**Registration Reference No.\_\_\_ (PLENARY TALK**

**Yeast Diversity United**

**Teun Boekhout**

*CBS Fungal Biodiversity Centre (CBS-KNAW), Uppsalalaan 8, 3584 CT Utrecht, The Netherlands*

*E-mail:* *t.boekhout@cbs.knaw.nl*

**Keywords**: Yeast biodiversity, phylogeny, taxonomy, identification

|  |
| --- |
|  |

**Session selection**: Keynote talk

Our knowledge of yeast biodiversity is rapidly advancing. In the 5th edition of The Yeasts, a Taxonomic Study (2011) ca. 1500 species are described. However, large parts of earth remain undersampled or are not sampled at all. Conceptual and operational strategies to define species are available and have been used with variable success. For higher level classifications, e.g., at the generic and ordinal levels, concepts are much less clear. I will illustrate this with some examples from the basidiomycetous yeasts, a rapidly expanding fungal domain. The current generic classification of these yeasts is mainly based on phenotypic criteria, which has resulted in description of many polyphyletic genera. This is not only disadvantageous from a scientific point of view but may also hamper technological innovations using non-conventional yeasts that are wrongly classified. Names such as *Candida* and *Cryptococcus* have a prime trigger to represent human pathogens. Presently, yeast taxonomy is being revised completely, because of improved phylogenetic signal in multigene- and genomics-based phylogenies; the introduction of the ‘one species-one name’ concept; and ongoing species discovery that add species to new or hardly sampled lineages. In addition, we need to consider the classification of many species that result from metagenomics approaches.

New species discovery resulted in the recognition of technologically and clinically important species. We will illustrate this with recent insights from species that belong to genera such as *Malassezia* and *Cryptococcus*. A genotype of *Cr. gattii*, that most likely represents a separate species, is involved in major outbreaks in Canada and the USA, and is emerging in Mediterranean Europe. Detailed genotyping and coalescence analysis demonstrated that this lineage originated in the lowland rainforest of Brazilian Amazonia and subsequently spread to other parts of the world. Climate change may be contributing to the survival and expansion of new populations in the outbreak regions.

Identification of yeast isolates has traditionally used phenotypic properties. However, developments in DNA-barcoding and proteomics-based diagnostics (MALDI-TOF MS) largely increased the accuracy of identifications, and significantly contributed to new species discovery. We will present results from a multicenter study on the reliability of MALDI-based diagnostics of clinically relevant yeasts.