurs stochastically with a half-life of approximately 1/sec, which is based on information from *E. coli* MinD (5). (vii) MinD dimers that come in close proximity of MinJ, represented as the surface area at the polar caps, will remain attached to MinJ for some time, so that approximately 25 % of MinD dimers is associated with MinJ, reminiscent of the septal localization of the D40A variant (Fig. S3). We simulated 10^7 time steps, corresponding to about 100 s real time, when the system is in steady state. Simulation details are described in the material and methods, and a full list of parameters and their typical values considered in simulations is presented in Table S1.

When we applied these rules and ran the simulation, a strong accumulation of MinD at the poles was observed, but no gradient (Fig. 8A). In this simulation, the chance that MinD can form a dimer is the same for monomers in the cytoplasm and those that are attached to the membrane. However, it is likely that dimer formation in the latter situation is more likely since monomers attached to the membrane by their C-terminal amphipathic helix will diffuse slower and therefore spend more time in close proximity and, importantly, they have the same spatial orientation, which will facilitate dimerization. However, when we repeated the simulation, and implemented that membrane attached monomers have a 2-fold higher chance of forming dimers than monomers in the cytoplasm, the localization pattern did not change (Fig. 8B).

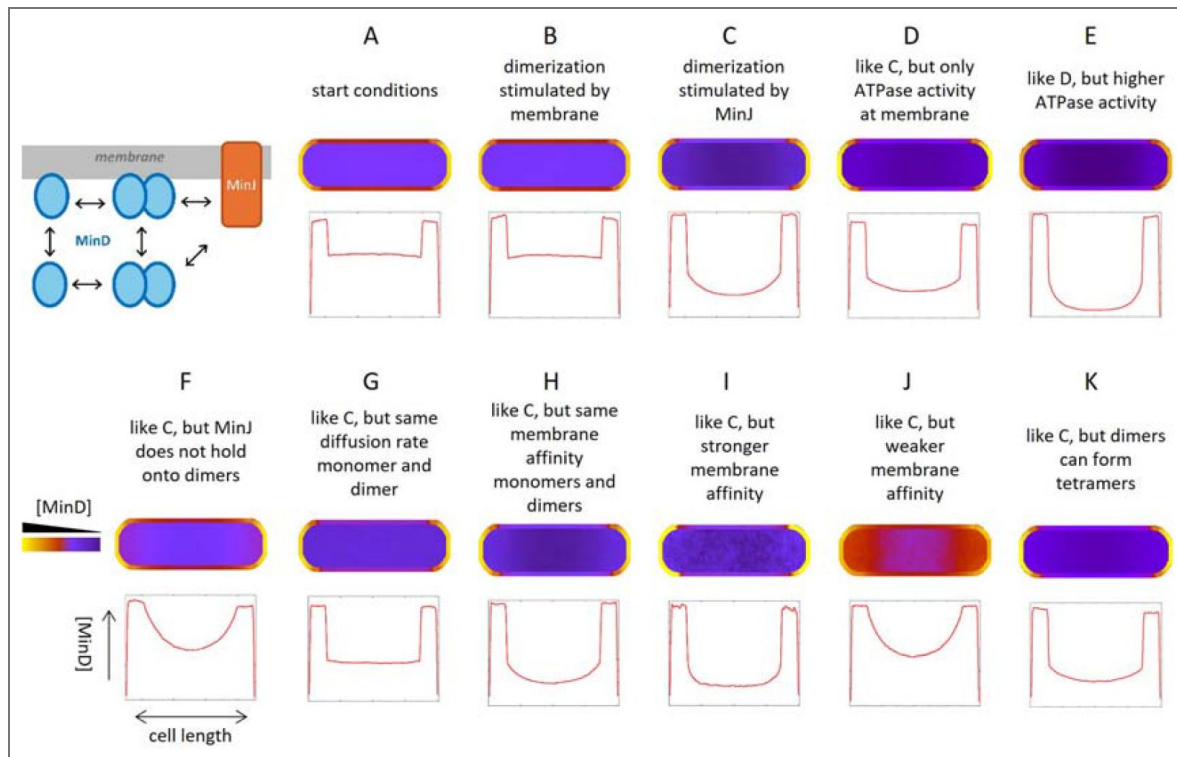


Fig. 8. Kinetic Monte Carlo simulations of MinD localization

Whole-cell kinetic Monte-Carlo simulations of MinD distribution, taking into account dimer-to-monomer transition rates (ATPase activity), membrane affinities, and MinJ interaction (schematic model). The following conditions have been simulated: (A) Start situation whereby (i) diffusion along the membrane is 10-fold slower compared to cytoplasm, (ii) MinD dimer diffuses 2-fold slower compared to the monomer in both environments, (iii) 10 % stronger membrane affinity for dimer, (iv) membrane dwell time of monomers and dimers on average 1.4-4.5 sec, (v) dimerization and monomerization rates such that dimers and monomers are approximately in a 1:1 ratio, (vi) transition from dimer to monomer occurs stochastically with a half-life of approximately 1/sec, and (vii) MinD dimers in close proximity of polar regions (peak MinJ concentration) will remain attached for some time, so that approximately 25 % of MinD dimers is associated with the polar caps, representing MinJ. (B) Same as simulation A, but membrane attached monomers have a 2-fold higher chance of forming dimers compared to cytoplasmic monomers. (C) Same as simulation A, but MinJ also stimulates MinD dimerization. (D) Same as simulation C, but MinD ATPase activity, i.e. dimer-to-monomer transition, only occurs at the membrane. (E) Same as simulation D, but with a 10-fold higher ATPase activity, i.e. dimer-to-monomer transition. (F) Same as simulation C, but MinD dimers are not retained by MinJ. (G) Same as simulation C, but diffusion rates of monomer and dimer are the same. (H) Same as simulation C, but the membrane affinity of MinD monomers and dimers is the same. (I) Same as simulation C, but membrane affinity of MinD is stronger, such that the diffusion is a further 10-fold slower on the membrane. (J) Same as simulation C, but membrane affinity of MinD is 2-fold weaker. (K) Same as simulation C, but now MinD dimers can also form tetramers. Graphs indicate the average lateral projection of MinD in simulated cells.

Since it seems that MinJ interacts with the dimer form of MinD (Fig. 2C), there is the possibility that MinJ actually stimulates MinD dimerization. Interestingly, when this property was added to the simulation, a clear MinD gradient emerged along the cell length, together with a strong polar localization signal (Fig. 8C), a pattern that is in good agreement with the longitudinal fluorescence intensity profiles observed *in vivo* (Fig. 1A). This pattern did not change when we included the condition that only membrane attached dimers are able to revert to monomers (Fig. 8D, E), in agreement with a recent report showing that the ATPase activity of MinD depends on its interaction with lipid membranes (57). In the simulation of Fig. 8E, we repeated the simulation of Fig. 8D, but increased the ATPase activity, i.e. dimer-to-monomer transition 10-fold. This enhances MinD gradient formation.

When we performed the simulation of Fig. 8C but now with the assumption that MinJ only stimulates dimerization and does not bind MinD dimers, a MinD gradient is still formed, although the strong accumulation at the polar caps was abolished (Fig. 8F). Subsequently, we repeated the simulation of Fig. 8C under conditions whereby there was no difference in the diffusion rate of monomer and dimer (Fig. 8G). In this case the MinD gradient was completely lost, showing that the differential diffusion of monomers and dimers is necessary to create a steady-state gradient.

Next, we tested the role of the membrane affinity in gradient formation. First, the simulation of Fig. 8C was repeated without a difference between the membrane affinity of the MinD monomer and dimer (Fig. 8H). Interestingly, under these conditions the MinD protein gradient is still being formed. When we repeated the simulation of Fig. 8C and kept the 10 % difference in membrane affinity between MinD monomer and dimer, but made their membrane affinities stronger, the gradient was reduced (Fig. 8I), in good agreement with our *in vivo* observation with a MinD variant containing a tandem membrane anchor (Fig. 5B). We then tested what happens when the simulation of Fig. 8C was repeated with a weaker membrane affinity of MinD. As shown in Fig. 8J, a clear gradient is formed, again in line with what was found when the membrane targeting amphipathic helix of MinD was replaced with the weaker amphipathic helix 2 from Hepatitis C virus protein NS4B (Fig. 5C).

It has been shown that purified *E. coli* MinD can form large polymers in the presence of ATP (58), and when bound to membranes can stimulate multimerization (59). Multimerization might further increase the diffusion difference between monomer and dimer, thus contributing to the formation of a protein gradient. Multimerization is challenging to model in our simulation setup, but as an approximation we tested what happens when MinD dimers can form tetramers. We ran a simulation whereby the baseline rates of dimer to tetramer and tetramer to dimer formations were equal. However this did not lead to a dramatic change in MinD gradient (Fig. 8K). In conclusion, our kinetic Monte Carlo simulations suggests that the formation of a MinD gradient requires: (i) a reversible and not too strong interaction of MinD with the membrane, (ii) a clear difference between the diffusion rates of monomer and dimer, (iii) an ATPase driven dimer-monomer cycle, and (iv) the stimulation of dimerization at the cell poles and division sites. Importantly, a difference in membrane affinity between monomer and dimer is not required.

Discussion

Protein gradients in bacteria

Due to their small size, proteins diffuse rapidly throughout bacterial cells, in a matter of seconds, yet stable protein gradients can be found in a large variety of bacteria. What these systems have in common, including the MinD gradient, is a locally reduced diffusion rate of the proteins involved, which allows stable protein concentration gradients to form. The viscosity of the cell membrane is roughly 100 times larger compared to the cytoplasm (60, 61), and the Min system uses attachment to the cell membrane to slow down diffusion. Another approach to reduce diffusion is to bind to DNA, which occurs in the ParABS system involved in chromosome segregation in the asymmetric bacterium *Caulobacter crescentus* (62). This system consists of the ParA ATPase, which belongs to the same ATPase family as MinD (63) and ParB that binds to *parS* DNA binding sites. The ParA

dimers associate with DNA nonspecifically whereby ParB stimulates ATP hydrolysis of ParA dimers, resulting in the dissociation from DNA. The localized dissociation and subsequent increased diffusion rate results in a ParA concentration gradient away from the *parS* locus (64). The cyanobacterium *Synechococcus elongatus* uses the ParA-like protein McdA to position carboxysomes along the longitudinal axis. In this system, the protein McdB, which interacts with carboxysomes, stimulates McdA ATPase activity and its release from DNA, resulting in an oscillation of McdA over the nucleoid (65). Recently it was described that *Staphylococcus aureus* trigger factor (TF) forms a gradient by interacting with the cell division protein FtsK, resulting in an increased TF concentration towards the septal region (66). How TF reduces its diffusion in *S. aureus* cells is still unclear but might be a consequence of the fact that the chaperone directly interacts with ribosomes (67), which diffuse much slower due to their size and association with mRNA and nascent polypeptide chains.

Previous MinD gradient modelling studies

As mentioned in the introduction, there are many mathematical models describing the oscillating MinD gradient of *E. coli* but so far only two mathematical models focused on the MinD gradient of *B. subtilis* (36, 37). Both models make use of the reversible interaction of MinD with the cell membrane. The first study, almost 20 years ago, modelled the localization of DivIVA and MinD by a reaction-diffusion system in one spatial dimension (36). At that time neither MinJ nor the localization mechanism of DivIVA were known. In this early study both MinD and DivIVA were assumed to cycle between the membrane and the cytosol, and the membrane attachment of DivIVA would depend on MinD, whereas the membrane attachment of the latter would be stabilized at the cell poles by DivIVA. However, we now know that DivIVA binds to the membrane by itself, and there is no interaction between MinD and DivIVA (34).

The ATPase stimulated monomer-dimer cycle of MinD was not included in this early model, but it was used in a recent study that employed a minimal reaction-diffusion system in three-dimensional cellular space (37). In this model *B. subtilis* MinD cycles between the cell membrane and cytosol, whereby the membrane detached MinD is in the ADP-bound state and can only rebind after exchanging ADP for ATP, like in *E. coli*. By assuming that the membrane recruitment rate is higher at the poles and septa due to the presence of MinJ or due to a kinetic increase of diffusional impacts with the membrane due to the curved geometry at poles, a steep MinD gradient could be simulated (37).

New data on MinD localization

Here, we have shown that monomeric MinD, both in its ATP-bound and unbound state, has a membrane affinity that is comparable to that of the dimeric form of MinD, which is clearly different from *E. coli* MinD that requires dimerization for membrane association. In fact, it has been shown that the C-terminal membrane targeting amphipathic helix of *E. coli* is considerably weaker than that of *B. subtilis* MinD, and that stable membrane binding is only possible when a dimer is formed so that there are two membrane targeting domains (24). Our findings are in good agreement with a recent report showing a strong membrane affinity for purified monomeric *B. subtilis* MinD for liposomes, independent of the presence of ATP (57).

We have also shown that MinJ is not required for the membrane recruitment of MinD (Fig. 2). We have no explanation for the differences between our findings and that of the previous studies in which it has been shown that MinJ is needed for the membrane localization of MinD (32, 37). However, since the membrane-targeting amphipathic alpha helix of *B. subtilis* MinD is by itself sufficient to recruit GFP to the cell membrane, even in *E. coli*, which does not contain a MinJ homologue (24, 50), it is difficult to envision how the absence of MinJ would bring MinD to the cytosol.

In another study, it has been suggested that the C-terminal amphipathic helix of MinD by itself is sufficient to recruit GFP to cell division sites, even in the absence of either MinJ or DivIVA (68). However, as indicated in Fig. 1, the presence of two perpendicular-observed membranes that are formed during septum synthesis gives a higher fluorescence membrane signal, which might

have been mistakenly interpreted as septal localization. In addition, in our hands a GFP fusion with the C-terminal amphipathic helix of *B. subtilis* MinD shows a clear fluorescence membrane stain but no accumulation at division sites (Fig. 4B).

Kinetic Monte Carlo model

Our *in vivo* findings warranted a new mathematical model to study the formation of the *B. subtilis* MinD gradient (see Methods for more details). The kinetic Monte Carlo model showed that a membrane attachment-detachment cycle is not required to form a protein gradient, but that a dynamic ATP-driven cycle between monomer and dimer is crucial, coupled to the differences in diffusion rates. We have shown that the MinD dimer associates with MinJ, but this by itself, even when the interaction was reversible, was not enough to create a gradient. We ascribe this to the fact that both monomers and dimers bind to the membrane with small difference in affinities in our model, whereas in (37) the monomer state is not membrane-associated. To establish a gradient in our simulations, we needed to include the requirement that MinJ stimulates and/or stabilizes MinD dimerization, but this MinJ activity remains speculative. It should be stressed that MinJ is not crucial for MinD dimerization, since a *minJ* mutant shows a strong filamentous phenotype that can be suppressed by a *minC* deletion, indicating that MinD dimerization, required for MinC activity, also occurs in the absence of MinJ.

Although a difference in membrane affinity between monomer and dimer is not necessary to establish a gradient, the modelling shows that a transient and reversible membrane binding of MinD is necessary. This was also confirmed by the reduced formation of a gradient when the membrane affinity of MinD was increased by using a tandem C-terminal amphipathic helix (Fig. 5B). This can be explained by considering the emergent length scale over which the gradient develops. As in reaction-diffusion models for morphogenesis, this length scale is given by the square root of a diffusion coefficient over a reaction rate. Our simulations suggest that a possible formula is given by $l \sim \sqrt{\frac{D_m - D_d}{k_m}}$, with D_d and D_m the dimer and monomer diffusion (the relevant rate is that on the membrane), and k_m the rate of conversion between dimers and monomers. Increasing the interaction with the membrane leads to a decrease in diffusivity, and concomitantly a reduction in the length scale over which the gradient can be observed.

In our modelling, MinJ is simply represented by the polar cap area. FRAP studies have shown that the recruitment of MinJ to cell poles and division sites is quite dynamic with a fluorescence recovery rate close to a minute (37). However, the fluorescence recovery rate of MinD is approximate 8-fold higher (37). Because of this large difference in diffusion rates, we have ignored the diffusion of MinJ in our modelling. We do not foresee different results if we were to include MinJ diffusion in our Monte Carlo simulations, provided that in steady state MinJ is on average localized at the poles.

Another aspect that we have only partially addressed in the simulations is MinD polymerization. It has been shown that purified *E. coli* MinD can form large polymers in the presence of ATP (58), and, when bound to membranes, can stimulate multimerization (59). In our simulations we tested the effect of MinD tetramerization, however, this did not improve MinD gradient formation (Fig. 8K). It should be mentioned that formation of large polymers was not found with purified *B. subtilis* MinD (48). Moreover, FRAP experiments with *B. subtilis* shows a fluorescence recover rate of seconds for MinD at division sites (37), suggesting that if such polymers exist, they are not very stable. Thus, it remains to be seen whether MinD multimerization is relevant in *B. subtilis* cells.

In conclusion, we have shown here that a dynamic cyclic change in membrane affinity of MinD is not required for the formation of a concentration gradient in the cell. Instead, our modelling suggests that stimulation of MinD-dimerization at cell poles and cell division sites is needed. It will be interesting to see whether future experiments proves this suggestion right or wrong.

Material and methods

Bacterial strains, growth conditions and media

Luria-Bertani (LB) agar was used for the routine selection and maintenance of both *B. subtilis* and *E. coli* strains. For *B. subtilis*, cells were grown in LB medium or Spizizen minimal salt medium supplemented with 0.05 % yeast extract (SMMY). SMMY consists of 2 g/l $(\text{NH}_4)_2\text{SO}_4$, 14 g/l K_2HPO_4 , 6 g/l KH_2PO_4 , 1 g/l sodium citrate, 2 g/l MgSO_4 , 5 g/l fructose, 2 g/l tryptophan, 0.2 g/l casamino acids and 2.2 g/l ammonium ferric citrate. All strains were grown at 37 °C. The supplements were added as required: 100 µg/ml ampicillin, 5 µg/ml chloramphenicol, 5 µg/ml kanamycin, 100 µg/ml spectinomycin, 10 µg/ml tetracycline and 1 µg/ml erythromycin. The *B. subtilis* strains used are listed in Table S2. The mutant strains kindly provided by other labs were transformed into our laboratory strain to ensure that all strains were isogenic.

Strain constructions

Molecular cloning, PCR and transformations were carried out by standard techniques. Plasmids and oligonucleotides used in this study are listed in Table S3 and S4, respectively. The *minC*, *minD*, *minCD* and *minJ* gene deletions were introduced from existing strains listed in Table S2 by standard natural transformation (69). The *aprE*-integration vector containing mCherry under an IPTG-inducible promoter (*Pspac*) was constructed as follows. The spectinomycin marker of pAPNC213 (70) was replaced with a chloramphenicol resistance cassette (*cat*) using In-Fusion cloning (Clontech). For this aim pAPNC123 was PCR-linearized with oligonucleotide pair HS05/HS06 and the *cat* cassette was amplified from pSG2 (71) with oligonucleotide pair HS07/HS08. These PCR products were fused together with In-Fusion cloning, resulting in pAPNC*cat*, this plasmid was verified by sequencing. Next, the mCherry encoding gene was amplified using oligonucleotide pair HS437/HS438 and plasmid template pSS153 (72) as template. Sall and BamHI restriction sites were inserted into the primers. The mCherry PCR product and the pAPNC*cat* were digested with Sall and BamHI and ligated. The resulting plasmid was verified by sequencing and named pHJS112.

The IPTG-inducible mCherry-*minC* fusion was constructed as follows. A PCR fragment containing *minC* was amplified with oligonucleotide pair LB1/LB2 and genomic DNA of the wild type strain 168 as template. BamHI and EcoRI restriction sites were inserted into the primers. The PCR product and the *aprE*-integration vector pHJS112 were digested with BamHI and EcoRI restriction enzymes and ligated. The resulting plasmid pLB11 was verified by sequencing and transformed into *B. subtilis* competent cells, resulting in strain LB31. The *aprE* integration was verified by PCR, amplifying the genomic DNA with oligonucleotide pair HS508/HS509 and sequencing.

The *amyE*-integration vector pSG1730 containing GFP fused to *minD* under a xylose-inducible promoter (13) was used to exchange the *minD* residue glycine 12 to valine (G12V) and aspartic acid 40 to alanine (D40A), by incorporation of the corresponding mutation using the QuickChange site-directed mutagenesis reaction (Stratagene) and the oligonucleotide pairs HS320/HS321 and HS322/HS323, respectively. The resulting plasmids were verified by sequencing and named pHJS115 and pHJS116, respectively. The plasmid pHJS113 containing GFP fused to *B. subtilis minD* coding sequence with the lysine 16 to alanine (K16A) exchange under a xylose-inducible promoter was reported previously (50).

Plasmid pSG1729 (44), containing GFP under a xylose-inducible promoter, was used to generate a construct with GFP fused to the native *minD* membrane targeting amphipathic helix (KGMMAKIKSFFG). This domain was amplified from *B. subtilis* wild type strain 168 with oligonucleotide pair FB136/FB149. EcoRI and BamHI restriction sites were inserted into the primers. The PCR product and the plasmid pSG1729 were digested with EcoRI and BamHI restriction enzymes and ligated. The new plasmid was verified by sequencing and named pHJS117. Plasmid pHJS117 was used to generate a construct with GFP fused to two *minD* amphipathic helices in tandem with a short linker of glycines in between (2xAH). This tandem membrane targeting sequence was created by amplification with oligonucleotides FB138/FB149

and pHJS117 as template. The primer FB138 carries a long overhang that generates an extra MinD membrane targeting amphipathic helix fused to the existing membrane targeting domain (KGMMAKIKSFFGVRS~~GGVLEE~~QNKGMMAKIKSFFG). EcoRI and BamHI restriction sites were inserted into the primers. The PCR product and the plasmid pSG1729 were digested with *EcoRI* and *BamHI* restriction enzymes and ligated. The new plasmid was verified by sequencing and named pHJS119.

Another construct with GFP fused to the NS4B amphipathic helix 2 from Hepatitis C virus (NS4B-AH) was generated as follows. Plasmid pSG1729 was amplified with oligonucleotides FB141/FB149. The primer FB141 carries a long overhang that generates the NS4B-AH anchor (TVTQLLRRLHQWI). EcoRI and BamHI restriction sites were inserted into the primers. The PCR product and the plasmid pSG1729 were digested with *EcoRI* and *BamHI* restriction enzymes and ligated. The new plasmid was verified by sequencing and named pHJS121.

We constructed two different *amyE*-integration plasmids with GFP fused to *minD* with different membrane targeting sequences. The native *minD* amphipathic helix was either replaced with two *minD* amphipathic helices in tandem with a short linker of glycines in between (MinD2xAH) or with the Hepatitis C virus NS4B amphipathic helix 2 (MinDNS4B-AH). The *minD* gene was amplified from the *B. subtilis* genome (strain 168) with oligonucleotides pairs FB135/FB138 and FB135/FB141, respectively. BamHI and EcoRI restriction sites were inserted into the primers. The primers FB138 and FB141 carry a long overhang that generates the 2xAH and the NS4B-AH, respectively. The digested PCR fragments were ligated with BamHI/*EcoRI*-linearized pSG1729, containing GFP under a xylose-inducible promoter. The new plasmids were verified by sequencing and named pHJS123 and pHJS125, respectively.

Plasmids pSG1730, pHJS113, pHJS115, pHJS116, pHJS123 and pHJS125 were used as template for the QuickChange site-directed mutagenesis reaction (Stratagene) with oligonucleotide pair HS410/HS411 to introduce the A206K exchange in the GFP coding sequence to reduce protein dimerization (mGFP). The resulting plasmids were verified by sequencing and named pLB21, pLB22, pLB23, pLB24, pLB49 and pLB50 respectively. Plasmids pLB21 and pLB24 were used to further exchange the *minD* isoleucine 260 to glutamic acid (I260E) by QuickChange site-directed mutagenesis reaction (Stratagene) with oligonucleotide pair HS205/HS206. The resulting plasmids were verified by sequencing and named pLB71 and pLB72, respectively. These constructs were integrated at the *amyE* locus in different genetic backgrounds.

Western blot analysis

To detect the cellular levels of the different GFP-MinD variants the strains were induced with 0.1 % xylose for three doublings. 2 ml of cultures, with comparable ODs were centrifuged and the cell pellets flash frozen in liquid nitrogen. The pellets were then resuspended in 200 µl of buffer containing 10 mM Tris-HCl pH 8, 100 mM NaCl and 1 % TritonX-100. The cells were lysed with 100 µg/ml lysozyme during 15 min incubation at room temperature. Cell debris were spun down (20 min Eppendorf centrifuge, 14000 rpm, 4°C) and 10 µl of samples were loaded onto a 10 % SDS-PAGE followed by separation by electrophoresis at 150 V for 60 min. The proteins were then transferred to a PVDF membrane (Thermo Scientific) with transfer buffer (14.4 g/l glycine, 3 g/l Tris base and 15 % methanol) using mini-wet electroblotting system (Bio-Rad) at 55 V for 130 min. The transferred membrane was then blocked in blocking buffer (1 % skimmed milk powder in TBST buffer 50 mM Tris, 150 mM NaCl and 0.05 % Tween-20) overnight and rinsed twice for 5 min in TBST. The proteins were probed with a 1:2000 dilution of rabbit anti-GFP primary antibody (Invitrogen) in 10 ml TBST incubated 1 h, the membrane was washed 3x in TBST and incubated in a 1:20 000 dilution of secondary antibody goat anti rabbit IR dye (Li-cor Biosciences) in 10 ml TBST during 1 h. The immunoblot was developed by using an Odyssey® imaging system (Li-cor Biosciences).

Microscopy

Microscopy was performed on an inverted fluorescence Nikon Eclipse Ti microscope equipped with a CFI Plan Apochromat DM 100x oil objective, an Intensilight HG 130bW lamp and C11440-22CU Hamamatsu ORCA camera. Images were analysed using ImageJ v.1.48d5 (National Institutes of Health) software and the plugin ObjectJ (73). To measure the transverse fluorescence intensity profiles (FIP), line-scans perpendicular to the cell axis were marked. The polar gradient areas, marked in red in figures, were manually assigned by means of visual inspection of the fluorescence gradient of the FIPs. The membrane affinity was estimated as the ratio valley/peaks of the transverse FIP, using an average of at least 30 cells per data set. When appropriate, data was analyzed with t-tests (p-values) using GraphPad Prism for Mac, GraphPad Software.

For microscopy, cells were grown to exponential phase by diluting 1:100 a starter culture grown overnight in liquid medium (SMMY) into fresh medium, and allowing at least three doublings before mounting on microscopy slides covered with a thin film of 1 % agarose. 0.1 % xylose and 0.01 mM IPTG were used for the induction since these concentrations complemented a $\Delta minCD$ deletion strain, preventing minicell formation. Membranes were stained with the fluorescent membrane dye FM-95 (0.5 μ g/ml final concentration), incubated for 5 min prior to mounting onto microscope slides covered with a thin film of 1 % agarose. Dissipation of the proton motive force (pmf) was carried out by the addition of 100 μ M carbonyl cyanide m-chlorophenylhydrazone (CCCP) for 10 min. CCCP was dissolved in DMSO (0.1 % final concentration of DMSO). As control, cells were incubated with 0.1 % DMSO.

Kinetic Monte Carlo simulations

To model the formation of a steady state gradient in *B. subtilis* wild-type cells and mutants, kinetic Monte Carlo simulation were performed. Kinetic Monte Carlo is a stochastic algorithm which is known to be equivalent to molecular dynamics for sufficiently small local moves (55, 56). The system simulated consisted in a collection of 1000 MinD proteins enclosed inside a spherocylinder (aspect ratio 4, sizes 80 by 20 in simulation units) modelling a *B. subtilis* cell. MinD proteins can be in one of two states, either monomeric (M) or dimeric (D). The M and D states have both affinities for the membrane (the surface of the spherocylinder). To model this, we introduce an attractive potential, a square well with range 1 and strength e_M and e_D for the M and D state respectively. Given our experimental results that the dimer is only weakly stickier than the monomer, we ran our simulations with $e_D = 1.1e_M = 1 k_B T$. Additionally, the D state, but not the M state, may interact with the caps (poles) in the spherocylinders, with an extra interaction again represented by a square well, with range 1 and strength e_C . This interaction simulates binding between dimeric MinD and MinJ. Various cases were considered but results are reported, for simplicity for two cases only: $e_C = 0$ (no additional polar interaction), or $e_C = 0.7 e_M$. A third parameter which varies between M and D is the diffusion coefficient: for simplicity, unless otherwise stated, we assume this to scale inversely with molecular weight, so that the diffusivity of the dimer, D, is half that of the monomer, M.

Key to the formation of the gradient is the fact that the reaction between the M and D states of MinD is not in thermodynamic equilibrium, as it is linked to ATP hydrolysis. In our model, D turns into M, due to ATP hydrolysis, at a constant rate k_{ATP} , in all cases. We consider instead three cases for the dimerization reaction. In our baseline model the conversion of M into D also occurred at the same rate in the cytoplasm, at the membrane and at the pole. We have set this rate such that the M and D state are on average comparable in steady state, as suggested by our experiments. We also considered the case where dimerization at the membrane occurs 2-fold more often at the membrane, and a third case where polar localization (through MinJ interaction) strongly stimulates dimerization, so that the M to D transition occurs at a rate $k_{pole} \gg k_{ATP}$ at poles. When considering polar stimulation, dimerization occurs at a rate $k_{ATP}/10$ in the cytosol; otherwise, rates of dimerization and monomerization in the cytoplasm are equal. The diffusion of monomeric MinD was set to 0.0033 in simulation units (corresponding to approximately 2 micron square per second, see below), where the hydrolysis rate k_{ATP} was set to 10^{-5} (corresponding to 1/s, which is of the same order as used in previous modeling studies (5)). When considering polar stimulation, we

set k_{pole} such that dimerization at the pole occurs with unit probability during a timestep (we have verified though that the results are qualitatively similar down to at least a value of k_{pole} equal to $100 k_{\text{ATP}}$). More details on the parameters used in the model are given in the caption of **Fig. 8**, and Table S1.

To simulate the monomer (K16A) and dimer (D40A) mutants, we used another version of the same model, in which all particles were of type M or D respectively, and the rate of interconversion between the two was set to 0.

Simulation units may be mapped to physical units by noting that 1 space and time units in simulations can be made to correspond to 0.08 microns and 10 microseconds, respectively. Simulations were run typically for 10^7 time steps. Snapshots shown are for systems which have reached equilibrium, so representing steady-state behaviour.

Data availability

All data is present in the manuscript. Strains are available upon request.

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Additional files

[Supplementary Information](#)

Additional information

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Peer reviews

Reviewer #1 (Public review):

The authors used fluorescence microscopy, image analysis, and mathematical modeling to study the effects of membrane affinity and diffusion rates of MinD monomer and dimer states on MinD gradient formation in *B. subtilis*. To test these effects, the authors experimentally examined MinD mutants that lock the protein in specific states, including Apo monomer (K16A), ATP-bound monomer (G12V) and ATP-bound dimer (D40A, hydrolysis defective), and compared to wild-type MinD. Overall, the experimental results support the conclusions that reversible membrane binding of MinD is critical for the formation of the MinD gradient, but the binding affinities between monomers and dimers are similar.

The modeling part is a new attempt to use the Monte Carlo method to test the conditions for the formation of the MinD gradient in *B. subtilis*. The modeling results provide good support for the observations and find that the MinD gradient is sensitive to different diffusion rates between monomers and dimers. This simulation is based on several assumptions and predictions, which raises new questions that need to be addressed experimentally in the future.

<https://doi.org/10.7554/eLife.101520.2.sa2>

Reviewer #3 (Public review):

This important study by Bohorquez et al examines the determinants necessary for concentrating the spatial modulator of cell division, MinD, at the future site of division and the cell poles. Proper localization of MinD is necessary to bring the division inhibitor, MinC, in proximity to the cell membrane and cell poles where it prevents aberrant assembly of the division machinery. In contrast to *E. coli*, in which MinD oscillates from pole-to-pole courtesy of a third protein MinE, how MinD localization is achieved in *B. subtilis*-which does not encode a MinE analog-has remained largely a mystery. The authors present compelling data indicating that MinD dimerization is dispensable for membrane localization but required for concentration at the cell poles. Dimerization is also important for interactions between MinD and MinC, leading to the formation of large protein complexes. Computational modeling, specifically a Monte Carlo simulation, supports a model in which differences in diffusion rates between MinD monomers and dimers lead to concentration of MinD at cell poles. Once there, interaction with MinC increases the size of the complex, further reinforcing diffusion differences. Notably, interactions with MinJ-which has previously been implicated in MinCD localization, are dispensable for concentrating MinD at cell poles although MinJ may help stabilize the MinCD complex at those locations.

Comments on revisions:

I believe the authors put respectable effort into revisions and addressing reviewer comments, particularly those that focused on the strengths of the original conclusions. The language in the current version of the manuscript is more precise and the overall product is stronger.

<https://doi.org/10.7554/eLife.101520.2.sa1>

Author response:

The following is the authors' response to the original reviews.

Reviewer #1 (Public review):

The authors used fluorescence microscopy, image analysis, and mathematical modeling to study the effects of membrane affinity and diffusion rates of MinD monomer and dimer states on MinD gradient formation in B. subtilis. To test these effects, the authors experimentally examined MinD mutants that lock the protein in specific states, including Apo monomer (K16A), ATP-bound monomer (G12V), and ATPbound dimer (D40A, hydrolysis defective), and compared to wild-type MinD. Overall, the experimental results support the conclusion that reversible membrane binding of MinD is critical for the formation of the MinD gradient, but that the binding affinities between monomers and dimers are similar.

The modeling part is a new attempt to use the Monte Carlo method to test the conditions for the formation of the MinD gradient in B. subtilis. The modeling results provide good support for the observations and find that the MinD gradient is sensitive to different diffusion rates between monomers and dimers. This simulation is based on several assumptions and predictions, which raises new questions that need to be addressed experimentally in the future. However, the current story is sufficient without testing these assumptions or predictions.

Reviewer #2 (Public review):

Summary:

Bohorquez et al. investigate the molecular determinants of intracellular gradient formation in the B. subtilis Min system. To this end, they generate B. subtilis strains that express MinD mutants that are locked in the monomeric or dimeric states, and also MinD mutants with amphipathic helices of varying membrane affinity. They then assess the mutants' ability to bind to the membrane and form gradients using fluorescence microscopy in different genetic backgrounds. They find that, unlike in the E. coli Min system, the monomeric form of MinD is already capable of membrane binding. They also show that MinJ is not required for MinD membrane binding and only interacts with the dimeric form of MinD. Using kinetic

Monte Carlo simulations, the authors then test different models for gradient formation, and find that a MinD gradient along the cell axis is only formed when the polarly localized protein MinJ stimulates dimerization of MinD, and when the diffusion rate of monomeric and dimeric MinD differs. They also show that differences in the membrane affinity of MinD monomers and dimers are not required for gradient formation.

Strengths:

The paper offers a comprehensive collection of the subcellular localization and gradient formation of various MinD mutants in different genetic backgrounds. In particular, the comparison of the localization of these mutants in a delta MinC and MinJ background offers valuable additional insights. For example, they find that only dimeric MinD can interact with MinJ. They also provide evidence that MinD locked in a dimer state may co-polymerize with MinC, resulting in a speckled appearance.

The authors introduce and verify a useful measure of membrane affinity in vivo.

The modulation of the membrane affinity by using distinct amphipathic helices highlights the robustness of the B. subtilis MinD system, which can form gradients even when the

membrane affinity of MinD is increased or decreased.

Weaknesses:

The main claim of the paper, that differences in the membrane affinity between MinD monomers and dimers are not required for gradient formation, does not seem to be supported by the data. The only measure of membrane affinity presented is extracted from the transverse fluorescence intensity profile of cells expressing the mGFP-tagged MinD mutants. The authors measure the valley-to-peak ratio of the profile, which is lower than 1 for proteins binding to the membrane and higher than 1 for cytosolic proteins. To verify this measure of membrane affinity, they use a membrane dye and a soluble GFP, which results in values of ~0.75 and ~1.25, respectively. They then show that all MinD mutants have a value - roughly in the range of 0.8-0.9 - and they use this to claim that there are no differences in membrane affinity between monomeric and dimeric versions.

While this way to measure membrane affinity is useful to distinguish between binders and non-binders, it is unclear how sensitive this assay is, and whether it can resolve more subtle differences in membrane affinity, beyond the classification into binders and non-binders. A dimer with two amphipathic helices should have a higher membrane affinity than a monomer with only one such copy. Thus, the data does not seem to support the claim that "the different monomeric mutants have the same membrane affinity as the wildtype MinD". The data only supports the claim that *B. subtilis* MinD monomers already have a measurable membrane affinity, which is indeed a difference from the *E. coli* Min system.

While their data does show that a stark difference between monomer and dimer membrane affinity may not be required for gradient formation in the *B. subtilis* case, it is also not prevented if the monomer is unable to bind to the membrane. They show this by replacing the native MinD amphipathic helix with the weak amphipathic helix NS4AB-AH. According to their membrane affinity assay, NS4AB-AH does not bind to the membrane as a monomer (Figure 4D), but when this helix is fused to MinD, MinD is still capable of forming a gradient (albeit a weaker one). Since the authors make a direct comparison to the *E. coli* MinDE systems, they could have used the *E. coli* MinD MTS instead or in addition to the NS4AB-AH amphipathic helix. The reviewer suspects that a fusion of the *E. coli* MinD MTS to *B. subtilis* MinD may also support gradient formation.

The paper contains insufficient data to support the many claims about cell filamentation and minicell formation. In many cases, statements like "did not result in cell filamentation" or "restored cell division" are only supported by a single fluorescence image instead of a quantitative analysis of cell length distribution and minicell frequency, as the one reported for a subset of the data in Figure 5.

The paper would also benefit from a quantitative measure of gradient formation of the distinct MinD mutants, instead of relying on individual fluorescent intensity profiles.

The authors compare their experimental results with the oscillating *E. coli* MinDE system and use it to define some of the rules of their Monte Carlo simulation. However, the description of the *E. coli* Min system is sometimes misleading or based on outdated findings.

The Monte Carlo simulation of the gradient formation in *B. subtilis* could benefit from a more comprehensive approach:

(1) While most of the initial rules underlying the simulation are well justified, the authors do not implement or test two key conditions:

(a) Cooperative membrane binding, which is a key component of mathematical models for the oscillating *E. coli* Min system. This cooperative membrane binding has recently been attributed to MinD or MinCD oligomerization on the membrane and has been experimentally observed in various instances; in fact, the authors themselves show data supporting the formation of MinCD copolymers.

(2) Local stimulation of the ATPase activity of MinD which triggers the dimer-to-monomer transition; *E. coli* MinD ATP hydrolysis is stimulated by the membrane and by MinE, so *B. subtilis* MinD may also be stimulated by the membrane and/or other components like MinJ. Instead, the authors claim that (a) would only increase differences in diffusion between the monomer and different oligomeric species, and that a 2-fold increase in dimerization on the membrane could not induce gradient formation in their simulation, in the absence of MinJ stimulating gradient formation. However, a 2-fold increase in dimerization is likely way too low to explain any cooperative membrane binding observed for the *E. coli* Min system. Regarding (b), they also claim that implementing stimulation of ATP hydrolysis on the membrane (dimer-to-monomer transition) would not change the outcome, but no simulation result for this condition is actually shown.

(3) To generate any gradient formation, the authors claim that they would need to implement stimulation of dimer formation by MinJ, but they themselves acknowledge the lack of any experimental evidence for this assertion. They then test all other conditions (e.g., differences in membrane affinity, diffusion, etc.) in addition to the requirement that MinJ stimulates dimer formation. It is unclear whether the authors tested all other conditions independently of the "MinJ induces dimerization" condition, and whether either of those alone or in combination could also lead to gradient formation. This would be an important test to establish the validity of their claims.

Reviewer #3 (Public review):

This important study by Bohorquez et al examines the determinants necessary for concentrating the spatial modulator of cell division, MinD, at the future site of division and the cell poles. Proper localization of MinD is necessary to bring the division inhibitor, MinC, in proximity to the cell membrane and cell poles where it prevents aberrant assembly of the division machinery. In contrast to *E. coli*, in which MinD oscillates from pole to pole courtesy of a third protein MinE, how MinD localization is achieved in *B. subtilis* - which does not encode a MinE analog - has remained largely a mystery. The authors present compelling data indicating that MinD dimerization is dispensable for membrane localization but required for concentration at the cell poles. Dimerization is also important for interactions between MinD and MinC, leading to the formation of large protein complexes. Computational modeling, specifically a Monte Carlo simulation, supports a model in which differences in diffusion rates between MinD monomers and dimers lead to the concentration of MinD at cell poles. Once there, interaction with MinC increases the size of the complex, further reinforcing diffusion differences. Notably, interactions with MinJ-which has previously been implicated in MinCD localization, are dispensable for concentrating MinD at cell poles although MinJ may help stabilize the MinCD complex at those locations.

Reviewer #1 (Recommendations for the authors):

(1) The title could be modified to better reflect the emphasis on MinD monomer and dimer diffusion rather than the fact that membrane affinity is not important in MinD gradient formation. In addition, because membrane association requires affinity for the membrane, this title seems inconsistent with statements in the main text, such as Lines 246-247: a reversible membrane association is important for the formation of a MinD gradient along the cell axis.

We agree with the reviewer that the title can be more accurate, and we have now changed it to “Membrane affinity difference between MinD monomer and dimer is not crucial to MinD gradient formation in *Bacillus subtilis*”

(2) This paper reports that the difference in diffusion rates between MinD monomers and dimers is an important factor in the formation of Bs MinD gradients. However, one can argue for the importance of MinD monomers in the cellular context. Since the abundance of ATP in cells often far exceeds the abundance of MinD protein molecules under experimental conditions, MinD can easily form dimers in the cytoplasm. How does the author address this problem?

It is a good point that ATP concentration in the cell likely favours dimers in the cytoplasm. However, what is important in our model is that there is cycling between monomer and dimer, rather than where exactly this happens. In fact, the gradients work essentially equally well if dimers can become monomers only whilst they are at the membrane, as we have mentioned in the manuscript (lines 324-326 in the original manuscript). However, in the original manuscript this simulation was not shown, and now we have included this in the new Fig. 8D & E.

(3) The claim “This oscillating gradient requires cycling of MinD between a monomeric cytosolic and a dimeric membrane attached state.” (Lines 46, 47) is not well supported by most current studies and needs to be revised since to my knowledge, most proposed models do not consider the monomer state. The basic reaction steps of Ec Min oscillations include ATP-bound MinD dimers attaching to the membrane that subsequently recruit more MinD dimers and MinE dimers to the membrane; MinE interactions stimulate ATP hydrolysis in MinD, leading to dissociation of ADP-bound MinD dimers from the membrane; nucleotide exchange occurs in the cytoplasm.

Here the reviewer refers to a sentence in a short “Importance” abstract that we have added. In fact, such abstract is not necessary, so we have removed it. Of note, the *E. coli* MinD oscillation, including the role of MinE, is described in detail in the Introduction.

A recent reference is a paper by Heermann et al. (2020; doi: 10.1016/j.jmb.2020.03.012), which considers the MinD monomer state, which is not mentioned in this work. How do their observations compare to this work?

The Heermann paper mentions that MinD bound to the membrane displays an interface for multimerization, and that this contributes to the local self-enhancement of MinD at the membrane. In our Discussion, we do mention that *E. coli* MinD can form polymers in vitro and that any multimerization of MinD dimers will further increase the diffusion difference between monomer and dimer, and might contribute to the formation of a protein gradient (lines 459-467). We have now included a reference to the Heermann paper (line 461).

(4) Throughout the manuscript, errors in citing references were found in several places.

We have corrected this where suggested.

(5) The introduction may be somewhat misleading due to mixed information from experimental cellular results, in vitro reconstructions, and theoretical models in cells or in vitro environments. Some models consider space constraints, while others do not. Modifications are recommended to clarify differences.

See below for responses

(6) The citation for MinD monomers:

The paper by Hu and Lutkenhaus (2003, doi: 10.1046/j.1365-2958.2003.03321.x) contains experimental evidence showing monomer-dimer transition using purified proteins. Another paper by the same laboratory (Park et al. 2012, doi: 10.1111/j.1365-2958.2012.08110.x.) explained how ATP-induced dimerization, but this paper is not cited.

The Park et al. 2012 paper focusses at the asymmetric activation of MinD ATPase by MinE, which goes beyond the scope of our work. However, we have cited several other papers from the Lutkenhaus lab, including the Wu et al. 2011 paper describing the structure of the MinD-ATP complex.

Other evidence comes from structural studies of Archaea Pyrococcus furiosus (1G3R) and Pyrococcus horikoshii (1ION), and thermophilic Aquifex aeolicus (4V01, 4V02, 4V03). As they may function differently from Ec MinD, they are less relevant to this manuscript.

We agree.

(7) Lines 65, 66: Using the term 'a reaction-diffusion couple' to describe the biochemical facts by citing references of Hu and Lutkenhaus (1999) and Raskin and de Boer (1999) is not appropriate. The idea that the Min system behaves as a reaction-diffusion system was started by Howard et al. (2001), Meinhardt and de Boer (2001), and Huang et al. (2003) et al. In addition, references for MinE oscillation are missing.

We have now corrected this (line 52).

(8) Lines 77-79: Citations are incorrect.

ATP-induced dimerization: Hu and Lutkenhaus (2003, DOI: 10.1046/j.1365-2958.2003.03321.x), Park et al. (2012). C-terminal amphipathic helix formation: Szeto et al. (2003), Hu and Lutkenhaus (2003, DOI: 10.1046/j.1365-2958.2003.03321.x).

Citations have been corrected.

(9) Line 78: The C-terminal amphipathic helix is not pre-formed and then exposed upon conformational change induced by ATP-binding. This alpha-helical structure is an induced fold upon interaction with membranes as experimentally demonstrated by Szeto et al. (2003).

We have adjusted the text to correct this (lines 64-66).

(10) Line 102: 'cycles between membrane association and dissociation of MinD' also requires MinE in addition to ATP.

We believe that in the context of this sentence and following paragraph it is not necessary to again mention MinE, since it is focused on parallels between the E. coli and B. subtilis MinD membrane binding cycles.

(11) In the introduction, could the author briefly explain to a general audience the difference between Monte Carlo and reaction-diffusion methods? How do different algorithms affect the results?

The main difference between the kinetic Monte Carlo and typical reaction-diffusion methods which is relevant to our work is that the first is particle-based, and naturally includes statistical fluctuations (noise), whereas the second is field-based, and is in the normal implementation deterministic, so does not include noise. Whilst it should be noted that one can in principle include noise in the field-based reactiondiffusion methods, this is done rarely. Additionally, although we do not do this here, the kinetic MonteCarlo can also account, in principle, for particle shape (sphere versus rod), or for localized interactions (as sticky

patches on the surface): therefore the kinetic Monte Carlo is more microscopic in nature. We have now shortly described the difference in lines 102-105.

(12) Lines 126-128: The second part of the sentence uses the protein structure of *Pyrococcus furiosus* MinD (Ref 37) to support a protein sequence comparison between *Ec* and *Bs* MinD. However, the structure of the dimeric *E. coli* MinD-ATP complex (3Q9L) is available, which is Reference 38 that is more suited for direct comparison.

To discuss monomeric MinD from *P. furiosus*, it will be useful to include it in the primary sequence alignment in Figure S1.

We do not think that this detailed information is necessary to add to Figure S1, since the mutants have been described before (appropriate citations present in the text).

(13) Lines 127, 166: Where Figure S1 is discussed, a structural model of MinD will be useful alongside with the primary sequence alignment.

We do not think that this detailed information is necessary to understand the experiments since the mutants have been described before.

(14) Lines 131-132: Reference is missing for the sentence of "the conserved..."; Reference 38. In Reference 38, there is no experimental evidence on G12 but inferred from structure analysis. Reference 26 discusses ATP and MinE regulation on the interactions between MinD and phospholipid bilayers; not about MinD dimerization.

We have corrected this and added the proper references.

For easy reading, the mutant MinD phenotypes can be indicated here instead of in the figure legends, including K16A (apo monomer), MinD G12V (ATP-bound monomer), and MinD D40A (ATP-bound dimer, ATP hydrolysis deficient).

We have added the suggested descriptions of the mutants in the main text.

(15) Lines 150-151: Unlike *Ec* MinD, which forms a clear gradient in one half of the cell, *Bs* MinD (wild type) mainly accumulates at the hemispheric poles. What percentage of a cell (or cell length) can be covered by the *Bs* MinD gradient? How does the shaded area in the longitudinal FIP compare to the area of the bacterial hemispherical pole? If possible, it might be interesting to compare with the range of nucleoid occlusion mechanisms that occur.

Part of the MinD gradient covers the nucleoid area, since the fluorescence signal is still visible along the cell lengths, yet there is no sudden drop in fluorescence, suggesting that nucleoid exclusion does not play a role.

(16) Line 160: In addition to summarizing the membrane-binding affinity, descriptions of the differences in the gradient distribution or formation will be useful.

We have done this in lines 155-156 of the original manuscript: "The monomeric ATP binding G12V variant shows the same absence of a protein gradient as the K16A variant".

(17) Line 262: 'distribution' is not shown.

We do not understand this remark. This information is shown in Fig. 5B (now Fig. 6B).

(18) Line 287: Wrong citation for reference 31.

Reference has been corrected.

(19) Line 288 and lines 596 regarding the Monte Carlo simulation:

(a) An illustration showing the reaction steps for MinD gradient formation will help understand the rationale and assumptions behind this simulation.

We have added an illustration depicting the different modelling steps in the new Fig. 8.

(b) Equations are missing.

(c) A table summarizing the parameters used in the simulation and their values.

(d) For general readers, it will be helpful to convert the simulation units to real units.

(e) Indicate real experimental data with a citation or the reason for any speculative value.

The Methods section provides a discussion of all parameters used in the potentials on which our kinetic Monte-Carlo algorithm is based. We have now also provided a Table in the SI (Table S1) with typical parameter values in both simulation units and real units. The experimental data and reasoning behind the values chosen are discussed in the Methods section (see “Kinetic Monte Carlo simulation”).

(20) Lines 320-321: Reference missing.

The interaction between MinJ and the dimer form of MinD is based on our findings shown in the original Fig. S4, and this information has not been published before. We have rephrased the sentence to make it more clear. Of note, Fig. S4 has been moved to the main manuscript, at the request of reviewer #2, and is now new Fig. 2.

(21) Lines 355-359: Is the statement specifically made for the Bs Min system? Is there any reference for the statement? Isn't the differences in diffusion rates between molecules 'at different locations' in the system more important than reducing their diffusion rates alone? It is unclear about the meaning of the statement "the Min system uses attachment to the membrane to slow down diffusion". Is this an assumption in the simulation?

The statement is generic, however the reviewer has a good point and we have made this statement more clear by changing “considerably reduced diffusion rate” to “locally reduced diffusion rate” (line 359).

(22) Line 403: Citation format.

We have corrected the text and citation.

(23) Lines 442-444: The parameters are not defined anywhere in the manuscript.

Discussed in the M&M and in the new Table S1.

(24) Lines 464-465: Regarding the final sentence, what does 'this prediction' refer to? Hasn't the author started with experimental observations, predicted possible factors of membrane affinity and diffusion rates, and used the simulation approach to disapprove or support the prediction?

We have changed “prediction” to “suggestion”, to make it clear that it is related to the suggestion in the previous sentence that “our modelling suggests that stimulation of MinD-dimerization at cell poles and cell division sites is needed.” (line 471).

(25) Materials and Methods: Statistical methods for data analyses are missing.

Added to “Microscopy” section.

(26) References: References 34, 40, 51 are incomplete.

References 34 and 40 have been corrected. Reference 51 is a book.

(27) Figures: The legends (Figures 1-7) can be shortened by removing redundant details in Material and Methods. Make sure statistical information is provided. The specific mutant MinD states, including Apo monomer, ATP-bound dimer, ATP hydrolysis deficient, and non-membrane binding etc can be specified in the main text. They are repeated in the legends of Figures 1 and 2.

We have removed redundant details from the legends and provided statistical information.

(28) Supporting information:

Table S1: Content of the acknowledgment statement may be moved to materials and methods and the acknowledgment section. Make sure statistical information is provided in the supporting figure legends.

We are not sure what the reviewer means with the content acknowledgement in Table S1 (now Table S2). Statistical information has been added.

Figure S1. Adding a MinD structure model will be useful.

We do not think that a structural model will enlighten our results since our work is not focused at structural mutagenesis. The mutants that we use have been described in other papers that we have cited.

Reviewer #2 (Recommendations for the authors):

The authors should cite and relate their data to the preprint by Feddersen & Bramkamp, BioRxiv 2024. ATPase activity of B. subtilis MinD is activated solely by membrane binding.

We have now discussed this paper in relation to our data in lines 407-409.

I am not convinced the authors are able to make the statement in lines 160-161 based on their assay: "This confirmed that the different monomeric mutants have the same membrane affinity as wild-type MinD". It is unclear if measuring valley-to-peak ratios in their longitudinal profiles can resolve small differences in membrane affinity. Wildtype MinD should at least be dimeric, or (as the authors also note elsewhere) may even be present in higher-order structures and as such have a higher membrane affinity than a monomeric MinD mutant. The authors should rephrase the corresponding sections in the manuscript to state that the MinD monomer already has detectable membrane affinity, instead of stating that the monomer and dimer membrane affinity are the same.

We agree that "the same affinity" is too strongly worded, and we have now rephrased this by saying that the different monomeric mutants have a comparable membrane affinity as wild type MinD (line 152).

According to the authors' analysis, MinD-NS4B would not bind to the membrane as it has a valley-to-peak ratio higher than 1, similar to the soluble GFP. However, the protein is clearly forming a gradient, and as such probably binding to the membrane. The authors should discuss this as a limitation of their membrane binding measure.

The ratio value of 1 is not a cutoff for membrane binding. As shown in Fig. 1F, GFP has a valley-to-peak ratio close to 1.25, whereas the FM5-95 membrane dye has a ratio close to 0.75. In Fig. 3C (now Fig. 4C) we have shown that GFP fused with the NS4B membrane anchor has a lower ratio than free GFP, and we have shown the same in Fig. 4D (now Fig. 5D) for GFP-MinD-NS4B. The difference are small but clear, and not similar to GFP.

The observation that MinD dimers are localized by MinJ is interesting and key to the rule of the Monte Carlo simulation that dimers attach to MinJ. However, the data is hidden in the supplementary information and is not analysed as comprehensively, e.g., it lacks the analysis of the membrane binding. The paper would benefit from moving the fluorescence images and accompanying analysis into the main text.

We have moved this figure to the main text and added an analysis of the fluorescence intensities (new Fig. 2).

The authors should show the data for cell length and minicell formation, not only for the MinDamphipathic helix versions (Fig. 5), but also for the GFP-MinD, and all the MinD mutants. They do refer to some of this data in lines 145-148 but do not show it anywhere. They also refer to "did not result in cell filamentation" in line 213 and to "resulted in highly filamentous cells" and "Introduction of a minC deletion restored cell division" in lines 167-160 without showing the cell length and minicell data, but instead refer to the fluorescence image of the respective strain. I would suggest the authors include this data either in a subpanel in the respective figure or in the supplementary information.

The effect of uncontrolled MinC activity is very apparent and leads to long filamentous cells. Also the occurrence of minicells is apparent. Cell lengths distribution of wild type cells is shown in Fig. 6B, and minicell formation is negligibly small in wild type cells.

The transverse fluorescence intensity profiles used as a measure for membrane binding are an average profile from ~30 cells. In the case of the longitudinal profiles that display the gradient, only individual profiles are displayed. I understand that because of distinct cell length, the longitudinal profiles cannot simply be averaged. However, it is possible to project the profiles onto a unit length for averaging (see for example the projection of profiles in McNamara. et al., BioRxiv (2023)). It would be more convincing to average these profiles, which would allow the authors to also quantify the gradients in more detail. If that is impossible, the authors may at least quantify individual valley-to-peak ratios of the longitudinal fluorescence profiles as a measure of the gradient.

We agree that in future work it would be better to average the profiles as suggested. However, due to limited time and resources, we cannot do this for the current manuscript.

Regarding the rules and parameters used for the Monte Carlo simulation (see also the corresponding sections in the public review):

(1) The authors mention that they have not included multimerization of MinD in their simulation but argue in the discussion that it would only strengthen the differences in the diffusion between monomers and multimers. This is correct, but it may also change the membrane residence time and membrane affinity drastically.

Simulation of multimerization is difficult, but we have now included a simulation whereby MinD dimers can also form tetramers (lines 341-348), shown in the new Fig. 8K. This did not alter the MinD gradient much.

(2) The authors implement a dimer-to-monomer transition rate that they equate with the stochastic ATP hydrolysis rate occurring with a half-life of approximately 1/s (line 305). They claim that this rate is based on information from E. coli and cite Huang and Wingreen. However, the Huang paper only mentions the nucleotide exchange rate from ADP to ATP at 1/s. Later that paper cites their use of an ATP hydrolysis rate of 0.7/s to match the E. coli MinDE oscillation rate of 40s. From the authors' statement, it is unclear to me whether they refer to the actual ATP hydrolysis rate in Huang and Wingreen or something else. For E. coli MinD, both the membrane and MinE stimulate ATPase activity. Even if B. subtilis lacks MinE, ATP hydrolysis may still be stimulated by the membrane,

which has also been reported in another preprint (Feddersen & Bramkamp, BioRxiv 2024). It may also be stimulated by other components of the Min system like MinJ. The authors should include in the manuscript the Monte Carlo simulation implementing dimer to monomer transition on the membrane only, which is currently referred to only as "(data not shown)".

The exact value of the ATP hydrolysis rate is not so important here, so 1/s only gives the order of magnitude (in line with 0.7/s above), which we have now clarified in lines 631-632. We have now also added the "(data not shown)" results to Fig. 8, i.e. simulations where dimer to monomer transitions (i.e. ATPase activity) only occurs at the membrane (Fig. 8D & E, and lines 319-322).

(3) How long did the authors simulate for? How many steps? What timesteps does the average pictured in Figure 7 correspond to?

We simulated 10^7 time steps (corresponding to 100 s in real time). We have checked that the simulation steps for which we average are in steady state. Typical snapshots are recorded after 10^6 time steps, when the system is in steady state. We have added this information in lines 299-300.

There are several misconceptions about the (oscillating E. coli) Min system in the main text:

(1) Lines 77-78: "In case of the E. coli MinD, ATP binding leads to dimerization of MinD, which induces a conformational change in the C-terminal region, thereby exposing an amphipathic helix that functions as a membrane binding domain" and "This shows a clear difference with the E. coli situation, where dimerization of MinD causes a conformational change of the C-terminal region enabling the amphipathic helix to insert into the lipid bilayer" in lines 400-403 are incorrect. There is no evidence that the amphipathic helix at the C-terminus of MinD changes conformation upon ATP binding; several studies have shown instead that a single copy of the amphipathic helix is too weak to confer efficient membrane binding but that the dimerization confers increased membrane binding as now two amphipathic helices are present leading to an avidity effect in membrane binding. Please refer to the following papers (Szeto et al., JBC (2003); Wu et al., Mol Microbiol (2011); Park et al., Cell (2011); Heermann et al., JMB (2020); Loose et al., Nat Struct Mol Biol (2011); Kretschmer et al., ACS Syn Biol (2021); Ramm et al., Nat Commun (2018) or for a better overview the following reviews on the topic of the E. coli Min system Wettmann and Kruse, Philos Trans R Soc B Biol (2018), Ramm et al., Cell and Mol Life Sci (2019); Halatek et al., Philos Trans R Soc B Biol Sci (2018).

This is indeed incorrectly formulated, and we have now amended this in lines 64-66 and lines 403-406. Key papers are cited in the text.

(2) The authors mention that E. coli MinD may multimerize, citing a study where purified MinD was found to polymerize, and then suggest that this is unlikely to be the case in B. subtilis as FRAP recovery of MinD is quick. However, cooperativity in membrane binding is essential to the mathematical models reproducing E. coli Min oscillations, and there is more recent experimental evidence that E. coli MinD forms smaller oligomers that differ in their membrane residence time and diffusion (e.g., Heermann et al., Nat Methods (2023); Heermann et al., JMB (2020);) I would suggest the authors revise the corresponding text sections and test the multimerization in their simulation (see above).

As mentioned above, simulating oligomerization is difficult, but in order to approximate related cooperative effects, we have simulated a situation whereby MinD dimers can form tetramers. This simulation did not show a large change in MinD gradient formation. We have added the result of this simulation to Fig. 8 (Fig. 8K), and discuss this further in lines 341-348 and 459-467.

(3) Lines 75-76 and lines 79-80: The sentences "MinC ... and needs to bind to the Walker A-type ATPase MinD for its activity" and "The MinD dimer recruits MinC ... and stimulates its activity" are misleading. MinC is localized by MinD, but MinD does not alter MinC activity, as MinC mislocalization or overexpression also prevents FtsZ ring formation leading to minicell or filamentous cells, as also later described by the authors (line 98). There is also no biochemical evidence that the presence of MinD somehow alters MinC activity towards FtsZ other than a local enrichment on the membrane. I would rephrase the sentence to emphasize that MinD is only localizing MinC but does not alter its activity.

We have rephrased this sentence to prevent misinterpretation (lines 66-67).

Minor points:

(1) I am not quite sure what the experiment with the CCCP shows. The authors explain that MinD binding via the amphipathic helix requires the presence of membrane potential and that the addition of CCCP disturbs binding. They then show that the MinD with two amphipathic helices is not affected by CCCP but the wildtype MinD is. What is the conclusion of this experiment? Would that mean that the MinD with two amphipathic helices binds more strongly, very differently, perhaps non-physiologically?

This experiment was "To confirm that the tandem amphipathic helix increased the membrane affinity of MinD", as mentioned in the beginning of the paragraph (line 224).

(2) Lines 456-457: Please cite the FRAP experiment that shows a quick recovery rate of MinD.

Reference has been added.

(3) Figure 4D: It is unclear to me to which condition the p-value brackets point.

This is related to a statistical t-test. We have added this information to the legend of the figure.

(4) Line 111, "in the membrane affinity of the MinD". I think that the "the" before MinD should be removed.

Corrected

(5) Typo in line 199 "indicting" instead of indicating.

Corrected

(6) Typo in line 220 "reversable" instead of reversible.

Corrected

(7) Lines 279, 284, 905: "Monte-Carlo" should read Monte Carlo.

Corrected

Reviewer #3 (Recommendations for the authors):

Introduction: As written, the introduction does not provide sufficient background for the uninitiated reader to understand the function of the MinCD complex in the context of assembly and activation of cell division in *B. subtilis*. The introduction is also quite long and would benefit from condensing the description of the Min oscillation mechanism in *E. coli* to one or two sentences. While highlighting the role of MinE in this system is important for understanding how it works, it is only needed as a counterpoint to the situation in *B. subtilis*.

Since the Min system of *E. coli* is by far the best understood Min system, we feel that it is important to provide detailed information on this system. However, we have added an introductory sentence to explain the key function of the Min system (line 46-48).

Line 248: Increasing MinD membrane affinity increases the frequency of minicells - however it is unclear if cells are dividing too much or if it is just a Min mutant (i.e. occasionally dividing at the cell pole vs the middle)? Cell length measurements should be included to clarify this point (Figures 4 and 5).

This information is presented in Fig. 5B (Cell length distribution), which is now Fig. 6B, indicating that the average cell length increases in the tandem alpha helix mutant, a phenotype that is comparable to a MinD knockout.

Figure 5: I am a bit confused as to whether increasing MinD affinity doesn't lead to a general block in division by MinCD rather than phenocopying a minD null mutant.

Although the tandem alpha helix mutant has a cell length distribution comparable to a minD knockout, the tandem mutant produces much less minicells than the minD knockout, indicating that there is still some cell division regulation.

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