



Call for 2022 Chinese Postdoctoral Applicants under the Helmholtz – OCPC Program

Title of the project:

Microbiome and Virome in human health and phage therapy

Helmholtz Centre and institute:

Helmholtz Centre Munich, Institute of Virology, Group of 'viruses in Nature and Health'

Project leader:

Professor Dr. Li Deng

Contact Information of Project Supervisor: (Email, telephone)

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Web-address:

<https://www.helmholtz-munich.de/en/viro/research-groups/emmy-noether-research-group-virus-in-nature-and-health>

<https://www.virologie.med.tum.de/en/research-groups-tum/li-deng/>

Department: (at the involved Helmholtz centre or Institute)

Molecular Targets and Therapeutics Center

Programme Coordinator (Email, telephone)

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Description of the project (max. 1 page):

As German Research Center for Environmental Health, Helmholtz Centre Munich pursues the goal of developing personalized medical approaches for the prevention and therapy of major common diseases. On the base of results obtained in molecular studies, the institute of Virology develops novel diagnostic and therapeutic concepts against viral infections, and uses viruses as therapeutic tools. Focusing on bacterial viruses (phages), the group 'Viruses in Nature and Human Health' uses an integrated approach to investigate microbes-viruses interactions by combining microcosm experiments employing model microbes and viruses, and culture-independent, high-throughput metagenomics.

The role of the human microbiome for maintenance of health resp. development of infectious, but also noninfectious chronic diseases is increasingly recognized. However, an important group of the spectrum – phages – is largely overlooked in the human microbiome. Although during the last years diverse phenomena critical to the biology of microbes have been described to be driven by phages in Nature, and they are now considered as ubiquitous players that impact microbial



communities through mortality and horizontal gene transfer to modulate microbial metabolism. The view that phages are “only” parasites is no longer valid but phages rather are able to transfer and store genetic information of their hosts and to some extent, regulate the metabolism of their host.

In this project, we seek to understand the overall impact of environmental factor driving the structure of phages colonizing the various human organs, especially lung surface, and to investigate their impacts on human health and diseases development. Various cutting-edge omics tools (e.g. viral-tagged metagenomics, transcriptomics) will be applied. The successful applicant will be involved in the development and the use of new methods and tools for handling, analyzing and interpreting microbial and viral metagenomic sequencing data, as well as further development and/or application of multiomics intergradation.

Our Offer:

- Working in an innovative, well- equipped and scientifically stimulating surrounding.
- Working as part of a young and motivated team.
- Further training opportunities.
- The possibility to work with first-hand state-of-the-art datasets.

Related publication:

- Mirzaei MK, Xue J, Costa R, Ru J, Schulz S, Taranu SE & Deng L, Challenges of studying the human virome- relevant emerging technologies. (2020) *Trends in Microbiology*
- Dzungova M, Low SJ, Daly JN, Deng L, RinkeC, Hugenholtz P. Defining the human gut host-phage network through single-cell viral tagging. (2019) *Nature Microbiology*
- Elbehery AHA, Feichtmayer J, Singh D, Griebler C & Deng L. The Human Virome Protein Cluster Database (HVPC): A Human Viral Metagenomic Database for Diversity and Function Annotation. (2018). *Frontiers in Microbiology*
- Deng L, Ignacio-Espinoza JS, Gregory A, Poulos PT, Weitz JS, Hugenholtz P, Sullivan MBViral tagging reveals discrete populations in *Synechococcus* viral genome sequence space,. (2014) *Nature*.

Description of existing or expected Chinese cooperation institution (not necessary):

Chinese Universities or institutions with strong programme and expertise in either the general science and technology, or medical oriented are welcome to apply. The expertise in the following list are beneficial: (1) bioinformatics, (2) molecular biology or virology, (3) biotechnology especially synthetic biology.

Required qualification of the post-doc:

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- Recent PhD in Computational Biology, Bioinformatics, genomics, Microbiology or a related field.
 - Experience in any of the following areas: phage biology, viral genomics, metagenomics, microbial ecology.
 - Strong experience in scripting tools (e.g. Perl or Python) in order to mine data files.
 - Good experience with processing and analysis of genomic/metagenomic data using compute clusters / high-performance computing.



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- Good experience with using standard bioinformatics tools and databases programming (e.g. SQL).
 - Good experience with using analytic tools (e.g. R or Matlab).
 - Fluency in English both spoken and written.
 - Knowledge Biology/Biochemistry and understanding of key and complex biological concepts (genes, pathways, microbial phylogeny and microbial ecology.).
 - Ability to independently carry out creative research with tenacity and of the highest quality standards.
 - At least one first author paper in an international peer reviewed journal.