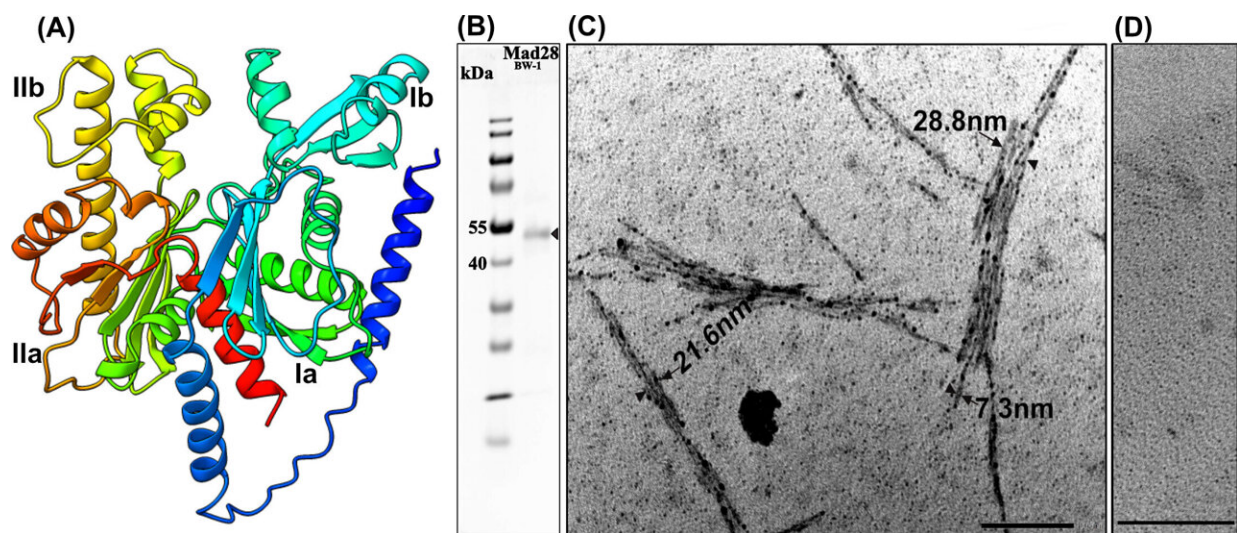


Biosynthesis of magnetic sensor in magnetic bacteria revealed through expression of foreign proteins

October 30 2023, by Jennifer Opel



(A) Three-dimensional structure model of Mad28 from BW-1 predicted by *AlphaFold*. The four actin domains, Ia, Ib, IIa, and IIb, are indicated in the structure. (B) SDS-PAGE of the purified N-terminal His-tagged Mad28_{BW-1} from *E. coli*. (C) *In vitro* polymerization of Mad28_{BW-1} in the presence of ATP- γ -S and without ATP (D) visualized by TEM. Scale bar, 100 nm. Credit: *mBio* (2023). DOI: 10.1128/mbio.01649-23

A German-French research team led by Bayreuth microbiologist Dirk Schüler presents [new findings](#) on the functionality of proteins in magnetic bacteria in the journal *mBio*. The research is based on [previous](#)

[results](#) published recently in the same journal.

In this study, the Bayreuth scientists used [bacteria](#) of the species *Magnetospirillum gryphiswaldense* to decipher the function of genes that are presumably involved in the biosynthesis of magnetosomes in other magnetic bacteria that are difficult to access.

Chains of magnetosomes act like compass needles

Magnetic bacteria contain [magnetic particles](#) consisting of nanocrystals of an iron mineral inside their cells. These organelle-like particles are known in research as magnetosomes. Like links in a chain, well over 20 of these particles are regularly lined up one after the other. The magnetic moments of the individual crystals add up so that the chain—similar to a compass needle—has the function of a magnetic sensor: It aligns the bacterial cell in the relatively weak magnetic field of the Earth.

The structure and spatial alignment of the chain are supported by fibers to which the particles attach. The main component of these cytoskeletal fibers, which act like a stabilizing scaffold, is the protein MamK. It belongs to the actin family and is present in all known species of magnetic bacteria, but also has relatives with quite different functions in most non-magnetic bacteria.

Gene transfer overcomes hurdles for research

The functions performed by the actin protein MamK in magnetic bacteria of the species *M. gryphiswaldense* have already been extensively investigated in previous studies: It has a significant influence on the chain formation process and causes the chain to be positioned exactly in the middle of the bacterial cell. During cell division, this ensures that the magnetosome chains are bisected and that the two

daughter cells receive sections of equal length.

Until now, however, little was known about whether other species of magnetic bacteria rely on MamK for magnetosome biosynthesis in the same way, or whether they use other proteins or even mechanisms for this purpose. This question is of particular interest to researchers, not least for the following reason: Numerous other species of magnetic bacteria produce magnetosomes and magnetosome chains that differ significantly from *M. gryphiswaldense* in terms of shape and size of their crystalline building blocks as well as their cellular arrangement.

The question as to what extent the mechanisms of biosynthesis unveiled in *M. gryphiswaldense* are universal remained unresolved mainly because the necessary studies on numerous other species of magnetic bacteria are very difficult: In some cases, the magnetic bacteria in question are not amenable to genetic study; in other cases, the mud-dwelling organisms can not be grown in the laboratory.

Mutants of *M. gryphiswaldense* produce foreign proteins

The new study published in *mBio* presents a novel approach to circumvent these difficulties. The Bayreuth researchers have laid the groundwork for this in a previous study also published in *mBio*. Here, they were successful in expressing proteins that control the production of magnetosomes in foreign species of magnetic bacteria, in *M. gryphiswaldense* mutants. The introduced proteins even could be shown to replace the functions of *M. gryphiswaldense*'s own proteins, whose genes had previously been eliminated—thus demonstrating functional equality of the foreign proteins in magnetosome formation.

In their new study, microbiologists from the University of Bayreuth, the

University of Aix-Marseille and the University of Lyon 1 have now applied this promising method to actins that were suspected of having a controlling influence on the linkage of magnetosomes in other magnetic bacteria. Mutants of *M. gryphiswaldense* produced these foreign actins, whose function could now be studied for the first time.

As it turned out, all the foreign actins studied affected chain formation. Some were even capable of producing scaffolds for chains that are very similar to the "original chains" in *M. gryphiswaldense*. In addition, a previously discovered, only distantly related novel actin-like protein termed Mad28 proved to be able to support the formation of the cytoskeletal fiber scaffold, and thus the formation of well-ordered magnetosome chains.

Key proteins control the linkage of magnetosomes

"Our research has clearly revealed that in addition to the already well-studied MamK, there are other actin-like proteins in the evolutionarily diverse group of magnetic bacteria that influence the production and positioning of magnetosome chains. In addition, we have discovered previously unknown proteins that perform similar functions in other bacteria in the formation of their magnetic compass needle. This sheds new light on the function of key proteins in the bacterial biosynthesis of magnetosomes," explains Ram Prasad Awal, Ph.D., the first author of the two studies.

"Our research results prove that the bacterium *M. gryphiswaldense* is very suitable as a model organism to decipher the functions of biosynthetic magnetosome proteins from foreign bacteria. These findings could also be used in the future for biotechnological and biomedical applications of magnetosomes," says Prof. Dr. Dirk Schüler, who is Chair of Microbiology at the University of Bayreuth.

Insights into evolution

Finally, the new study also provides an insight into the evolutionary history of the unique ability of magnetic bacteria to synthesize cellular magnetic sensors. Using special bioinformatic methods on the computer, the German-French team has succeeded for the first time in reconstructing the putative sequence of amino acids of an evolutionary predecessor protein of MamK. This is presumably the last common ancestor of all known representatives of this family.

Notably, this artificially generated protein, named MamK-LUCA, was able to perform a similar function in the extant magnetic bacterium *M. gryphiswaldense* as this model organism's own [protein](#).

More information: Ram Prasad Awal et al, Experimental analysis of diverse actin-like proteins from various magnetotactic bacteria by functional expression in *Magnetospirillum gryphiswaldense*, *mBio* (2023). [DOI: 10.1128/mbio.01649-23](https://doi.org/10.1128/mbio.01649-23)

Ram Prasad Awal et al, Functional expression of foreign magnetosome genes in the alphaproteobacterium *Magnetospirillum gryphiswaldense*, *mBio* (2023). [DOI: 10.1128/mbio.03282-22](https://doi.org/10.1128/mbio.03282-22)

Provided by Bayreuth University

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