## **Invited speaker 8.5**

## Omics and meta'omics dataflows in mycology

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Omics data from individual organisms and meta'omics data from organismic associations or communities in environmental samples like soil, host tissues, water or air, populate an increasing number of databases and are redistributed to the public via data portals and web services. These data mostly concern nucleotide and translated protein sequences from genes and genomes, patterns of hybridisation signals from transcripts or translation products, as well as manifold information on molecular structures or pathways.

While gene and transcriptome data of individual organisms are nowadays routinely processed, the handling of meta'omics data is still challenging. An ulterior scope is even emerging: the joining of omics and meta'omics data with ecosystem metadata, such as site characteristics, methodological details, organismic traits, and information on sample deposition in repositories.

For comprehensive analysis of such diverse data, the content of different databases has to be linked. Data nodes with database registries and data record ID resolvers are preconditioned for providing this data integration. Mechanisms, which collect and redistribute such identifiers among data nodes, need to be established. Currently, networks of web services and platforms are set up, allowing for the presentation and downstream analysis of content-enriched omics and environmental meta'omics data.