

Saccharomyces cerevisiae var. 'boulardii' infections: from diagnosis to in-host microevolution

Alexandra Imre^{1,2}, Hanna Rácz^{1,3}, Péter Oláh^{4,5}, Zsuzsa Antunovics⁶, Ilona Dóczy⁷, László Majoros⁸, Renátó Kovács^{8,9}, Ksenija Lopandic¹⁰, Zsigmond Benkő¹, István Pócsi¹, Walter P. Pfliegler¹

- 1) Department of Molecular Biotechnology and Microbiology, University of Debrecen, Debrecen, Hungary
- 2) Kálmán Laki Doctoral School of Biomedical and Clinical Sciences, University of Debrecen, Debrecen, Hungary
- 3) Doctoral School of Nutrition and Food Sciences, University of Debrecen, Debrecen, Hungary
- 4) Department of Dermatology, Venereology and Oncodermatology, University of Pécs, Pécs, Hungary
- 5) Department of Dermatology, University Hospital of Düsseldorf, Düsseldorf, Germany
- 6) Department of Genetics and Applied Microbiology, University of Debrecen, Debrecen, Hungary
- 7) Institute of Clinical Microbiology, University of Szeged, Szeged, Hungary
- 8) Department of Medical Microbiology, University of Debrecen, Debrecen, Hungary
- 9) Faculty of Pharmacy, University of Debrecen, Debrecen, Hungary
- 10) Institute of Biotechnology, University of Natural Resources and Life Sciences, Vienna, Austria

Saccharomyces 'boulardii'

•Recently, the subtype *S. 'boulardii'* has become an ingredient in many **probiotic supplements**.

•Positive health effects:

- effect against *Clostridium difficile* and cholera toxins
- antimicrobial activity
- modulation of gut flora
- reduction of inflammatory cytokine levels

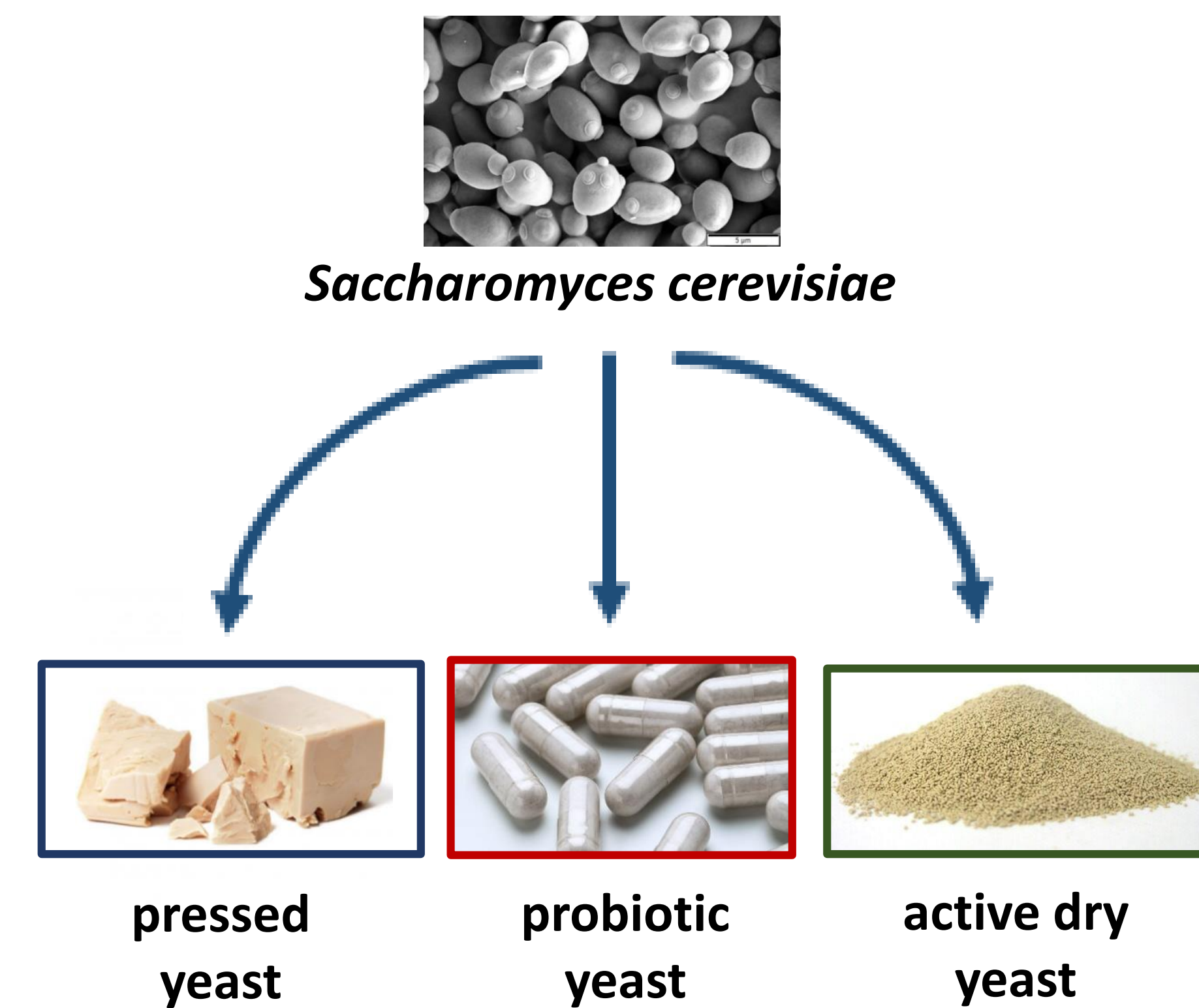
•**Treatment:** diarrheal disorders (acute colitis, *C. difficile*-related diarrhea)

Diagnosis of yeast probiotic infection

Subtyping

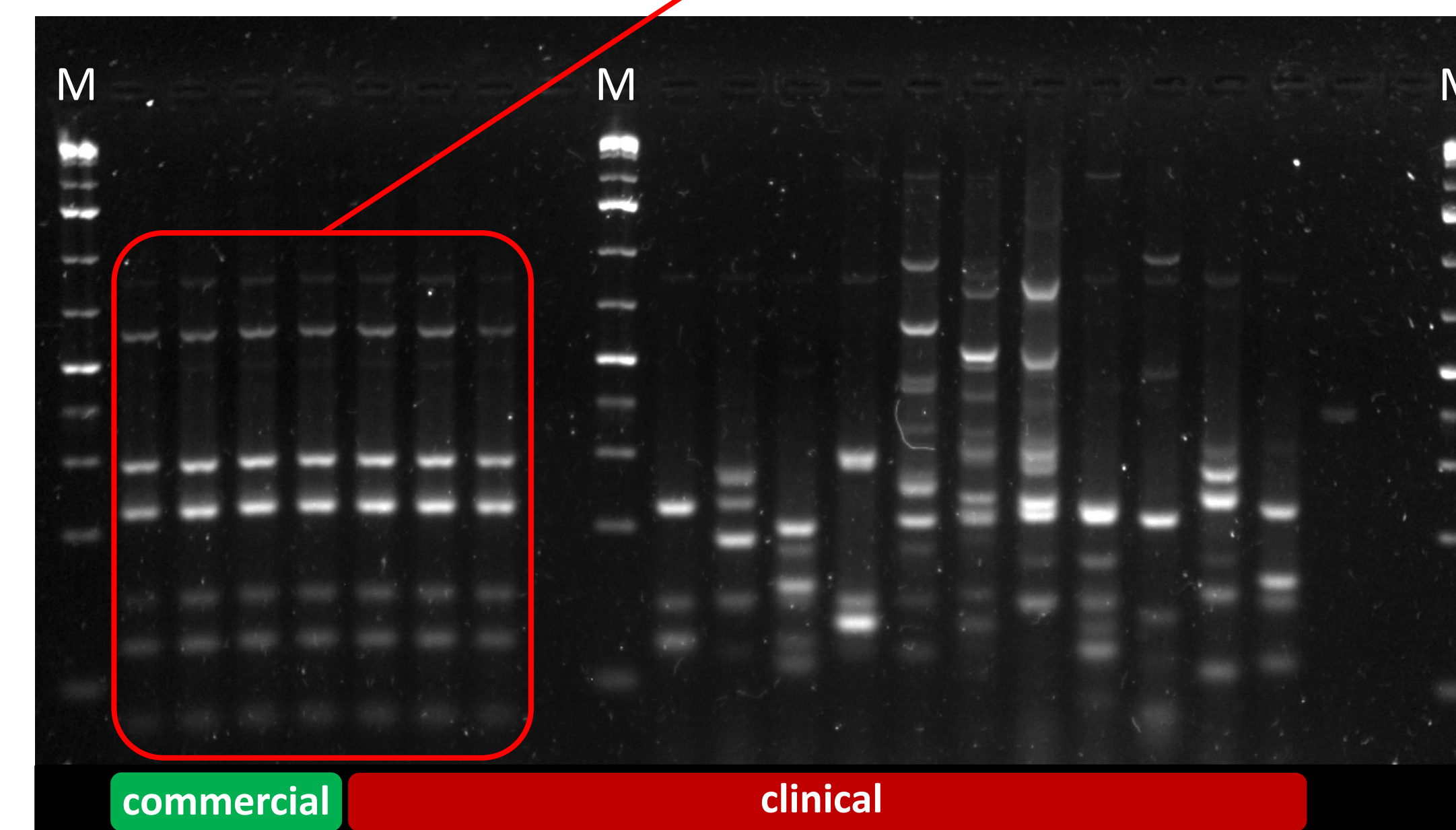
S. cerevisiae is a potentially emerging fungal pathogen and as a species it is not homogeneous. Instead it can be divided into clades and several clinical isolates have been identified in these phylogenetic groups. Although PCR-fingerprinting methods are applicable for subtyping, routine clinical mycological diagnostics rarely uses such methods.

However subtyping would be a prerequisite to understand how and why infections arise from products containing live yeasts, such as probiotics.



Multiplex PCR

Based on our genotyping results we combined interdelta, *YLR177w*, *YOR267c*, and the ITS region primers into a single multiplex reaction. For probiotics and probiotic-derived clinical isolates, our multiplex PCR resulted in an easily recognizable band pattern which consists of six bands in three groups plus a single band. The other, non-probiotic related clinical isolates displayed different band patterns clearly distinguishing them from the probiotic group.



Imre A. et al., A new, rapid multiplex PCR method identifies frequent probiotic origin among clinical *Saccharomyces* isolates, *Microbiological Research* **227**, 126298 (2019)

Live Q&A session:

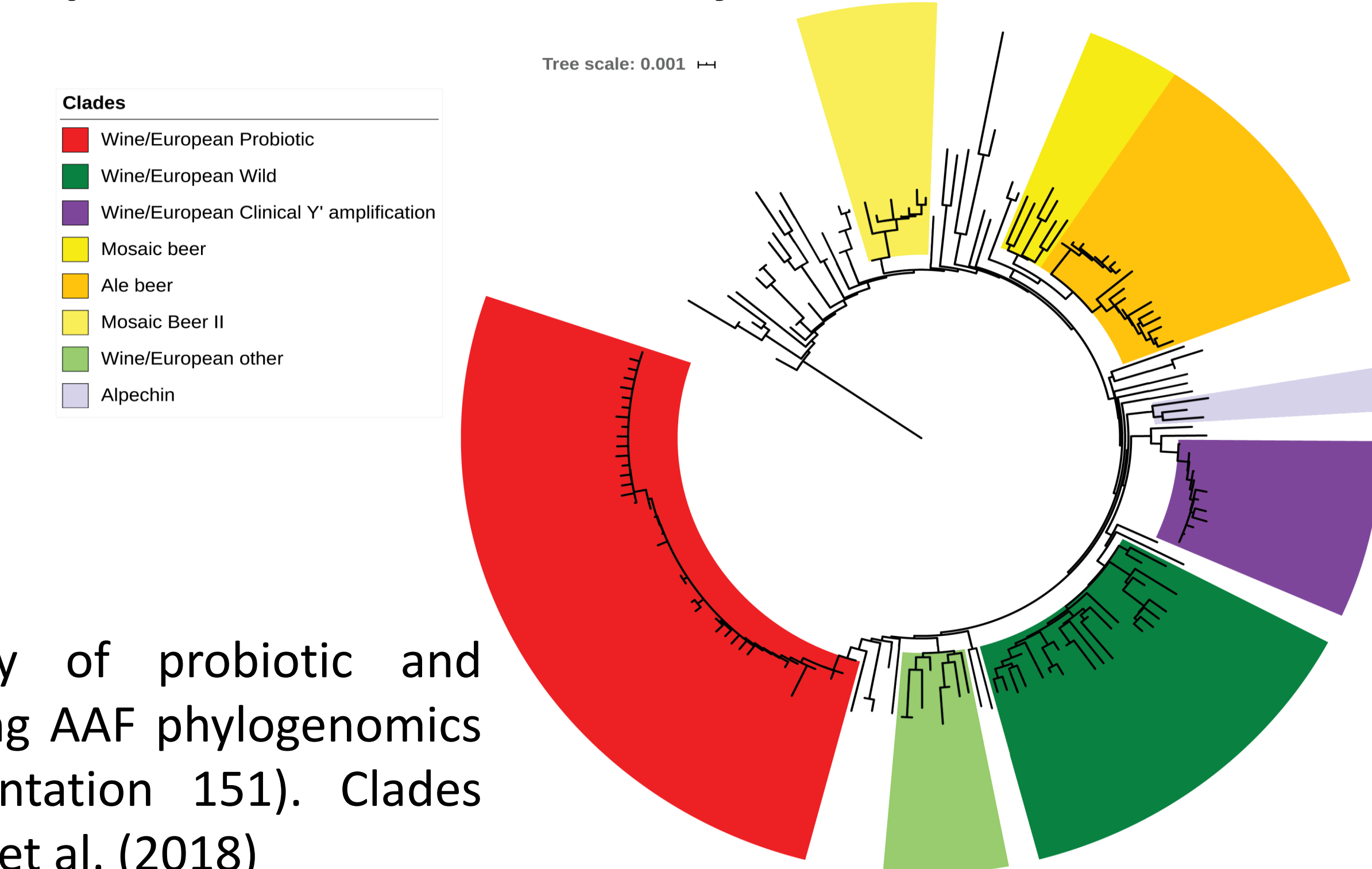
Tuesday, April 28
2:02 - 2:04 PM

@alexandra_imre_
alexandra-imre-a1a0b3110

E-mail: imre.alexandra@science.unideb.hu

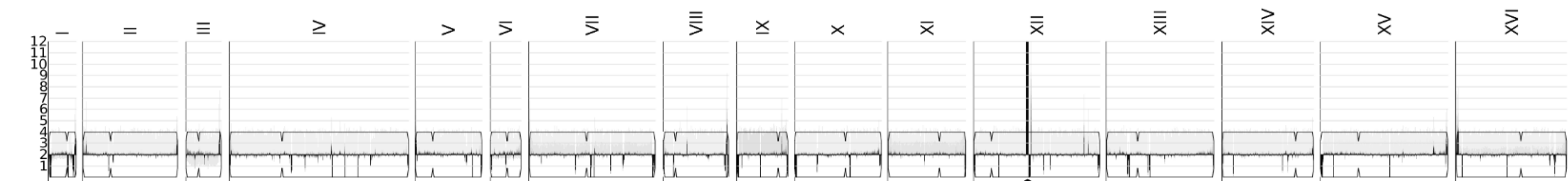


mtDNA and genome structure variation analysis in probiotic-derived clinical yeasts



mtDNA phylogeny of probiotic and related yeasts using AAF phylogenomics (see PEQG presentation 151). Clades according to Peter et al. (2018)

Combined coverage plot for 43 probiotic and derived clinical isolates shows that genome structure variations are rare (1 tetraploid, 4 aneuploid (> diploid), 1 aneuploid (<diploid), 37 diploid)



Problems

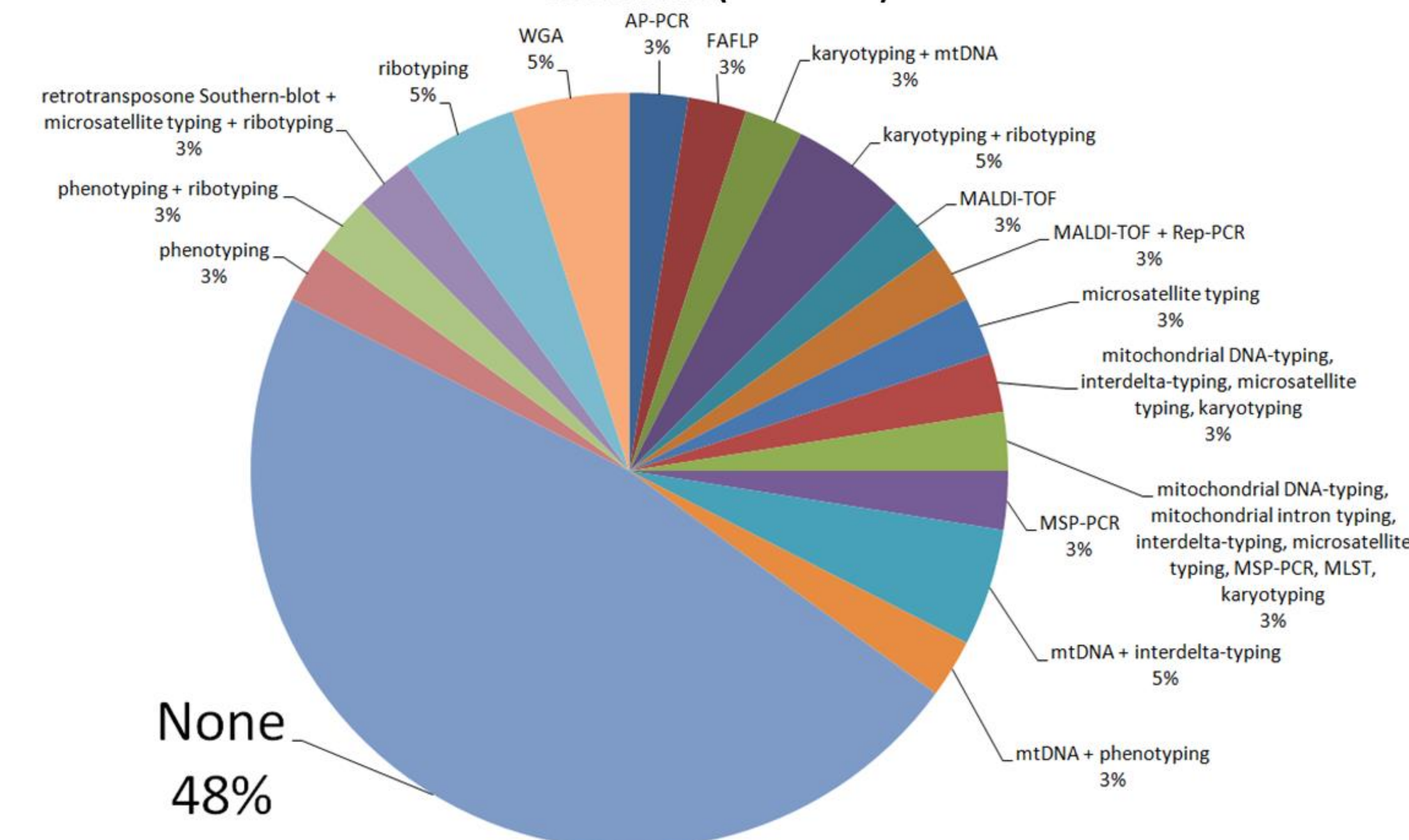
Yeast probiotics infections (first in 1991)

- local or systemic mycosis
- published fungemia cases

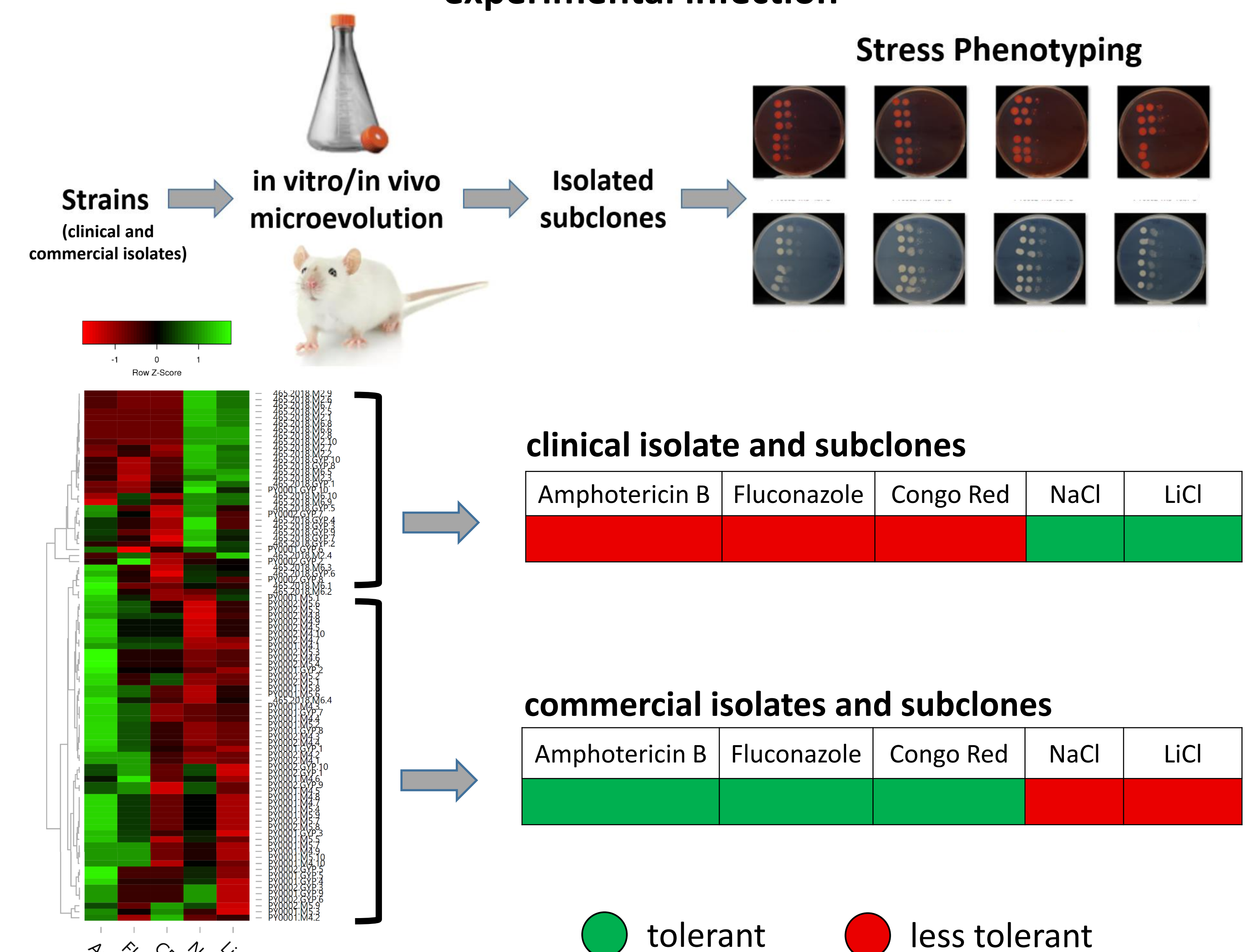
Predisposing factors

- critical illness; ICU admission
- antibiotics and probiotics use
- immunosuppression

Methods used for strain-level typing of presumably probiotic-derived yeast infections (1999-2019)



Identification of traits under selection during experimental infection



● tolerant ● less tolerant