



Conference Abstract

Resolving classification problems in yeasts-a unified method

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Abstract

In our research, we established unified criteria for yeast species and genera delineation by integrating DNA and physiological characters. Specifically, we focused on Sequence Identity (SI) and Evolutionary Distance (ED) derived from the combination of ITS1-2 and LSU rDNA markers, as well as a new parameter—Distance Between Physiological Profiles (DPP). We first constructed a phylogenetic tree based on the combined sequences and calculated SI between all yeast pairs on the tree. Yeast physiological traits were then encoded using a binary system (presence or absence of the character i.e., presence = 1, absence = 0), and these profiles were compared to build a physiological dendrogram. Notably, the physiological dendrogram closely mirrored the genetic dendrogram. Using both dendrograms, we visualized and identified robust taxonomic boundaries within the *Kazachstania* and *Starmarella* clades, further supported by rDNA phylogenetic trees (1-4). Strong correlations between SI and ED confirmed the reliability of our DNA-based approach, while the integration of DPP further enhanced species delineation. Together, these criteria provide a comprehensive framework for taxon delineation, generalizable to all yeast species and genera.

Keywords

Yeast systematics, Sequence identity, Evolutionary distance, Distance between physiological profiles, *Kazachstania*, *Starmarella*

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Author contributions

- **Roumen Dimitrov:** Conceptualization, methodology development, and bioinformatic analysis.
- **Dilnora Gouliamova:** Methodology development

Conflicts of interest

The authors have declared that no competing interests exist.

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