Micro**Commentary**

Snapping magnetosome chains by asymmetric cell division in magnetotactic bacteria

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Summary

The mechanism by which prokaryotic cells organize and segregate their intracellular organelles during cell division has recently been the subject of substantial interest. Unlike other microorganisms, magnetotactic bacteria (MTB) form internal magnets (known as magnetosome chain) for magnetic orientation, and thus face an additional challenge of dividing and equipartitioning this magnetic receptor to their daughter cells. Although MTB have been investigated more than four decades, it is only recently that the basic mechanism of how MTB divide and segregate their magnetic organelles has been addressed. In this issue of *Molecular Microbiology*, the cell cycle of the model magnetotactic bacterium, *Magnetospirillum gryphiswaldense* is characterized by Katzmann and co-workers. The authors have found that *M. gryphiswaldense* undergoes an asymmetric cell division along two planes. A novel wedge-like type of cellular constriction is observed before separation of daughter cells and magnetosome chains, which is assumed to help cell cope with the magnetic force within the magnetosome chain. The data shows that the magneto-

some chain becomes actively recruited to the cellular division site, in agreement with the previous suggestions described by Staniland *et al.* (2010), and the actin-like protein MamK is likely involved in this fast polar-to-midcell translocation. With the use of cryo-electron tomography, an arc-shaped Z ring is observed near the division site, which is assumed to trigger the asymmetric septation of cell and magnetosome chain.

Magnetotactic bacteria (MTB) are a physiologically diverse group of microorganisms with a broad ecological distribution from freshwater to marine ecosystems (Amann *et al.*, 2007; Lin *et al.*, 2011a). Based on the 16S rRNA gene analyses, MTB are affiliated to the *Alphaproteobacteria*, *Deltaproteobacteria*, *Gammaproteobacteria*, phylum *Nitrospirae*, and the candidate division OP3 (Amann *et al.*, 2007; Kolinko *et al.*, 2011; Lefèvre *et al.*, 2011; Lin *et al.*, 2011b). The hallmark of MTB is that these bacteria produce intracellular membrane-enveloped iron minerals of magnetite (Fe_3O_4) and/or greigite (Fe_3S_4), known as magnetosomes (Faivre and Schüler, 2008). As a consequence of evolution and natural selection, the individual sizes of magnetosomes are generally between 35 and 120 nm, falling into a range of stable single domain, which are normally organized into one or multiple regular chain structures in order to optimize the magnetic moment (Bazylinski and Frankel, 2004; Pan *et al.*, 2004; Faivre and Schüler, 2008). In recent years, MTB have become an attractive model system for investigating the molecular mechanisms of organelle-like structure formation in prokaryotic cells (e.g. Murat *et al.*, 2010a). It has been demonstrated that the entire process of magnetosome formation is strictly controlled by a group of genes that are clustered within a coherent genomic fragment described as magnetosome island (Ullrich *et al.*, 2005; Schüler, 2008; Jogler and Schüler, 2009; Murat *et al.*, 2010b).

As a representative prokaryotic organelle-like structure, the magnetosome chain is believed to facilitate MTB to search for their favourable low-oxygen environments in nature (Frankel *et al.*, 2007), and therefore plays an

important role in the adaptive evolution of MTB populations (Jogler *et al.*, 2009). Notwithstanding, dividing the magnetosome chain to the daughter cells is a challenge to MTB cell. The mechanism of division in diverse MTB has so far received much less attention than it deserves, partially because of the limited availability of pure cultures and lack of powerful genetic and visualization tools. To date, only a few studies have attempted to examine this issue. For instance, a recent study based on the direct visualization through transmission electron microscopy has revealed that, in the single chain of *Magnetospirillum gryphiswaldense*, the nascent magnetosome chain migrates from cell pole to midcell (the future division site) rapidly after division, and the division subsequently occurs in the middle of the cell as well as the magnetosome chain (Staniland *et al.*, 2010). This stirs up debates on basic yet important issues that need to be addressed in MTB division. What is the molecular mechanism behind the recognition and localization of magnetosome chain to the division site? How do MTB overcome the intra-chain magnetic force and effectively divide the chain into the daughter cells? And how do MTB ensure that both daughter cells will inherit equal fractions of the divided magnetosome chains?

In the current issue of *Molecular Microbiology*, using transmission electron microscopy, time-lapse light microscopy, and cryo-electron tomography, Katzmann and co-workers have provided the first detailed description of cytokinesis of *M. gryphiswaldense* (Katzmann *et al.*, 2011). This article is of note because the authors provide evidence that, similar to other prokaryotic organelles, the magnetosome chain division in *M. gryphiswaldense* is well co-ordinated with the cell division. Nascent magnetosome chain only transiently locates at the cell pole immediately after cell separation and then quickly migrates towards the midcell in pre-divisional cell as previously suggested (Staniland *et al.* 2010). By comparing localization and division of magnetosome chain in wild type and several mutants, Katzmann *et al.* (2011) demonstrated that the actin-like protein gene, *mamK*, which was previously implicated in chain assembly (Komeili *et al.*, 2006), likely plays a key role in this process. In a mutant in which *mam*K was deleted, the magnetosome chain was not properly localized at midcell (the future division site), and the chains became no longer recruited to the multiple constriction sites of filamentous cells, in which final septation and cell separation were blocked by the antibiotic cephalexin. This finding supports the hypothesis suggested by previous studies that MamK may have a dynamic role in actively positioning and assembly of the magnetosome chain (Pradel *et al.*, 2006, Komeili, 2007, Staniland *et al.*, 2010). This protein was first suggested to form cytoskeletal filaments for magnetosome chain alignment (Komeili *et al.*, 2006), but was recently realized to perform multiple functionalities (Katzmann *et al.*, 2010; Draper *et al.*, 2011).

Another key question of MTB cell division is how do MTB overcome the intra-chain magnetic force during division? In MTB cell, the arrangement of stable single domain magnetosomes in chain structure results in a net magnetic moment equal to the sum of each magnetosome's magnetic moment, which behaves as a permanent bar magnet. During the cell division, MTB have to overcome the existing intra-chain magnetic force. Katzmann *et al.* have found that *M. gryphiswaldense* undergoes an asymmetric cell division along two axes, somewhat reminiscent of cellular differentiation in *Caulobacter crescentus* and other bacteria (Margolin, 2000; Shapiro *et al.*, 2002). The authors discovered that, during the cell and magnetosome chain division, a wedge-like constriction and snapping of cell occurred by the formation of an arc-shaped Z ring (Fig. 1). *M. gryphiswaldense* displays this unique asymmetric constriction to cope with the magnetic force in the magnetosome chain structure. Katzmann *et al.* found that the snapping mechanism could reduce the force required to separate magnetosome chain by a factor of nearly five when compared with separating the chain by exerting a force along its chain axis. It has been calculated that the force generated by cell constriction, which in *Escherichia coli* and other bacteria was estimated to be in the range of about 10 pN (Erickson *et al.*, 2010), is sufficient to divide the magnetosome chain in *M. gryphiswaldense* through the snapping mechanism. One should note, however, that the intra-chain magnetic force needs to be overcome in *Magnetospirillum* bacteria is likely the lowest limit, as a magnetosome chain with larger and elongated magnetosomes, or multiple magnetosome chains in other MTB should have much stronger intra- and/or inter-chain magnetic interaction. Katzmann *et al.* additionally observed that the snapping of cell and concomitant division of magnetosome chain was a relatively fast process and occurred within short time period (i.e. several minutes) of the entire cell cycles, which took nearly about 4.5 h for completion (Katzmann *et al.*, 2011).

So far the processes of bacterial cell division are well characterized in several model organisms, such as *E. coli*, *C. crescentus*, and *Bacillus subtilis*. The article by Katzmann *et al.* provides a detailed analysis of this unique fascinating mode of cell division (Katzmann *et al.*, 2011). In *E. coli*, a complete tubulin-like Z ring assembles at midcell regulated by the Min system and nucleoid occlusion, and ultimately constricts symmetrically to bring about cell division (Fig. 1) (Margolin, 2001; Adams and Errington, 2009). In contrast to *E. coli* but much like *C. crescentus* (Li *et al.*, 2007), *M. gryph-*
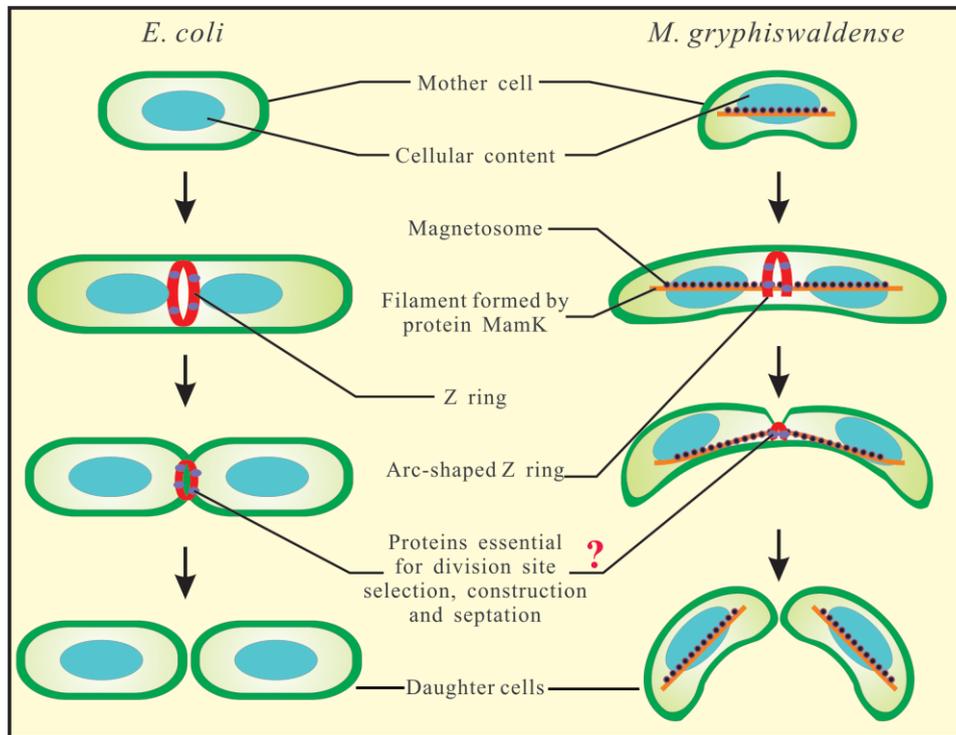
Fig. 1. Two different models of cytokinesis in *E. coli* and *M. gryphiswaldense* respectively. The Z ring in *E. coli* symmetrically constricts to bring about cell division; whereas, in *M. gryphiswaldense*, the arc-shaped Z ring is likely to cause an asymmetric wedge-like constriction. This novel leverage bending mechanism is assumed to overcome the magnetic force generated by magnetosome chain structure.

iswaldense produces an arc-shaped Z ring near the division site, where it displays an asymmetrically wedge-like constriction to snap the cell and magnetosome chain (Fig. 1). It is reasonable to assume that *Magnetospirillum* bacteria have developed this specific division system by evolution to efficiently pass on the magnetic receptor to their daughter cells. The exciting study by Katzmann and co-workers makes an important contribution to the field of prokaryotic cytokinesis. Notably, it demonstrates that an active and dedicated mechanism exists for positioning, segregation, and equipartitioning of magnetic organelles, which is analogous to mechanisms that have been recently discovered for other bacterial organelle-like structures and protein complexes, such as plasmids, chemoreceptors, carboxysomes and PHB granules (Thompson *et al.*, 2006; Savage *et al.*, 2010; Galán *et al.*, 2011).

The molecular mechanism of asymmetric division in *Magnetospirillum* bacteria is still not fully understood. One hypothesis is that this specific division is a consequence of a particular genetic organization. Comparative genomics has shown that, unlike most other bacteria that only have a single *ftsZ* gene, *Magnetospirillum* species have an additional *ftsZ*-like gene within an operon encoding other magnetosome proteins (Richter *et al.*, 2007; Ding *et al.*, 2010), which is suggested by the authors to be involved in the asymmetric division. However, future studies are needed to elucidate the roles and contributions of both *ftsZ* and *ftsZ*-like genes in the division of *Magnetospirillum*. Furthermore, more work has to be done to further characterize the cytokinesis mechanism in MTB. Emerging questions are, for example, what is the recognition mode of division site by magnetosome chain and perhaps by direct physical interaction of the actin-like MamK protein with the tubulin-like FtsZ protein or other divisome constituents? And finally, is the described mechanism of cell and magnetosome chain division universal and common to all other MTB, or do MTB with multiple and more intricate magnetosome chains use other or even more complex mechanisms?

Acknowledgements

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