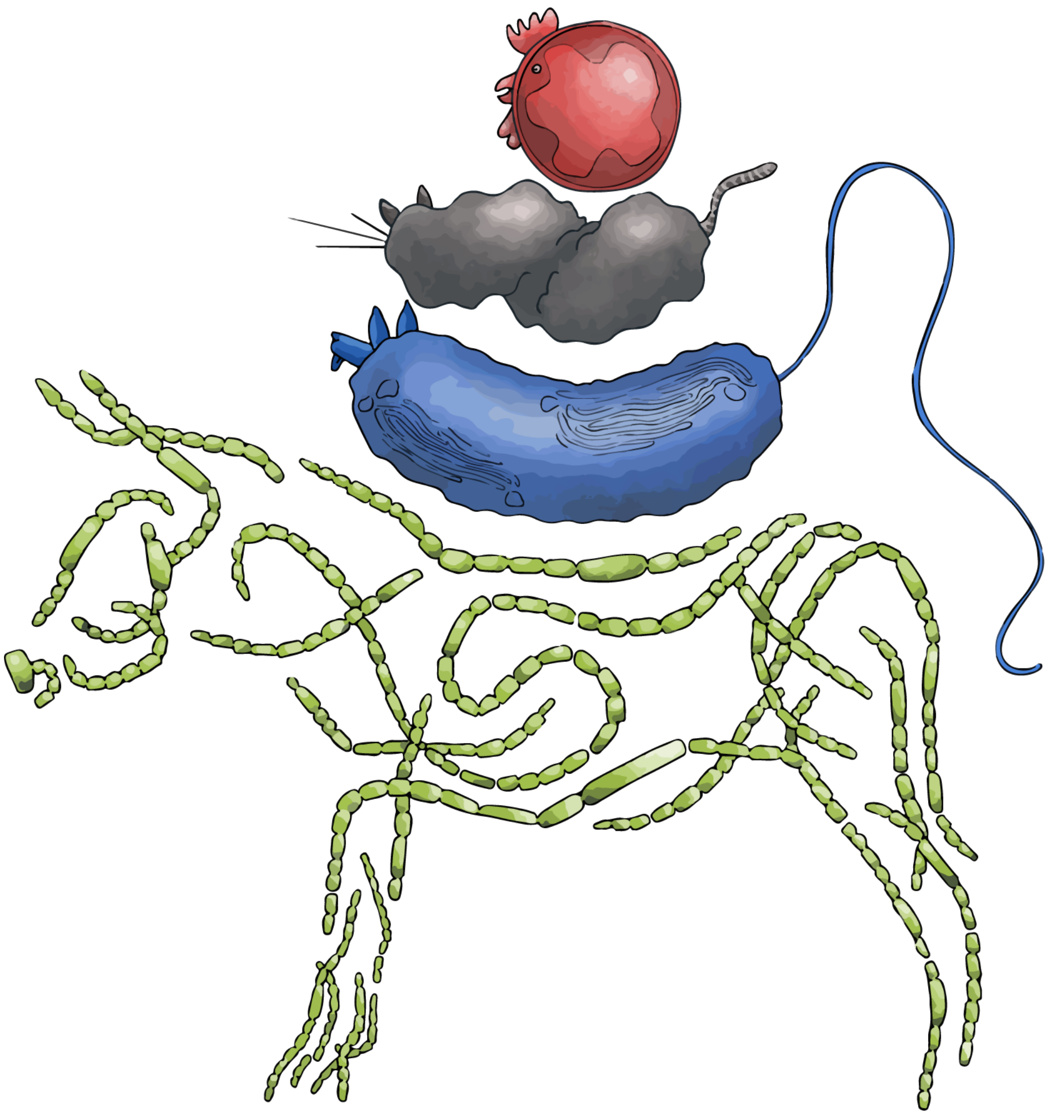
ICoN9

JUNE 22–26 2025
BREMEN, GERMANY



ABSTRACT BOOKLET

A high-throughput screening platform for the discovery of biological nitrification inhibitors in plant germplasm

Alexandros E. Kanellopoulos[1], Andrea Malits[2], Arindam Ghatak[3,4], Cristina López-Hidalgo[3], Hugo Ribeiro[1], Yuhang Meng[3], Florian Schindler[3], Shuang Zhang[3], Jiahang Li[3], Steffen Waldherr[3], Melina Kerou[2], Logan Hodgskiss[2], Maximilian Dreer[2], Reyazul Rouf Mir[5], Sandeep Sharma[6], Gert Bachmann[3], Palak Chaturvedi[3], Wolfram Weckwerth[3,4], Dimitrios G. Karpouzas[1], Christa Schleper[2], Evangelia S. Papadopoulou[7]

[1]Laboratory of Plant and Environmental Biotechnology, Department of Biochemistry and Biotechnology, University of Thessaly, Larissa, Greece

[2]Archaea Biology and Ecogenomics Unit, Department of Functional and Evolutionary Ecology, Faculty of Life Sciences, University of Vienna, Vienna, Austria

[3]Molecular Systems Biology Lab (MOSYS), Department of Functional and Evolutionary Ecology, Faculty of Life Sciences, University of Vienna, Vienna, Austria

[4]Vienna Metabolomics Center (VIME), University of Vienna, Vienna, Austria

[5]Division of Genetics & Plant Breeding, Faculty of Agriculture (FoA), SKUAST-Kashmir, Wadura Campus, Sopore-193201, Kashmir, J&K, India

[6]Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi 221005, India

[7]Laboratory of Environmental Microbiology and Virology, Department of Environmental Sciences, University of Thessaly, Larissa, Greece

Excessive nitrogen fertilization disrupts the global nitrogen cycle, causing nitrate leaching and nitrous oxide emissions. Biological nitrification inhibitors (BNIs) offer an environmentally friendly alternative to synthetic nitrification inhibitors (SNIs) for controlling soil nitrification and reducing nitrogen losses, yet their discovery remains limited, particularly across large plant germplasm collections. Here, we present a novel high-throughput screening platform for BNI discovery, utilizing a diverse set of soil-relevant ammonia-oxidizing bacteria (AOB) and archaea (AOA) strains, including *Nitrosospira multiformis*, *Nitrosomonas ureae*, *Nitrosomonas communis*, *Nitrososphaera viennensis*, and *Ca.* Nitrosocosmicus franklandianus. These ecophysiologically and phylogenetically diverse strains were specifically selected to closely represent natural nitrification processes, providing a realistic environment for evaluating BNI activity in plant root exudates. We applied this system to screen root exudates from 44 diverse wheat genotypes from India and Austria, revealing significant variation in BNI activity. Distinct inhibition profiles among the genotypes highlighted the capacity of the platform for rapid and sensitive BNI assessment. An advanced machine-learning approach further identified key metabolites associated with strong BNI activity, offering insights into the molecular drivers of nitrification inhibition. Validated with established SNIs and BNIs, this high-throughput platform provides a critical tool for screening large germplasm collections, accelerating the identification of BNI-producing plant genotypes. Its integration into the design and development of modern breeding programs holds promise for enhancing nitrogen use efficiency and mitigating the environmental impact of nitrogen fertilizers, advancing sustainable nitrogen management in agriculture.