

EXPLOITING THE UNEXPLOITED: FUNCTIONAL METAGENOMICS OF LICHEN AND MOSS ASSOCIATED MICROBIOTA

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» Identification of antimicrobial volatile organic compounds
» Sourcing novel antimicrobial metabolites
» Elucidate the antibiotic resistome

BACKGROUND

The lichen *Lobaria pulmonaria* as well as the moss *Sphagnum magellanicum* are populated by bacteria of **GREAT TAXONOMIC DIVERSITY** (Fig. 1 A, B). The respective microbiomes each comprise a rich secondary metabolism. To a high share **ANTIFUNGAL AND ANTIBACTERIAL PROPERTIES** were attributed.^{1,2}

By functional metagenomics these previously untapped sources can be exploited more unmitigatedly, meaning getting a hold of the not cultivatable bacteria.

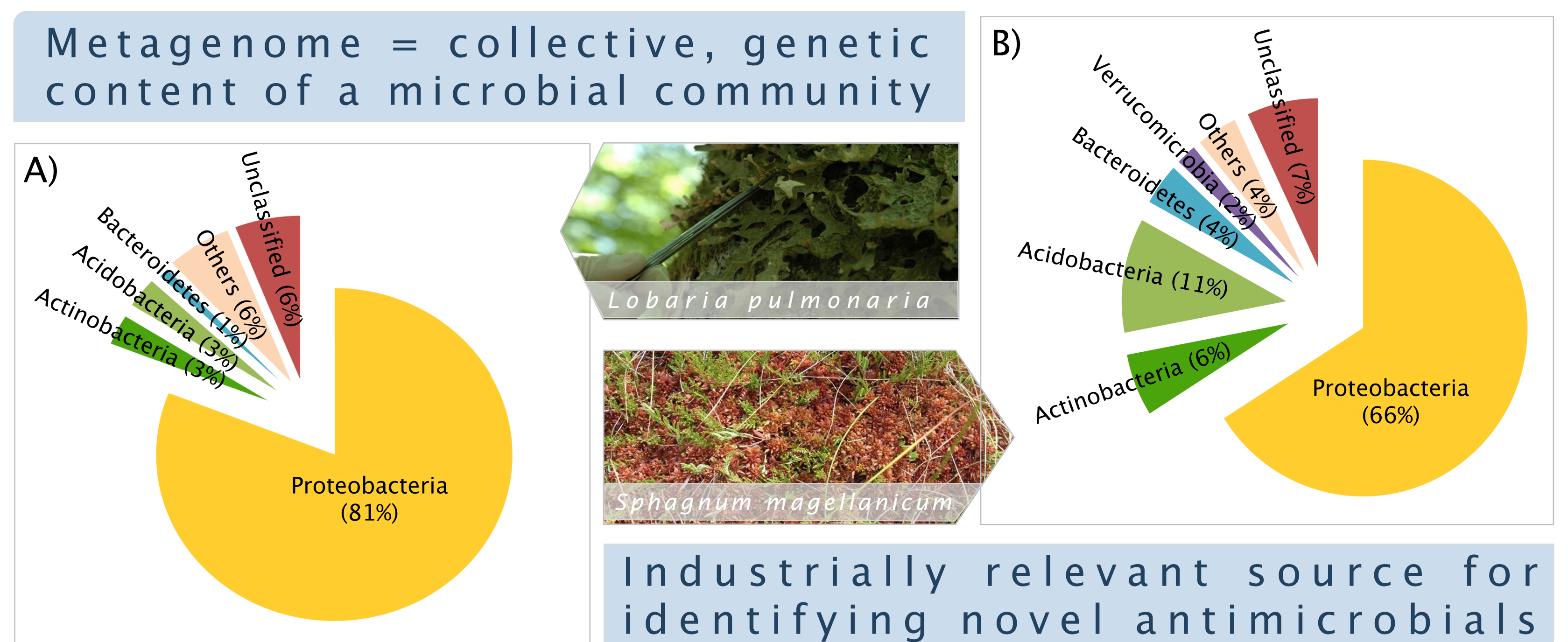
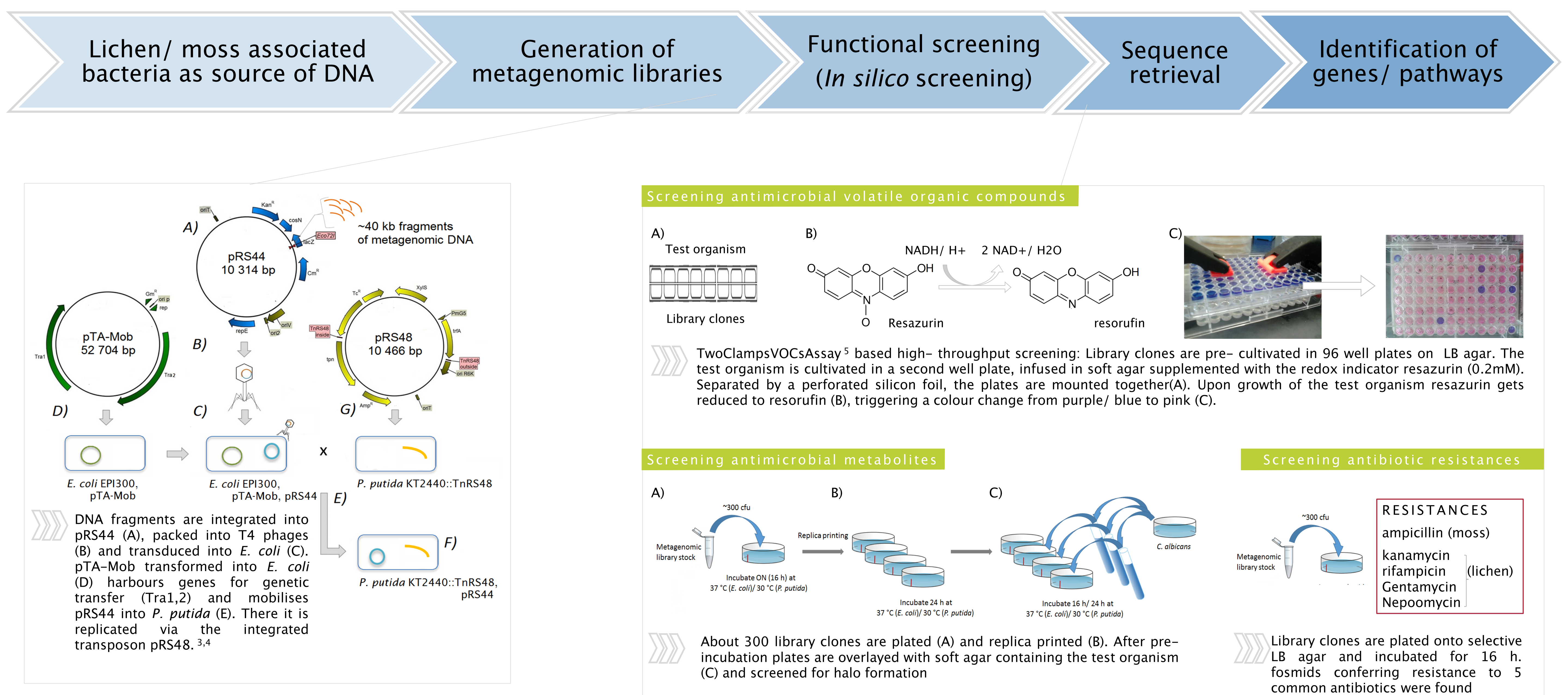


Figure 1: Taxonomic diversity. Bacterial community composition for the lichen *Lobaria pulmonaria* (A) and the moss *Sphagnum magellanicum* (B) as revealed by 16S rRNA analysis.^{1,2} Evaluation of the respective microbiome proved both to be industrially relevant.

Methodology: Bioprospecting lichen and moss associated bacteria as novel bio-resources for biotechnology and medicine



ECONOMIC & SCIENTIFIC BENEFIT

Antimicrobial volatile organic compounds can be applied in **BIOFUMIGATION** to develop **CROP WELFARE**. They, further, represent an effective remedy to **CONTROL MICROBIAL HAZARDS** in clinical environments and clean rooms. With the increasing emergence and spread of (mult-) resistances novel antimicrobials isolated from microorganisms of remote locations are promising, potential **NOVEL THERAPEUTICS**.

Elucidating antibiotic resistomes from environmental microbiomes will not only promote our knowledge about mechanisms of antibiotic resistances, but also aid understanding **THE ENVIRONMENT AS A SOURCE OF NOVEL ANTIBIOTIC RESISTANCES** in clinical isolates.



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