2026 Helmholtz – OCPC – Programme

for the involvement of postdocs in bilateral collaboration projects

PART A

Title of the project:
Mechanistic Dissection of Respiratory Bacteriome–Virome Interactions in Asthma

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Description of the project:

Asthma is a complex airway disease in which genetic predisposition interacts with environmental exposures and microbial stimuli, including viruses and bacteria. Dysbiosis of the airway microbiome, particularly an overrepresentation of Proteobacteria, has been linked to asthma development and exacerbations. Conversely, exposure to farm environments reduces asthma risk, partly by limiting colonization of the airway with bacteria such as *Moraxella*. The mechanisms underlying these protective effects, however, remain poorly understood.

Emerging evidence highlights phage communities (the phageome) as fundamental modulators of microbial ecosystems. Phages shape bacterial populations not only through lysis and horizontal gene transfer but also via auxiliary metabolic genes (AMGs) that may influence host immune responses. Bacterial metabolites and virome-encoded metabolites, such as short-chain fatty acids, further modulate immunity, suggesting that complex phage–bacteria–host interactions contribute to asthma pathogenesis and protection.

We hypothesize that phages contribute to airway dysbiosis and differentially modulate asthma risk in farm versus non-farm environments. The overarching goal of this project is to systematically dissect **cross-talk between the airway phageome and bacteriome** and its impact on asthma susceptibility.

We will pursue three specific aims:

1. **Characterize the upper airway bacteriome and phageome in asthma-protective environments** to identify microbial and viral signatures associated with reduced asthma risk.
2. **Define the role of phage–host interactions** in shaping microbial communities in the upper airway of asthma-protective environments.
3. **Isolate and cultivate representative bacteria and phages**, define synthetic microbial consortia and elucidate molecular mechanisms by which phages regulate bacterial communities and contribute to asthma prevention using in various in vitro systems.

This project integrates **mechanistic and systems-level approaches** to uncover how phage–microbiome interactions influence immune regulation and asthma susceptibility. By combining cultivation-based studies with **multi-omics analyses**—including microbiome, phageome, and metabolomics profiling—we aim to identify functional microbial networks relevant to disease prevention. Furthermore, we will leverage **recent advances in host-targeted, single-phage technologies**, enabling precise manipulation of bacterial populations and controlled study of phage–host interactions.

Validation of our hypothesis could directly inform the development of **precision microbiome-based interventions**. Specifically, designed phageomes could selectively target asthma-associated dysbiotic microbiota, offering **novel, highly specific therapeutic strategies** that minimize off-target effects and complement existing treatments. This approach has the potential to transform preventive and therapeutic strategies for asthma, particularly in high-risk populations.

In summary, this project will provide a mechanistic framework linking phage–bacteria interactions to asthma risk and protection, advance our understanding of airway microbial ecology, and lay the foundation for **innovative, clinically relevant phage-based therapies** aimed at preventing or mitigating asthma.

Description of existing or sought Chinese collaboration partner institute (max. half page)**:**

The proposed collaboration seeks to engage a leading Chinese university or research institute with a strong and well-established program in science and technology, or biomedical research. Suitable partner institutions are expected to demonstrate recognized expertise and a strong research track record in areas relevant to microbiome and virome research, and host–microbe interactions.

In particular, institutions with demonstrated strengths in **microbiome, virome**, **molecular microbiology**, **biotechnology**, and **bioinformatics and data science** are highly desirable. Expertise in **culturomics**, including advanced microbial cultivation strategies will be of significant value to the proposed research. Capabilities in microbiome and virome analysis, phage–host interaction studies, and functional characterization of microbial and viral communities using both culture-dependent and culture-independent approaches are especially advantageous.

In addition, access to high-throughput sequencing platforms, advanced computational infrastructure, and interdisciplinary research teams experienced in multi-omics data integration and mechanistic studies will strongly support the successful implementation of the project. Collaboration with such an institution will enable complementary expertise, facilitate bidirectional knowledge exchange, and promote joint innovation, thereby enhancing the scientific quality, translational relevance, and international impact of the proposed research.

Required qualification of the postdoc:

The postdoctoral researcher will contribute to analyzing airway bacteriome and virome data, isolating and cultivating representative bacteria and bacteriophages from asthma samples, and performing mechanistic studies of microbe–microbe, microbe-phages, and microbe–host interactions relevant to asthma development and prevention.

Qualifications:

- **Education:** PhD in **Microbiology, Virology, Bioinformatics**, or a closely related discipline.
- **Experience:**
  - Strong background in **microbial metagenomics or viral metagenomics** and associated bioinformatics analyses **OR**
  - Extensive experience in **microbial cultivation, molecular biology, and virology**, including bacterial and phage isolation and characterization.
- **Additional Skills:** Proficiency with **flow cytometry** and other relevant laboratory techniques.
- **Language:** Fluent in **spoken and written English**, which will be the primary language of communication within an **international research environment**

Candidates with interdisciplinary expertise bridging **computational analysis and experimental microbiology/virology** are particularly encouraged to apply.

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- Wang Y, et al. Distinct prophage gene profiles of *Staphylococcus aureus* strains from atopic dermatitis patients and healthy individuals. *Microbiol Spectr.* 2024;12:e00915-24.
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