



## ABSTRACT

**Title:** Life with more than 9000 genes- a genomic resource for *Rhodotorula* yeasts

**Authors:** Bettina Müller<sup>1</sup>, Adnan Niazi<sup>2</sup>, Erik Bongcam-Rudloff<sup>2</sup>, Christian Brandt<sup>3,4</sup>, Martin Hölzer<sup>3,5</sup>, Adrian Viehweger<sup>3,6</sup>, Giselle Martín-Hernández<sup>1</sup>, Sigurdur Davidsson<sup>1</sup>, Volkmar Passoth<sup>1</sup>

**Affiliations:** 1: Swedish University of Agricultural Sciences, Department of Molecular Sciences. 2: Swedish University of Agricultural Sciences, Department of Animal Breeding and Genetics. 3: nanozoo GmbH, Leipzig, Germany. 4: Institute for Infectious Diseases and Infection Control, Jena University Hospital, Jena, Germany. 5: RNA Bioinformatics and High-Throughput Analysis, Friedrich Schiller University Jena, Jena, Germany. 6: Department of Medical Microbiology, University Hospital Leipzig, Germany

**Presenting:** Volkmar Passoth

### Abstract content:

**Introduction:** The genus *Rhodotorula* has high biotechnological potential due to the ability to accumulate high amounts of lipids, carotenoids, and other interesting biochemicals. Still, tools for genetic and metabolic engineering are poorly developed and not much is known about genomics of *Rhodotorula* yeasts. These yeasts are highly diverse, with intraspecific variability sometimes as big as interspecific differences. Genes have several introns and alternative splicing variants.

**Objective:** Providing researchers access to comprehensive information about the genomes of a diverse set of *Rhodotorula* strains.

**Method:** Genome were sequenced using a combination of long-read (Nanopore) and short read (Illumina) techniques, enabling assembly of large contigs almost representing chromosomes. Genomes were annotated with a variety of annotation tools.

**Results:** The *Rhodotorula* Genome Database (RGDB) contains genomes of 19 strains. Users can search by gene name or perform BLAST searches. The integrated Genome Browser enables chromosome-level visualization of genomic features, and a built-in tool primer designing.

First investigations could correlate genetic changes (gene truncations) in one *R. toruloides* strain with diminished lipid- and carotenoid production. In another study, a first transformation system was established in another *Rhodotorula* species. Genome sequencing of transformants and comparison with the wild type strain in the database resulted in identifying integration sites in the genome.

**Conclusion:** The RDGB provides a valuable tool for research in this biotechnologically interesting genus. Based on the information, systematic research can be performed, enabling establishment of novel microbial cell factories and cell models for fundamental research based on these yeasts.