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# Poster abstract submission

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**Presenting author** Simona Huwiler

**Presenting author's email** simona.huwiler@uzh.ch

**Further authors (if any)**
Ting F. Lai, Denis Jankov, Jonas Grossmann, Bernd Roschitzki

**Affiliation(s)**
Department of Plant and Microbial Biology, University of Zurich

**Country** Switzerland

**Type of organization** Academic / research institution

**Poster title**
Quantitative proteome of bacterial periplasmic predation by Bdellovibrio bacteriovorus reveals a prey-lytic protease

**Poster abstract**
Gram-negative bacterium Bdellovibrio bacteriovorus raises hope as an potential alternative to antibiotics and is present in multiple environments. It serves as a model organism for predatory bacteria that invade Gram-negative bacteria as prey and replicate in their periplasm. The prey range includes many Gram-negative bacterial pathogens on top of the WHO priority pathogens list. Many processes in the predatory life cycle of B. bacteriovorus are enigmatic, especially in the last exit phase, where predator progeny exit the largely depleted prey cell crossing the prey's cell wall and outer membrane.

This project aims to learn from predatory bacteria through state-of-the-art quantitative proteomics, covering the entire predatory life cycle with a focus on the underexplored last exit phase. We generated the first quantitative proteome covering the complete predatory life cycle of B. bacteriovorus HD100 killing Escherichia coli K-12, quantifying 2195 predator proteins, which is about two-thirds of all B. bacteriovorus proteins. While describing systematically the most prominently regulated B. bacteriovorus proteins during the different predatory life cycle phases, we identified three highly abundant proteases (Bd2269, Bd2321 and Bd2692). We showed that predator protease Bd2269 causes E. coli cell lysis when expressed heterologous from within. Furthermore, we knocked out bd2269 in B. bacteriovorus and showed that the clean-deletion mutant strain exhibits a delayed predator progeny release from prey cells, confirming a critical involvement in the prey exit process.

This holistic quantitative predator proteome, allows an unprecedented detailed view on the predatory life cycle of a periplasmic predatory model organism. The generated dataset will inform current and future hypotheses investigating the complex predator-prey interaction interactions and help identify factors involved on the molecular level. This will contribute to advance the search for novel antimicrobial enzymes.

**Research topic** Microbiology