51st Annual International Conference on the Biology of the Myxobacteria

Monday 1st June – Thursday 4th June 2026

Abstract booklet

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Myxo Meeting 2026 Programme

Monday 1st June 2026

16:00 – 20:00 Registration. Accommodation check-in. Displaying of posters.

17:30 – 18:00 Welcome and orientation – Dave Whitworth and Emily Radford

18:00 – 19:00 Dinner

19:00 - 19:45 Session 1. Flash talks and Perspectives talks

Chair: Dave Whitworth

19:00 – 19:05 Raye Scotttow (Aberystwyth University)- Use of myxobacterial secondary metabolites as antimicrobials against bacterial.

19:05 – 19:10 Amy Deane (Aberystwyth University) – Genome editing enhanced myxobacterial predators for protection of diverse crop pathogens.

19:10 – 19:15 Abi Kennedy (Aberystwyth University)- Reducing the carriage of pathogens in the food chain using myxobacterial biological control.

19:15 – 19:25 Mitchell Singer (UC Davis) - Perspectives talk

19:30 – 19:40 Sébastien Wielgoss (ETH Zurich) - Perspectives talk

20:00 - 21:00 Session 2. Icebreaker - Maria Fernandes, Casulo Coaching

21:00 – 22:00 Social time. Followed by optional excursion to pub.

Tuesday 2nd June 2026

9:00 - 10:40 Session 3.

Chair: Emily Radford & Cole Stevens

9:00 - 9:20 Alex Welford (Aberystwyth University) - Entomopathogen control within the insects for food and feed industry using predatory myxobacteria.

9:25 – 9:45 Benjamin Garcia de Figueiredo (Princeton University) - Capillary forces control both the formation and healing of holes in *M. xanthus* monolayers.

9:50 – 10:10 Nada Rezania (INRS)- Beyond the Agar Plate:
Ecological Behavior of *Myxococcus xanthus* in Soil.

10:15 – 10:35 Anna Luca Ida Hampe (Ruhr-University Bochum) - T3SS*-dependent prey lysis by *Myxococcus xanthus* requires two TPR-containing chaperones with unique substrates.

10:40 – 11:10 Coffee break

11:10 - 12:50 Session 4.

Chair: Raye Scottow & Anke Treuner-Lange

11:10 – 11:30 Emily Radford (Aberystwyth University)-
Engineering myxobacterial super-predators to fight crop disease.

11:35 – 11:55 Nawal Shehata (University of Mississippi) - Investigation of Companionships in Myxobacterial Swarm Communities with WIMLSP-2 as a Model System.

12:00 – 12:20 Antoine Bignet (INRS) - Biosurfactant polysaccharide drives dispersal of exopolysaccharide-coated myxospores in *Myxococcus xanthus*.

12:25 – 12.45 Margret Holtz (University of Greifswald) - Predatory myxobacteria meet plants: the myxobacterial potential for biocontrol agents against plant pathogens.

12:0 – 14:00 Lunch

14:00 - 15:40, Session 5.

Chair: Penelope Higgs & Oleg Igoshin

14:00 – 14:20 Stephen Akemu (Aberystwyth University) - Newly isolated predatory myxobacteria can confer antifungal protection to edible insects.

14:25 – 14:45 Changsheng Wu (Shangdong University) – Chemistry and Biology of Natural Products from Predatory Myxobacteria.

14:50 – 15:10 Francisco Javier Marcos Torres (University of Granada)
- PhbR from *Myxococcus xanthus* modulates consumption of PHA from the prey.

15:15 – 15:35 Anke Treuner-Lange (Max-Planck-Institut für Terrestrische Mikrobiologie)- New insights in the transcriptional regulation of Type IV pilus formation in *Myxococcus xanthus.*

15:40 – 16:10 Coffee break

16:10 - 17:15 Session 6. Poster session

17:15 - 18:00 Session 7. Perspectives talks

Chair: Emily Radford

17:15 – 17:25 Egbert Hoiczyk - Perspectives talk

17:30 – 17:40 Yuen-Tsu Nicco Yu (ETH Zurich) – Perspectives talk

17:45 – 17:55 Dan Wall - Perspectives talk

18:00 – 19:00 Dinner

19:00 - 20:30 Session 8. Speed mentoring session - Maria Fernandes, Casulo Coaching

20:30 – 22:00 Quiz – Cwtch Bar in the Students' Union

Wednesday 3rd June 2026

9:00 - 10:40 Session 9.

Chair: Antoine Bignet & Egbert Hoiczyk

9:00 - 9:20 Penelope Higgs (Wayne State University) - Phenotypic heterogeneity and cell fate segregation in the *Myxococcus xanthus* life cycle.

9:25 – 9:45 Yuen-Tsu Nicco Yu (ETH Zurich) – Investigating T6SS-Mediated Antagonism and Resistance in Myxobacteria.

9:50 – 10:10 Gayathri Pananghat (Indian Institute of Science Education and Research) – Mechanism of the MglA GTPase activity regulators RomX and RomY.

10:15 – 10:35 Niels Jorgensen (University Copenhagen) - Myxobacteria as producers of off-flavour compounds in fish farms with water recirculation.

10:40 – 11:10 Coffee break

11:10 - 12:00 Session 10.

Chair: Maria da Costa & Gayathri Pananghat

11:10 – 11:30 Mitchell Singer (UC Davis) - Why do some Myxobacteria have two light recognition systems?

11:35 – 11:55 Luoyi Wang (Institute of Microbiology, Chinese Academy of Sciences) - Genetic Engineering of *Sorangium cellulosum*: A Platform for Decoding Myxobacterial Secondary Metabolism.

12:00 – 12:05 Excursion briefing – Dave Whitworth

12:05 – 13:00 Lunch

13.30 - 16:45 Excursion from Vale of Rheidol train station

18:30 – 20:30 Conference Banquet Dinner

20:30 - 21:45 Session 11 – Recorded Plenary.

Chair: Dave Whitworth & Amy Deane

20:30 – 20:50 Oleg Igoshin (Rice University) - Deep Learning Framework for Quantifying Self-Organization in *Myxococcus xanthus*.

20:55 – 21:15 Gregor Fuhrmann (Friedrich-Alexander-University Erlangen-Nürnberg) -Engineered myxobacterial vesicles as biogenic strategy for combating bacterial infections.

21:20 - 21:40 Cole Stevens (University of Mississippi)- Developing stable plasmids for use in Myxococcota.

21:45 – 22:00 Social time. Followed by optional excursion to pub.

Thursday 4th June 2026

9:00 - 10:40 Session 12.

Chair: Abi Kennedy & Mitchell Singer

9:00 - 9:20 Egbert Hoiczyk - Identification of novel bactofilin-interacting proteins.

9:25 – 9:45 Dan Wall (University of Wyoming) - Aggregative chimeric multicellularity in the absence of lethal kin discrimination.

9:50 – 10:10 Greg Velicir (ETH Zurich) - Testing for a tradeoff between sporulation versus fitness under early nutrient exposure after starvation.

10:15 – 10:35 Sébastien Wielgoss (ETH Zurich) - Endemic phage spread drives adaptive diversification in soil myxobacterial kin groups.

10:40 – 11:10 Coffee break

11:10 - 12:00 Prize giving and Business meeting

12:00 Collect packed lunch and depart

Abstract Booklet

Monday 1st of June

Use of myxobacterial secondary metabolites as antimicrobials against bacterial phytopathogens

Authors: Raye Scottow and David Whitworth

Affiliations: Aberystwyth University

Abstract:

The increasing threat of bacterial phytopathogens and antimicrobial resistance calls for the development of sustainable alternatives to conventional control methods [1]. This study evaluates the antimicrobial potential and predatory activity of *Myxococcus xanthus* strains CA010, CA023, and DK1622 against plant-associated bacteria [2].

Crude secondary metabolite extracts were assessed for antimicrobial activity using minimum inhibitory concentration (MIC) and minimum biofilm prevention concentration (MBPC) assays, alongside predation assays. Extracts exhibited concentration-dependent inhibition of planktonic growth but were weaker and more variable than commercially available antibiotics, with strong species-specific effects. Biofilm inhibition was limited and species-specific, with effects evident only at higher concentrations and, in some cases, stimulation of biofilm biomass growth at sub-inhibitory levels [3].

Predation assays demonstrated effective suppression of prey bacteria; however, predatory efficacy did not correlate with extract-based antimicrobial activity, indicating that these metabolites alone do not account for the full antimicrobial capacity of *M. xanthus* [4].

These findings highlight the mechanistic complexity of myxobacterial antimicrobial activity and support their potential as a source of novel strategies for controlling phytopathogenic bacteria.

References:

1. Košćak L, Lamovšek J, Đermić E, Prgomet I, Godena S. Microbial and plant-based compounds as alternatives for the control of phytopathogenic bacteria. *Horticulturae*. 2023;9(10):1124. Available from: https://www.mdpi.com/2311-7524/9/10/1124

2. Zhang L, Bao L, Li S, Liu Y, Liu H. Substances derived from myxobacteria that prevent and control plant pathogenic diseases and their prevention and control principles. *Front Microbiol*. 2024;14. Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC10800785/

3. Chimi LY, Bisso BN, Sedar G, Dzoyem JP. Antibiotic-potentiating effect of some bioactive natural products against planktonic cells, biofilms, and virulence factors of *Pseudomonas aeruginosa*. *Biomed Res Int*. 2023;2023:1–10.

4. Thiery S, Kaimer C. The predation strategy of *Myxococcus xanthus*. *Front Microbiol*. 2020;11:2. Available from: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6971385/

Genome Editing Enhanced Myxobacterial Predators for Protection of Diverse Crop Pathogens

Authors: Amy Deane

Affiliations: FoodBiosystems DTP, Aberystwyth University

Abstract:

Pathogens continue to pose a major challenge to global agriculture, accelerating spoilage, reducing yields, and undermining the resilience of emerging food-production systems such as hydroponics, insect farming, and cultured meat. As resistance to chemical pesticides rises, the need for sustainable alternatives becomes increasingly urgent. Myxobacteria are emerging as particularly promising biological control (biocontrol) agents due to their broad-spectrum predatory activity against diverse pathogens.

Recent genome-wide association studies have identified specific myxobacterial genes whose presence correlates with reduced predatory efficiency (Sutton *et al*., 2019). Deleting these *putative predation-inhibitory genes* (PPIGs) offers a potential route to enhance predatory performance and improve their value as biocontrol agents.

This project aims to identify PPIGs across multiple pathogen targets, engineer a CRISPR-Cas9 system to remove them, and evaluate whether these edits increase crop resilience to environmentally relevant pathogens. In vitro predation assays will first quantify how efficiently different myxobacterial strains prey upon agriculturally important pathogens. GWAS can then be used to identify PPIGs associated with reduced predation of individual or multiple pathogens. A CRISPR-Cas9 system will then be engineered to generate multiple unmarked deletions in myxobacteria, with successful gene loss confirmed through genome sequencing. Finally, genetically modified predator strains will be tested alongside wild-type myxobacteria in controlled assays, using metrics such as mortality, growth rate, and yield to assess improvements in biocontrol efficacy.

References:

Sutton, D., Livingstone, P.G., Furness, E., Swain, M.T. and Whitworth, D.E., 2019. Genome-wide identification of myxobacterial predation genes and demonstration of formaldehyde secretion as a potentially predation-resistant trait of Pseudomonas aeruginosa. *Frontiers in Microbiology*, *10*, p.2650.

Reducing the carriage of pathogens in the food chain using myxobacterial biological control

Authors: Abigail Kennedy

Affiliations: Aberystwyth University, OneZoo CDT, Edibl,

Abstract:

The pressure on global food systems has accelerated the development of novel protein sources, including commercial insect farming (Acheampong et al., 2025). While this offers opportunities for sustainable protein production, it also raises food safety and biosecurity challenges (Lisboa et al., 2024). High-density rearing environments can promote the persistence and transmission of entomopathogens and opportunistic or zoonotic microbes relevant to human health (Akemu et al., 2025). From a One Health perspective, the health of farmed insects, their associated microbiota, and human consumers are closely interconnected. Understanding and managing pathogen dynamics within these systems is therefore essential for ensuring food safety and sustainable insect production.

This PhD project aims to evaluate myxobacteria as biological control agents to reduce microbial pathogen carriage within insect-based food systems, using commercial cricket production as a model. It addresses interconnected risks to insect health, food safety, and human health by exploring biologically based alternatives to chemical disease control in intensive rearing systems.

Key methods include controlled exposure experiments to assess the effects of myxobacteria on insect survival, health, and pathogen load; microbiome sequencing to characterise shifts in microbial community composition; and in vitro antagonism and co-culture assays to evaluate the ability of selected strains to suppress relevant bacterial and fungal pathogens.

The project will create insights into the use of myxobacteria as a preventive biocontrol strategy. By integrating microbiome, host, and pathogen data, it will advance understanding of disease dynamics and contribute to safer, more sustainable insect-based food production systems.

References:

Acheampong, R., Osei Tutu, C., Akonor, P.T., Asiedu, B.K., Owusu-Bempah, J., Mahama, S., Kumador, D.K., Appiadu, D., Koranteng, A.F., Wiafe-Kwagyan, M., Kortei, N.K., Saalia, F.K., 2025. Edible insects for food security: Overcoming cultural, legal and tech barriers to wider adoption. Food Humanity 5, 100778. https://doi.org/10.1016/j.foohum.2025.100778

Akemu, S.E., Welford, A.E.G., Santer, R.D., Whitworth, D.E., 2025. Microbial pathogens of edible insects: a growing problem for the insect farming industry. Emerg. Top. Life Sci. 9, 13–24. https://doi.org/10.1042/ETLS20253013

Lisboa, H.M., Nascimento, A., Arruda, A., Sarinho, A., Lima, J., Batista, L., Dantas, M.F., Andrade, R., 2024. Unlocking the Potential of Insect-Based Proteins: Sustainable Solutions for Global Food Security and Nutrition. Foods 13. https://doi.org/10.3390/foods13121846

Tuesday 2nd June

Entomopathogen control within the insects for food and feed industry using predatory myxobacteria

Authors: Alex Welford & David Whitworth

Affiliations: Aberystwyth University

Abstract:

Current UN predictions estimate the global population will reach 8.5 billion by 2030 and 9.7 billion by 2050 [1.]. This continuing growth puts pressure on already unsustainable agricultural systems with increasing requirements for high-quality protein. 'Insects for food and feed' is a promising alternative protein stream, which also helps to tackle the need for more adaptable, sustainable and less environmentally damaging forms of agriculture. Insect rearing facilities are intensive - typically see high stocking densities, humidity and temperature, compounded by a lack of legislation as to the mandatory husbandry of insects. Such conditions promote pathogen outbreaks, resulting in potential economic losses and welfare issues.

Myxobacteria are soil-dwelling social bacteria which move and feed cooperatively in predatory groups [2.]. Their wide prey range and predatory characteristics mark myxobacteria as an exciting and promising candidates for new biocontrol treatments. We have been investigating the therapeutic effects of the myxobacterium *Myxococcus xanthus* when applied to desert locusts (*Schistocerca gregaria*, Orthoptera) infected with the entomopathogenic fungus *Metarhizium robertsii.* Survival studies showed that *M. xanthus* can protect *S. gregaria* from *M. robertsii* infection. We have also investigated the locust gut microbiome, which is diverse and variable, finding that *M. xanthus* can reach the insect gut without triggering systemic dysbiosis. Our current research is exploring the effects of myxobacterial treatments on the insect microbiome when challenged with an entomopathogen, and the potential benefits of the use of *Myxococcus xanthus* as a probiotic to reduce microbial loads within the insect gut prior to harvest.

References:

1. Żuk-Gołaszewska, K., Gałęcki, R., Obremski, K., Smetana, S., Figiel, S. and Gołaszewski, J., 2022. Edible insect farming in the context of the EU regulations and marketing—An overview. *Insects*, *13*(5), p.446.

2. Furness, E., Whitworth, D.E. and Zwarycz, A., 2020. Predatory interactions between myxobacteria and their prey. In *The ecology of predation at the microscale* (pp. 1-36). Cham: Springer International Publishing.

Capillary forces control both the formation and healing of holes in *M. xanthus* monolayers

Authors: Benjamin Garcia de Figueiredo, Joshua Shaevitz

Affiliations: Princeton University

Abstract:

When a colony of *M. xanthus* is grown on an agar plate, holes spontaneously form in the dense cell bulk, revealing the hydrogel underneath. From the point of view of active matter physics, this is a non-trivial behavior in cell density, since a simplified description of a gas of self-propelled rods would predict giant number fluctuations rather than biphasic behavior, with coexistence of a dense and a sparse phase. Previous work in our lab has shown that the formation of cell layers and holes is controlled by the coupling between cell orientation and self-propulsion, which renders the system an active nematic where inflow and outflow of cells is localized at features called topological defects [1-3]. More recent work has shown the importance of capillary forces due to the layer of fluid pulled by cells in their hydrated environment [4,5]. Here we show that the nucleation, persistence and eventual closing of holes in a monolayer is directly controlled by the fluid layer around individual cells. This fluid layer ordinarily acts as a cohesion factor, but once ruptured it becomes a stable interface which causes the realignment of cells at the boundary of a hole. We show the anchoring of cells at the meniscus suppresses the line tension that drives closure and promotes topological charge polarization at the interface. Altogether, these results highlight the role the thin fluid layer plays in the cell collective dynamics, suggesting a new paradigm of hydrated active matter.

References:

[1] **Copenhagen, K., Alert, R., Wingreen, N. S., Shaevitz, J. W.** "Topological defects promote layer formation in *Myxococcus xanthus* colonies." *Nat. Phys.* 17, 211–215 (2021).

[2] **Han, E., Fei, C., Alert, R., Copenhagen, K., Koch, M. D., Wingreen, N. S., Shaevitz, J. W.** "Local polar order controls mechanical stress and triggers layer

formation in *Myxococcus xanthus* colonies." *Nat. Commun.* 16, 952 (2025).
[3] **Copenhagen, K., Black, M., Shaevitz, J. W.** "3D Agent-Based Modeling without Chemical Signaling Recreates Collective Behaviors seen in *Myxococcus xanthus* Colonies." *PRX Life* 3, 043015 (2025).
[4] **Bourque, A. R., Hampshire, P. A. E., Alert, R., Shaevitz, J. W.** "Active surface waves drive rippling in *Myxococcus xanthus* colonies." *bioRxiv* 2025.11.28.691037 (2025).
[5] **Black, M. E., Fei, C., Alert, R., Wingreen, N. S., Shaevitz, J. W.** "Capillary interactions drive the self-organization of bacterial colonies." *Nat. Phys.* 21, 1444–1450 (2025).

Beyond the Agar Plate: Ecological Behavior of *Myxococcus xanthus* in Soil

Authors: Nada Rezania[1], Fares Saidi[2], Mamta Rani[3], Xavier Baril[1], Saji George[3], Philippe Constant[1], Jonathan Perreault[1], Salim T. Islam[1].

Affiliations: 1: INRS (National Institute of Scientific research)

2: EVAH corp

3: McGill university

Abstract:

The soil microbiome plays a central role in nutrient cycling, microbial interactions, and the maintenance of agricultural soil health. Soil microbial communities also contribute to plant protection by limiting the establishment and proliferation of pathogenic microorganisms through competition, antimicrobial production, and predatory interactions. Among soil microorganisms, the predatory bacterium *Myxococcus xanthus* stands out for its complex multicellular behaviors, coordinated motility systems, and predation strategies[1]. Although *M. xanthus* has been extensively characterized under laboratory conditions, its ecological behavior and adaptation within natural soil environments remain poorly understood. This project aims to investigate the responses of *M. xanthus* following implantation into Quebec agricultural soils under both sterile and non-sterile conditions. Several mutant strains associated with predation and motility behaviors, including Δ*pilA*, Δ*kilKLM* [2], and ΔT6SS, will be studied alongside the wild-type strain to evaluate how specific bacterial functions contribute to survival, adaptation within soil ecosystems, and nutrient acquisition mechanisms[3].

The study focuses on monitoring cell presence and morphology over time following soil implantation. By comparing sterile[4] and native microbial environments, the project seeks to determine how interactions with indigenous microorganisms influence the persistence and predatory behavior of *M. xanthus*.

Experimental approaches include fluorescence microscopy observations of single-cell organization following soil implantation of strains expressing mCherry. DNA-based

analyses, including 16S rRNA sequencing, will be used to monitor microbial community variation, while gas concentration measurements will help evaluate changes in microbial activity associated with the presence of *M. xanthus*. Preliminary observations suggest that soil conditions strongly influence cell organization and morphology.

This work contributes to a broader understanding of microbial predator ecology in complex environments and may support future applications involving soil microbiome modulation, biological control strategies[5], and sustainable agricultural soil management[6].

References:

1. Kroos L, Wall D, Islam ST, Whitworth DE, Muñoz-Dorado J, Higgs PI, et al. Milestones in the development of Myxococcus xanthus as a model multicellular bacterium. Journal of Bacteriology. 2025;207(7):e00071-25.
2. Seef S, Herrou J, de Boissier P, My L, Brasseur G, Robert D, et al. A Tad-like apparatus is required for contact-dependent prey killing in predatory social bacteria. Elife. 2021;10.
3. Ismaiel A, Lakshman DK, Millner P. Biocontrol Potential of Fungal and Oomycete Phytopathogens by Myxobacterial Strains. Applied Microbiology. 2025;5(3):85.
4. Li H, Liu L, Li C, Liu X, Ziadi N, Shi Y. Efficiency of Different Soil Sterilization Approaches and Their Effects on Soil Particle Size Distribution. Journal of Soil Science and Plant Nutrition. 2023;23(3):3979-90.
5. Bull CT, Shetty KG, Subbarao KV. Interactions Between Myxobacteria, Plant Pathogenic Fungi, and Biocontrol Agents. Plant Dis. 2002;86(8):889-96.
6. Ye X, Li Z, Luo X, Wang W, Li Y, Li R, et al. A predatory myxobacterium controls cucumber Fusarium wilt by regulating the soil microbial community. Microbiome. 2020;8(1):49.

Engineering myxobacterial super-predators to fight crop disease

Authors: Emily Radford and Dave Whitworth

Affiliations: Aberystwyth University

Abstract (250 words):

Myxobacteria exhibit broad-ranging antimicrobial activity as part of their predatory niche in the soil microbial community. They predate by killing, lysing and consuming nutrients from prey which include Gram-positive and -negative bacteria, fungi and oomycetes [1]. As such, this activity provides an opportunity for myxobacteria to be utilised in an alternative context: biological control.

Phytopathogens, such *Zymoseptoria tritici* - the causative fungal agent of septoria leaf blotch in wheat plants, threaten crop production by causing dramatic losses in yield and incurring substantial costs [2]. The use of biocontrol agents to prevent and/or treat crop diseases presents a more sustainable alternative to traditional chemical treatments and carries a smaller risk of resistance developing.

To assess the potential for myxobacteria to be used as a biocontrol for crop diseases, *in vitro* assays were used to demonstrate the strain-specific activity of a range of myxobacterial strains across genera. Predation activity against multiple strains of *Z. tritici* was assessed as well as the ability of the myxobacterial strains to prevent the formation of, and in some cases disrupt a mature, *Z. tritici* biofilm.

In addition, a genome-wide association study (GWAS) analysis was conducted to identify candidate genes with a role in determining predatory ability through assessing correlation of phenotype (*in vitro* predatory ability) with the presence/absence of individual genes in the genome of each myxobacterial strain. The resulting candidate genes are targets for gene editing techniques to create a novel strain/s which is/are expected to show enhanced predatory activity compared to the wild type.

References:

[1] Livingstone PG, Morphew RM, Whitworth DE. Myxobacteria are able to prey broadly upon clinically-relevant pathogens, exhibiting a prey range which cannot be explained by phylogeny. Front Microbiol 2017;8:1593. https://doi.org/10.3389/fmicb.2017.01593.

[2] Simón MR, Börner A, Struik PC. Editorial: Fungal Wheat Diseases: Etiology, Breeding, and Integrated Management. Front Plant Sci 2021;12:671060. https://doi.org/10.3389/FPLS.2021.671060.

Investigation of Companionships in Myxobacterial Swarm Communities with WIMLSP-2 as a Model System

Authors: Nawal Shehata, Cole Stevens

Affiliations: University of Mississippi

Abstract:

Understanding how predatory bacteria interact with neighboring microbes is key to understand the ecological and metabolic dynamics of soil communities. My research focuses on a naturally occurring bacterial consortium composed of the predatory myxobacterium Archangium and its associated partner Microvirga. While myxobacteria are typically characterized by broad predatory behavior, emerging evidence suggests that stable associations with non-prey organisms can form under specific conditions. In this study, I isolated and purified monocultures of both organisms from the WIMLSP-2 consortium using selective enrichment and serial passaging. I then reconstructed the consortium by reintroducing Microvirga into an Archangium monoculture and monitored its stability across multiple passages. The reconstituted system remained stable over time, providing a reproducible model for studying interspecies interactions. Time-course metabolomics revealed dynamic chemical communication within the consortium, including early production of acyl-homoserine lactone (AHL) signaling molecules and late-stage detection of gephyronic acid, a bioactive secondary metabolite. This temporal pattern mirrors that of the natural consortium and suggests coordinated metabolic activity between the two species. Genomic and metabolic analyses indicate potential cross-feeding interactions, where Microvirga may supply essential nutrients such as branched-chain amino acids, while Archangium contributes sulfur-containing metabolites involved in methionine biosynthesis. Predation assays further show that Archangium exhibits reduced predation toward Microvirga while maintaining activity against other bacteria such as Escherichia coli. Together, these findings support a model of interbacterial symbiosis that provides new insight into myxobacterial development, metabolism, and predation within polymicrobial communities.

References:

1) Khanal, S.; Walsh, S.; Shehata, N.; Ahearne, A.; Belin, D.; Larson, B.; Tabor, B.; Wall, D.; Stevens, C. S. Predator Avoidance Promotes Inter-Bacterial Symbiosis with Myxobacteria in Polymicrobial Communities. bioRxiv 2026. https://doi.org/10.64898/2026.02.12.705600

Biosurfactant polysaccharide drives dispersal of exopolysaccharide-coated myxospores in *Myxococcus xanthus*

Authors: Antoine Bignet, Nada Rezania, Salim T. Islam*

Affiliations: INRS, AFSB center, Laval, Quebec.

Abstract:

Bacterial spores are highly resilient cell forms, yet the organization of their protective surface layers in diderm species remains largely unexplored. For the social predatory soil bacterium *Myxococcus xanthus*, myxospore formation within multicellular fruiting body structures is a key ecological adaptation to surviving conditions of nutrient deprivation. These myxospores were long thought to be outwardly coated with so-called major spore coat (MASC) polysaccharide. Using polysaccharide-deficient mutant strains, electron microscopy, surface hydrophobicity assays, dye binding, and functional swarm complementation, we show that MASC instead forms a protective sub-surface outer-cortex layer, while the exopolysaccharide (EPS) glycocalyx inherited from vegetative cells constitutes the true outermost myxospore coat. EPS mediates inter-myxospore adhesion and supports collective behaviors, whereas secretion of biosurfactant polysaccharide (BPS) reduces myxospore surface stickiness, preventing excessive aggregation. BPS-deficient myxospores form persistent clumps, while EPS-deficient myxospores fail to aggregate or restore EPS-dependent swarm motility of vegetative cells. These results reveal a mechanistic interplay in which MASC serves as a sub-surface protective layer, EPS defines the exterior interface, and BPS tunes surface accessibility to regulate dispersal. Our findings overturn long-standing assumptions about myxospore architecture and illustrate a polysaccharide-driven strategy for controlling aggregation and readiness for germination. More broadly, these results highlight how social diderm bacteria leverage inherited and dynamically remodeled polysaccharide surfaces to coordinate multicellular development, in contrast to the rigid protein-based spore surfaces of Gram-positive species.

Predatory myxobacteria meet plants: the myxobacterial potential for biocontrol agents against plant pathogens

Authors: Groß, Verena[a]; Stettnisch, Anne[c]; Braun-Kiewnick, Andrea[b]; Holtz, Margret[a]; Gooch, Jesselyn[a]; Urich, Tim[a]; Babin, Doreen[b]

Affiliations: [a] Institute of Microbiology, Center for Functional Genomics of Microbes, University of Greifswald, Greifswald, Germany

[b] Julius Kühn Institute (JKI) - Federal Research Centre for Cultivated Plants, Institute for Epidemiology and Pathogen Diagnostics, Braunschweig, Germany

[c] Institute of Forest Sciences, Chair of Soil Ecology, Albert-Ludwigs-University Freiburg, Freiburg i. Br., Germany

Abstract:

Predatory myxobacteria play a crucial role in soil microbial food webs. Our previous metatranscriptomic study revealed that *Myxococcota*, particularly *Haliangiaceae* and *Polyangiaceae*, are prevalent micropredators in most soils, accounting for over 60% of all potential bacterivores identified. In vitro predation assays of understudied, but abundant representatives such as *Haliangium*, demonstrated high predation efficiency with a broad prey spectrum, including many Gram-positive and Gram-negative bacterial phyla, as well as yeasts and filamentous fungi. Thus, myxobacteria might be potent biocontrol agents against plant pathogens. The aim of this study was to determine whether myxobacteria could be used as a potential suppressors of the wheat pathogenic fungus *Gaeumannomyces tritici* (Ggt). Winter wheat seeds were inoculated with *Haliangium ochraceum* and *Myxococcus virescens* and grown for four weeks in Ggt-infected soil under greenhouse conditions. Ggt infection significantly reduced plant growth and resulted in an increase in potential plant-beneficial bacteria in the rhizosphere. Myxobacteria inoculation did not impair plant growth (with or without Ggt infection), with *M. virescens* exhibiting a slight plant growth-promoting effect. Notably, inoculating plants with myxobacteria reduced Ggt infestation symptoms by 50%, compared to non-inoculated controls. Our

study suggests that predatory myxobacteria might be promising candidates for novel plant-beneficial inoculants against the causative fungal agent of wheat take-all-disease.

References:

Petters, S.; Groß, V.; Söllinger, A.; Pichler, M.; Reinhard, A.; Bengtsson M. M.; Urich, T. (2021) 'The soil microbial food web revisited: Predatory myxobacteria as keystone taxa?', *The ISME Journal*, 15(9), pp. 2665–2675. Available at: https://doi.org/10.1038/s41396-021-00958-2.

Groß, V.; Reinhard, A.; Petters, S.; Pichler, M.; Urich, T. (2023) 'Adding complexity to soil food webs: Myxobacteria have broad predation spectra with bacteria, yeasts and filamentous fungi in vitro', *European Journal of Soil Biology*, 117, p. 103508. Available at: https://doi.org/10.1016/j.ejsobi.2023.103508.

Groß, V.; Stettnisch, A.; Braun-Kiewnick, A.; Holtz, M.; Gooch, J.; Urich, T.; Babin, D. (2026) 'Myxobacteria inoculation of wheat seeds – minor changes in the soil microbial community composition but potential for a reduction of take-all disease under greenhouse conditions', *Plant Soil.* Accepted for publication.

Newly isolated predatory myxobacteria can confer antifungal protection to edible insects

Authors: Akemu Stephen E, Whitworth David E, Santer Roger D

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Abstract:

Edible insects are emerging as a sustainable protein source; however, fungal diseases regularly disrupt large-scale insect production, reducing yield and endangering colony health. Current disease management strategies rely mainly on chemical treatments, resulting in a need for ecologically friendly biocontrol approaches. Myxobacteria are predatory soil bacteria known for producing a variety of bioactive secondary metabolites with antimicrobial capabilities; nevertheless, their potential applications in insect agriculture are mostly unknown. In this study, we isolated and characterised novel myxobacterial strains from environmental samples in Aberystwyth, and we tested their predatory ability and antifungal efficacy against entomopathogenic fungi initially isolated from deceased locusts. Phylogenetic analysis revealed several isolates that shared a low similarity with previously reported species, implying the presence of potentially novel taxa. In vitro studies revealed a potent inhibitory effect against locust-associated fungi with considerable decreases in fungal growth and spore germination. To determine functional significance in vivo, edible insect cohorts were exposed to fungal infections in the presence or absence of specific myxobacterial strains. When compared to untreated controls, treatment with live myxobacteria greatly increased insect survival and reduced obvious fungal colonisation. These findings highlight newly discovered myxobacteria as potential biocontrol agents for sustainable insect agriculture and contribute to a better understanding of beneficial microbial interactions in insect production systems.

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Chemistry and Biology of Natural Products from Predatory Myxobacteria

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Abstract:

Natural products (NPs) biosynthesized by myxobacteria are appealing due to their sophisticated chemical skeletons, remarkable biological activities, and intriguing biosynthetic enzymology. Our research group has been isolating myxobacteria from diverse ecological niches for nearly three decades. In this talk, we present an integrated strategy that advances both the chemical and biological investigation of myxobacterial NPs. On the chemical front, we established NMR-based metabolomics as a powerful alternative to conventional MS-based approaches for maximal excavation of this underexplored resource. We constructed MyxoDB (https://www.myxonpdb.sdu.edu.cn), the first freely available database dedicated to myxobacterial NPs, which greatly enhances NMR- and genomics-guided discovery of cryptic "dark matters." This pipeline led to the identification of structurally novel NPs, including archangiumide, myxadazole, and coralsterol, among others. On the biological front, to enable functional characterization and heterologous exploitation of myxobacterial biosynthetic gene clusters, we developed MxDIRECT, a novel and efficient genome editing technology specifically tailored for the model strain *Myxococcus xanthus* DK1622. We further constructed MxPKS, a proprietary chassis strain optimized for the high-efficiency heterologous expression of myxobacterial NP gene clusters. As a demonstration of the power of this integrated chemical-biological platform, we applied it to investigate coralinones, a newly discovered class of signaling molecules. Beyond structural elucidation, we elucidated their biosynthesis, performed biomimetic total synthesis, established structure–activity relationships, and uncovered their self-resistance mechanism. Intriguingly, coralinone exacerbates cellular aggregation of myxobacteria grown in liquid cultures by enhancing the secretion of extracellular matrix and is indispensable for fruiting body formation. Collectively, our findings—

combining NMR-based metabolomics, MyxoDB, MxDIRECT genome editing, and the MxPKS chassis—lay a solid foundation for the maximal excavation and functional study of these largely underexplored resources.

PhbR from *Myxococcus xanthus* modulates consumption of PHA from the prey

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Abstract:

Myxococcus xanthus is a facultative bacterial predator that preys upon other soil microorganisms to feed on and consume their macromolecules. Our research group is studying the predatory interaction between *M. xanthus* and the legume nitrogen-fixing symbiont *Sinorhizobium meliloti*. In a transcriptomic study of this interaction, we identified a gene cluster (MXAN_0214-MXAN_0220) harboring genes involved in fatty acid metabolism and a TetR-family transcriptional regulator, whose expression increases 4-12 fold during predation (Pérez et al., 2022). According to our data, this whole cluster is regulated by the TetR regulator (from now on named PhbR), and responds to the presence of PHA (polyhydroxyalcanoates) in the prey. PHA is a biological polyester with plastic properties and the capability of being degraded by certain microorganisms. These properties have turned PHA into one of the main alternatives to petrol-based bioplastics. Additional genes identified in the PhbR regulon suggest that this regulator mediates consumption of the prey PHA by controlling the expression of several PHA depolymerases, transmembrane transporters, and biosynthesis genes. Currently, we are investigating PhbR-dependent degradation of PHA, transport of its byproducts, and their assimilation into *M. xanthus'* biosynthetic routes.

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Wednesday 3rd June 2026

Phenotypic heterogeneity and cell fate segregation in the *Myxococcus xanthus* life cycle

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Abstract:

Myxococcus xanthus displays pronounced phenotypic heterogeneity during its complex lifecycle. Under nutrient-limited conditions, *M. xanthus* enters a developmental program (a specialized biofilm) in which cells segregate into two spatially distinct fates: fruiting bodies filled with spores and a persister-like peripheral rod population. Accumulation of MrpC, a major transcriptional regulator of the developmental program, is critical for appropriate cell fate segregation, but little is known about this regulated accumulation is achieved. The EspA and EspC histidine kinases function together to stimulate turnover of MrpC. We use a combination of single-cell reporters and in situ confocal microscopy to demonstrate that expression of the *esp* genes is enriched in the peripheral rods. We next identified three transcription factors necessary for *espA* and *C* transcriptional control: MrpC; FruA, a transcription factor that coordinates sporulation within fruiting bodies; and the xenobiotic response element, Xre0228. We demonstrate that MrpC directly activates *espA* and *espC*; FruA represses *espC* but not *espA*; and Xre0228 activates *espA* but represses *espC*. These genetic interactions fit common network motifs that promote or stabilize phenotypic heterogeneity. We propose a model by which cell fate segregation is directed, stabilized, and tuned to environmental conditions.

Investigating T6SS-Mediated Antagonism and Resistance in Myxobacteria

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Abstract:

To obtain nutrients and compete for space and limited resources, bacteria are constantly engaged in antagonistic interactions and microbial warfare within their environments. These competitive encounters drive the evolution of sophisticated offensive and defensive strategies that enable bacteria to eliminate rivals and secure ecological advantages. Myxobacteria, ubiquitous soil-dwelling social predators, employ a diverse arsenal of antagonistic and predatory mechanisms, including extracellular lytic enzymes, secondary metabolites, outer membrane exchange (OME) of toxins and contact-dependent killing strategies to lyse, and consume a broad range of microbial prey and inhibit competitors.

During social interactions, myxobacteria have a variety of mechanisms that determine who they cooperate with and who they antagonize, among which the Type VI Secretion System (T6SS) plays a central role. The T6SS is a contractile, phage-tail–like nanomachine that delivers toxic effectors directly into neighboring cells in a contact dependent manner, enabling interbacterial killing. The T6SS toxins target cell wall synthesis, membranes, nucleic acids, and protein synthesis; cognate immunity proteins protect kin cells and modulate community structure.

To understand the dynamics of T6SS-mediated antagonism between attacker and victim cells, we analyzed the T6SS-dependent killing effects of a DK1622 derivative on natural isolates to identify factors important for these hostile interactions. Using transposon-insertion mutagenesis,
we also attempted to identify mutations that might confer some degree of resistance to T6SS-mediated killing. Understanding the genetic basis of such resistance

could provide important insights into the mechanisms governing interbacterial competition and the complex interactions that occur within microbial “war zones.”

Mechanism of the MglA GTPase activity regulators, RomX and RomY

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Abstract:

Cell polarity specification and reversals are distinctive features of motility of the soil bacterium *Myxococcus xanthus*. The bacterial small Ras-like GTPase, MglA, serves as a key player orchestrating these polarity oscillations. RomR, a response regulator, along with its partner RomX, has been identified to function as a guanine nucleotide exchange factor (GEF) for MglA, crucial for its polar recruitment. Moreover, MglA uses RomY as a co-GAP, hypothesized to bind near the nucleotide binding pocket of MglA/$(MglB)_2$/RomY complex. Investigation of the mechanism of action of the GEF-ilke and co-GAP regulator of MglA through biophysical and structural characterization helped us identify putative active site residues for both the interacting partners, a key insight into the regulation of a prokaryotic GTPase and their regulators, a prokaryotic GAP and co-GAP.

Myxobacteria as producers of off-flavour compounds in fish farms with water recirculation

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Abstract:

Aquaculture production is increasing globally, but microorganisms that produce off-flavours, such as the earthy-smelling compound geosmin, may taint fish and reduce consumers' interest in farmed fish. Among potential off-flavour producers, myxobacteria have recently been detected in indoor recirculating aquaculture systems (RAS). In this study, we successfully isolated two geosmin-producing myxobacteria from RAS: *Myxococcus virescens* AT3 and *Corallococcus exiguus* AT4. Cell-specific geosmin production varied with nutrient concentration across media, but was highest in minimal medium and in water from RAS. Cultivation in RAS water also stimulated the production of other volatile organic compounds (VOCs), e.g., a ketone with a "forest" odour, an alcohol with "medicinal" and "chemical" odours, and a sesquiterpenoid described as "musty," "earthy," and "flowery". Myxobacteria have previously been proposed as keystone bacteria in the environment due to their predatory lifestyle. In predation assays with bacteria isolated from RAS, M. virescens AT3 and C. exiguus AT4 could successfully feed on 15 of 16 tested strains, suggesting a substantial influence on the microbiology of RAS microbiomes. The combination of predatory behaviour and potent production of geosmin and other VOCs underscores the ecological and sensory impact of these bacteria in RAS.

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Why do some Myxobacteria have two light recognition systems?

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Abstract:

Myxobacteria are soil-dwelling social bacteria that move by gliding motility in groups and form multicellular fruiting bodies when nutrients become scarce. In addition, the various different genera and species show distinct behavioral and pigment responses to light. In all known species of myxobacteria, , blue light activates the *carQRS* sigma-factor pathway to induce the production of carotenoid pigments that dissipate oxidative stress. What is interesting is that while this pathway is in all known species, a second light-activated transcriptional system has recently been identified. Recent genomic work has revealed that many species encode a red/far-red-sensing phytochrome, *bph.* In the two closely related *Myxococcus* species, *xanthus and macrosporus* only *M. macrosporus* contai ns this novel bacterial phytochrome. The question remains, why do some species contain two independent light-dependent regulatory systems? However, how defined light–dark cycles and wavelengths shape carotenoid production, growth dynamics, and potential rhythmic colony development in these two species remains poorly understood.

We hypothesize that varying light environments (wavelength and light–dark cycling) will differentially modulate carotenoid production and colony patterning

in *M. xanthus* versus *M. macrosporus*, with phytochromes in *M. macrosporus* generating unique, species-specific light responses beyond the CarQRS pathway. To test this, we are comparing growth and ring-like developmental patterns of both species under

Genetic Engineering of *Sorangium cellulosum*: A Platform for Decoding Myxobacterial Secondary Metabolism

Authors: Xiaotong Zhong, Shan Liu, Bingda Ma, Meiting Bu, Kaining Gao, Dayong Jiang, Yingshuo Hou, Luoyi Wang

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Abstract:

Sorangium cellulosum is a cellulolytic myxobacterium renowned for producing a vast array of complex natural products with diverse chemical scaffolds and biological activities, including the anticancer drug epothilones. Despite its remarkable biosynthetic potential, progress in understanding and harnessing these metabolites has been hampered by the lack of effective genetic manipulation tools. To address this challenge, we have developed a versatile genetic engineering method applicable across multiple *Sorangium cellulosum* strains, effectively overcoming their genetic intractability. This facilitated delineation of the biosynthetic pathways to several biologically important natural products including ambruticin, jerangolid and carolacton. Our findings reveal a series of biosynthetic steps characterised by remarkable enzymology, offering significant insights into the molecular machinery governing myxobacterial natural product biosynthesis. Our work establishes a robust platform for further pathway engineering of *Sorangium* strains, opening new avenues for expanding the chemical and biological diversity accessible from myxobacteria.

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Deep Learning Framework for Quantifying Self-Organization in *Myxococcus xanthus*

Authors: Jiangguo Zhang[a], Eduardo A. Caro[b], Peiying Chen[b], Trosporsha Tasnim Khan[b], Patrick A. Murphy[a], Lawrence J. Shimkets[f], Ankit B. Patel[c,d], Roy D. Welch[b], and Oleg A. Igoshin[a,e],

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Abstract:

Under starvation, *Myxococcus xanthus* bacteria initiate a multicellular developmental program in which cells move to form fruiting bodies and differentiate into distinct cell types. Many genes affecting this process have been identified, and it is assumed that perturbing genes within the same pathway induces similar changes in the phenotype, although these changes may be subtle or obscured by pleiotropy. However, these pathways cannot be systematically mapped because there are no reliable methods for quantifying phenotype similarity. Here, we applied deep learning techniques to quantify the phenotype patterns and self-organization dynamics of 292 genetically distinct strains. We integrated ResNet and StyleGAN2 into a Variational Autoencoder and trained it together with a Siamese network that learns phenotypic similarity. This end-to-end system encoded high-resolution microscopy images into 13-dimensional feature vectors, effectively capturing variation in aggregation patterns across time and strains. Human evaluation confirmed that our model's reconstructions were visually indistinguishable from real images and closely aligned with input phenotypes. Importantly, the feature space is interpretable: individual dimensions correlate with biological features such as aggregate number and size, and extrapolation along these dimensions produces predictable morphological changes. Remarkably, our model

revealed that developmental phenotypes and ultimate aggregation fate are predictable from the earliest images before visible aggregation begins. This predictability held across both genetic and environmental sources of variation, suggesting that subtle, early-stage phenotypic signatures carry critical information about developmental trajectories. These results demonstrate how machine learning can reveal hidden aspects of complex multicellular dynamics and provide methods for phenotypic analysis without manual annotation.

Engineered myxobacterial vesicles as biogenic strategy for combating bacterial infections

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Department Biology, Chair of Pharmaceutical Biology, Erlangen, Germany

Abstract:

Bacterial resistance to clinically used antibiotics has increased significantly in recent decades, making it one of the three major threats to humanity, according to the WHO. A promising way to address this challenge is the discovery of new natural products – such as those produced by myxobacteria – and in combination with their efficient delivery to the site of infection. Our research group is studying myxobacterial vesicles, which belong to the large group of cell-derived extracellular vesicles [1]. These vesicles are naturally produced by all cells and they are involved in cell-cell communication. The have sparked substantial interest in the area of drug delivery because of their natural origin, but we need reproducible methods for their characterization and drug loading, and a clear comprehension of their fate *in vivo* [2]. We have studied myxobacterial vesicles from *Cystobacter velatus* and *Cystobacter ferrugineus* and showed that they are naturally loaded with antimicrobial compounds, such as cystobactamids, while being non-toxic in cell assays [3]. To advance their translational development, we created novel biohybrid carriers by fusing drug loaded liposomes with vesicles as tunable platforms for drug delivery. We showed that the hybrids could eradicate bacterial biofilms and do not significantly alter the gut microbiome in a mouse model [4]. Most recently, we developed a surface engineering strategy based on a trivalent linker that allows modification of myxobacterial vesicles with targeting ligands. Such coupling to vancomycin significantly enhanced the antimicrobial effect of the vesicles. Using accessible techniques, we can thus engineer vesicles for better infection treatment.

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Developing stable plasmids for use in Myxococcota

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Abstract:

Synthetic biology approaches such as heterologous expression of biosynthetic gene clusters (BGCs) have leveraged growing capabilities to assume molecular details of natural products produced by sequenced bacteria from genetic data. Methodologies for heterologous expression of BGCs from *Streptomyces* spp. have benefited from incredible progress and enabled continued discovery of biologically active metabolites from Gram-positive actinobacteria. However, comparatively fewer synthetic biology techniques are available to other groups of bacteria known to be reliable sources of therapeutic leads. Myxobacteria are considered the Gram-negative reciprocal to actinobacteria when describing gifted producers of natural products and metabolites discovered from myxobacteria occupy chemical space unique from actinobacterial metabolites. Leveraging our collection of sequence data from myxobacterial isolates and included natural plasmids, we sought to synthesize plasmids suitable for gene expression in myxobacterial hosts. Utilizing replication and partitioning features from natural plasmids, we developed a series of plasmids and assessed their replication and stability in *Myxococcus xanthus*. Two of the developed plasmids can be efficiently transformed into *M. xanthus*, isolated using standard plasmid preparation kits, and transformed into *E. coli* for amplification to yield sufficient quantities for sequencing. No mutations, deletions, or insertions were present in sequenced plasmids suggesting stability in *M. xanthus*. Repeating this methodology with the only myxobacterial plasmid amenable to BGC heterologous expression in *M. xanthus* (pMF1) (1,2), we did not observe an assembly of pMF1 after multiple attempts. Provided access to these new plasmids, we are currently assessing their viability in a variety of myxobacterial hosts.

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Thursday 4th June 2026

Identification of novel bactofilin-interacting proteins

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Abstract:

Bactofilins are a recently identified broadly conserved class of cytoskeletal proteins found in bacteria, archaea, and selected eukaryotic oomycetes[1]. Although widely distributed, their roles in cell morphology, motility, chromosome segregation, and cellular polarity have thus far been characterized only in bacteria and archaea[2,3]. *Myxococcus xanthus* encodes four bactofilins: BacM (MXAN_7475), located within the *parA-parB* cell division operon, and BacN, BacO, and BacP (MXAN_4637-MXAN_4635), which are sequentially encoded in a separate operon[4]. Like all other bactofilins, these four proteins share a conserved architecture[1], comprising a central triangular b-helical bactofilin domain (DUF583) flanked by short N- and C-terminal regions. These terminal regions perform distinct functions: the widely conserved N-terminus mediates attachment to the cytoplasmic membrane, whereas the frequently proline-rich C-terminus is implicated in interactions with partner proteins, including endopeptidases[2] that function as output modules in bactofilin-mediated cellular processes. Among these processes, cell shape determination is currently the best characterized and

has been investigated in numerous rod-shaped, helical, and stalk-forming bacteria, including *M. xanthus, Helicobacter pylori, Proteus mirabilis, Caulobacter crescentus,* and *Asticcacaulis biprosthecum*. In most of these species, morphological phenotypes result from bactofilin-associated endopeptidases that remodel the peptidoglycan cell wall. However, in *M. xanthus*, no such enzyme has been identified as an interaction partner for the morphogenic bactofilin BacM[2,4]. Here we employed pulldown assays, bacterial two-hybrid, and split-luciferase BitLucOpt assays to identify novel BacM-interacting proteins. Combined with genetic analysis, quantitative Western blotting, and light microscopy, these approaches allowed us to characterize the functional significance of one of these newly identified interactions.

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Aggregative chimeric multicellularity in the absence of lethal kin discrimination

Authors: Michael L. Weltzer, Pravas C. Roy, Jack Govaerts**,** and Daniel Wall

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Abstract:

Myxobacteria transition to multicellularity by a cooperative aggregative strategy. This contrasts with plant and animal development, which proceeds through clonal expansion from a single progenitor cell, thus avoiding genetic conflicts and social cheating between divergent genotypes**.** *Myxococcus xanthus* and *Dictyostelium discoideum* are model organisms that share a common aggregative multicellular lifestyle where they form spore-filled fruiting bodies in response to starvation but differ in their mechanisms to reach clonality. *M. xanthus* uses lethal kin discrimination to eliminate nonclonal *M. xanthus* cells, while *D. discoideum* uses nonlethal mechanisms to segregate nonkin cells from their spore filled fruiting body head. Here, we examined aggregative multicellularity in divergent *M. xanthus* strains when their lethal kin discrimination mechanism, type VI secretion system (T6SS), were genetically inactivated. We found that strain mixtures of T6SS knockout mutants do not antagonize and form chimeric multicellular swarms and fruiting bodies with viable spores from both strains. Nevertheless, these T6SS mutant strains segregate, thus revealing that nonlethal kin discrimination mechanisms also exist in this species. Thus, lethal kin discrimination ensures homogeneous populations and monoclonal fruiting body development, while nonlethal mechanisms play a more subtle role**.**

Testing for a tradeoff between sporulation versus fitness under early nutrient exposure after starvation

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Abstract:

Genetically identical individuals in a microbial population can be phenotypically distinct. Such heterogeneity can help a population cope with environmental fluctuations and allows for the division of labor in clonal groups, such as in the multicellular-development program of the bacterium *Myxococcus xanthus*. Upon depletion of growth resources, *M. xanthus* initiates its development program in which many cells contribute to fruiting-body formation while only a minority become stress-resistant spores. Non-spore cells are thought to mostly die, whereas spores can survive extended starvation to germinate when conditions become favorable. An additional cell type present during development – peripheral rods – neither forms spores nor enters fruiting bodies but remains metabolically active and motile. This talk will present an evolution experiment we designed to test whether genotypes that commit fewer cells to the spore fate would have an evolutionary advantage over genotypes that convert more cells into spores when conditions allowing growth are encountered sooner rather than later after initiation of development.

Endemic phage spread drives adaptive diversification in soil myxobacterial kin groups

Authors: Sébastien Wielgoss, Marijn Ceelen, Alena Camenzind, Heike Keller, Gregory J. Velicer

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Abstract:

Interactions between bacteria and mobile genetic elements in spatially heterogeneous environments, such as soils, are highly localized; however, the ecological and evolutionary consequences of these interactions in nature remain poorly understood. Here, we demonstrate that an endemic bacteriophage promoted local adaptive diversification among kin groups of the cooperative soil bacterium *Myxococcus xanthus*. By analyzing genomes from densely sampled fruiting bodies, we show that a universally conserved CRISPR-Cas system functions as an adaptive immune hub in natural *M. xanthus* populations. Remarkably, one quarter of all informative spacers in our dataset mapped to a novel ~102kb tailed dsDNA phage infecting multiple isolates across several fruiting bodies. The latter hosts lacked newly acquired spacers, whereas nearby uninfected kin groups in the immediate neighborhood frequently carried novel spacers targeting the phage, consistent with highly localized and very recent phage transmission. Based on phylogenetic analysis, we propose naming the new *Myxococcus* phage Mx10. Finally, we conducted infection experiments with a focal kin group from nature that harbored multiple independently acquired spacers against Mx10, as well as co-occurring lipopolysaccharide (LPS) *O*-antigen mutants. Strikingly, independent LPS mutants displayed strong phage resistance at a substantial developmental cost, whereas CRISPR-mediated protection against phage infection was limited despite generally strong interference with plasmid-borne protospacers. This suggests the presence of phage immune evasion mechanisms. Our study moves bioinformatic inference to experimentally resolve phage-driven eco-

evolutionary dynamics *in situ* and reveals how localized viral spread can shape cooperation, immunity, and diversification in myxobacterial soil communitie

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