Research Interest

Identification of Virus-Host interactions

Our research is devoted to identify and characterize novel viruses-host interactions for pathogenic viruses using comprehensive and unbiased systems-based approaches. Virus systems currently established in the lab are HIV, HBV and Ebola trVLPs. Our efforts are directed towards gaining a better understanding of the mechanism of viral sensing and restriction as a response of the innate immune system to viral infections. Innate immunity is the first line of defense against foreign pathogen invasion. Viruses must evade these host protective mechanisms to establish productive infections, and thus, targeting these host-pathogen interactions is an attractive strategy for the development of novel antiviral therapies.

Furthermore, our lab has expanded to include data scientists, that focus on next-generation sequencing analysis and machine learning approaches. An additional subgroup addresses application of machine learning and text mining approaches to support regulators and assessors at PEI.

Our approach is

i) to understand the virus-host interplay, in particular innate sensing
ii) to identify and characterize cellular restrictions
iii) to establish novel platform technologies in science and regulation

1) Understanding the virus-host interplay and innate sensing

In ongoing projects funded by the Priority Program of the DFG SPP1923, we are interested in the innate sensing pathways directed towards HIV-1. Recently, our collaborators identified the proximal sensor for cGAS recognition specifically detecting HIV-1 in primary human dendritic cells, PQBP1 (Cell, 2015). This seminal work provided evidence that the interplay of regulatory and co-sensing factors within the pattern recognition receptor complex (PRR) is multifaceted, and that the PRR complex composition and PAMP recognition may vary for different viruses. In the ongoing projects, we aim to investigate in more detail the regulation of this novel sensing pathway (Yoh et al., BioRxiv 2022). Moreover, we have access to rare patients deficient in PQBP1. We generated an iPSC line from a patient mutated in the polar amino acid-rich domain of PQBP1 (Stem Cell Research 2019). The established iPSC model will serve as a tool to investigate the role of PQBP1 in both pathomechanistic and cellular processes.

2) Identify and characterize cellular restrictions

A key to understanding inefficient innate immunity leading to immune escape by HIV-1 and the potential role of SAMHD1 in tumor escape mechanisms will be the identification and validation of PTMs and regulators that control the activity of SAMHD1 (funding by SFB1292). In the ongoing project within the SFB1292, we are interested in understanding mutations of SAMHD1, their impact on cellular functions and on tumor development and immune escape (Schüssler et al., BioRxiv 2022; Schott et al., 2021; Schott et al., 2018)

3) Establish novel platform technologies

- CRISPR/Cas9 KO and KI screening approaches (Schüssler et al., BioRxiv 2022)
- iPSC technology (Fuchs et al., 2020, 2019)

- NGS/Metagenomics pipeline

  Newly funded BMG-project on AI-assisted virus surveillance using next-generation sequencing, metagenomics and AI.

- Artificial intelligence pipeline to support regulators

  Newly funded BMG-project on evaluation and validation of AI-based algorithms in regulation.
  Newly funded BMG-project on AI use for improved and standardized pre- and post-approval assessment.