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## CURRENT CHALLENGES IN YEAST TAXONOMY- WHERE ARE WE AND WHERE DO WE WANT TO GO?

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Recent years have witnessed a succession of dramatic changes in our understanding of yeast diversity and on its translation into a scientifically sound taxonomy. First, sequence-based species delimitations have promoted an incomparable step forward by providing the means for a (more) rational and an (almost) universal protocol for the delineation of yeast species. This has allowed for a significant increase in the number of described taxa, not only because of the availability of new tools but also because standardized and less obscure procedures for species descriptions were accessible to non-specialists. More recently, the abolition of the dual naming system for sexual and asexual forms started a new revolution in yeast nomenclature. This aspect is primarily illustrated by the impact of sequence-based classification in the delineation of yeast genera. Whereas redundant names are abolished the diminished relevance of the study of morphological traits, sexual states and ultimately phenotypes might have negative consequences. A problem that affects the new classification is that international nucleotide sequence databases lack community-curation and contain vast numbers of unnamed DNA sequences. Moreover, new taxa represented solely by environmental sequences are kept outside the classification. Finally, the limitations and future of barcoding using single-gene markers vs the power of genomics must also be taken into consideration. Through a series of examples, current challenges in yeast taxonomy and possible strategies to tackle them will be discussed.

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