



Inter- and intraspecies variability among yeasts isolated from dairy products

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INTRODUCTION & AIM

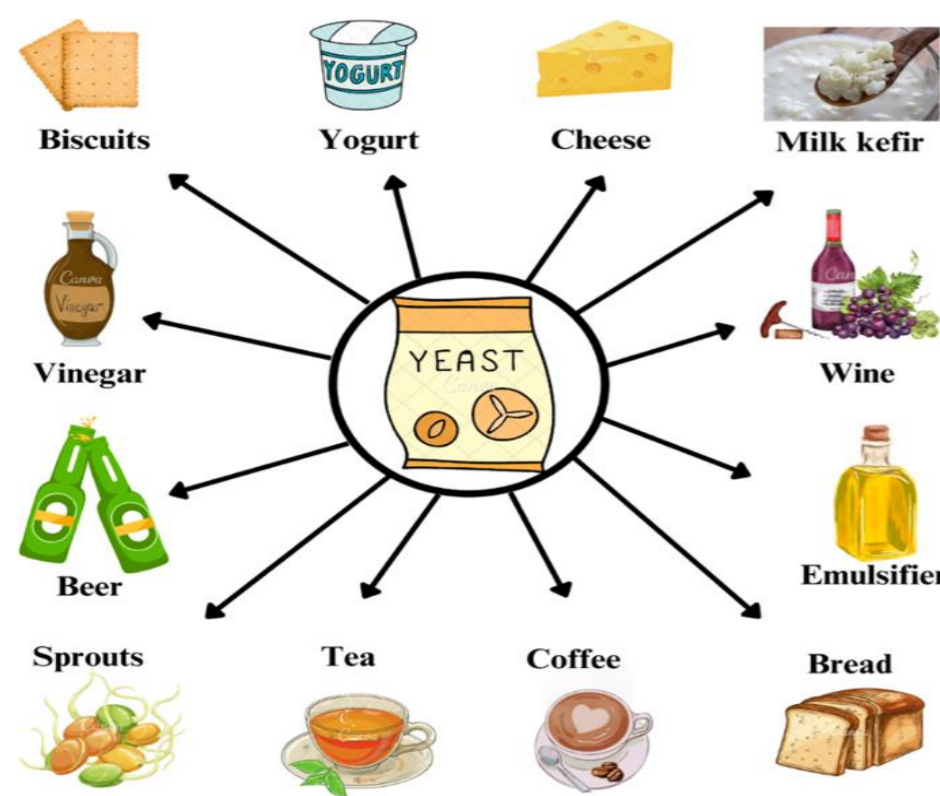


Figure 1. Application of yeasts in food industry [3]

Yeasts are microorganisms known and used by human for many years. They can be considered the spoiling agents of food products but they can also be used in many fermentation processes, in particular in dairy products (Fig. 1) contributing to the chemical composition, sensory quality, and typical characteristics of fermented food and even acting as probiotics [1, 2].

AIM of the study: to examine inter- and intraspecies variability among yeast species isolated from Ukrainian dairy products with the help of several molecular genetic markers.

METHODS

Objects: species of *Saccharomyces* (n=32), *Kluyveromyces* (n=26) and *Rhodotorula* (n=28) genera

Bioinformatic analysis was carried out on 18S rRNA, 26S rRNA and ITS-sequence from GenBank using the FaBox (1.41), MEGA 10.

Molecular genetic analysis: species were isolated from Ukrainian dairy products: yogurt, sour cream and soft cheese. Analysis was performed by ISSR PCR and RT-qPCR.

CONCLUSION.

1. The conserved genome regions (18S rRNA, 26S rRNA, ITS) are the most effective genetic markers of interspecies diversity;
2. The dispensable genome, in particular distribution of short repeats, allows studying the intraspecific polymorphism of yeasts;
3. Differential gene expression can serve as a molecular marker for the species heterogeneity.

REFERENCES

1. Jakobsen, Mogens, and Judy Narvhus. "Yeasts and their possible beneficial and negative effects on the quality of dairy products." *International dairy journal* 6.8-9 (1996): 755-768.
2. Arevalo-Villena, M., et al. "Biotechnological application of yeasts in food science: starter cultures, probiotics and enzyme production." *Journal of applied microbiology* 123.6 (2017): 1360-1372.
3. Doolam, B., Mishra, B., Surabhi, D. et al. A systematic review of potential bioactive compounds from *Saccharomyces cerevisiae*: exploring their applications in health promotion and food development. *Environ Dev Sustain* (2024).

RESULTS

Bioinformatic analysis.

Table 1. Inter- (A) and intraspecies (B) variability (sequence analysis)

Characteristics	Loci		
	18S rRNA	26S rRNA	ITS
Variable sites	43%	74%	61%
Parsimony informative	42%	31%	57%
Singletons	< 1%	43%	< 1%

Species	Loci		
	18S rRNA	26S rRNA	ITS
<i>S. cerevisiae</i>	1.5%	< 1%	0
<i>K.marxianus</i>	< 1%	0	< 1%
<i>R.mucilaginosa</i>	< 1%	2.3%	2%

Molecular genetic analysis

Table 2. Inter- (A) and intraspecies (B) variability (ISSR PCR)

Primer	Amplicon sizes, bp	TNB	NPB	PPB,%	PIC	Rp
(AC) ₈ C	400 - 3000	21	21	100	0.31	9.1
(AC) ₈ T	300 - 3000	16	16	100	0.31	7.8

Species	Amplicon sizes, bp	Total amplicon number	Polymorphism, %
<i>S. cerevisiae</i>	300 - 3000	20	80
<i>K.marxianus</i>	300 - 3000	33	100
<i>R.mucilaginosa</i>	300 - 1500	16	68

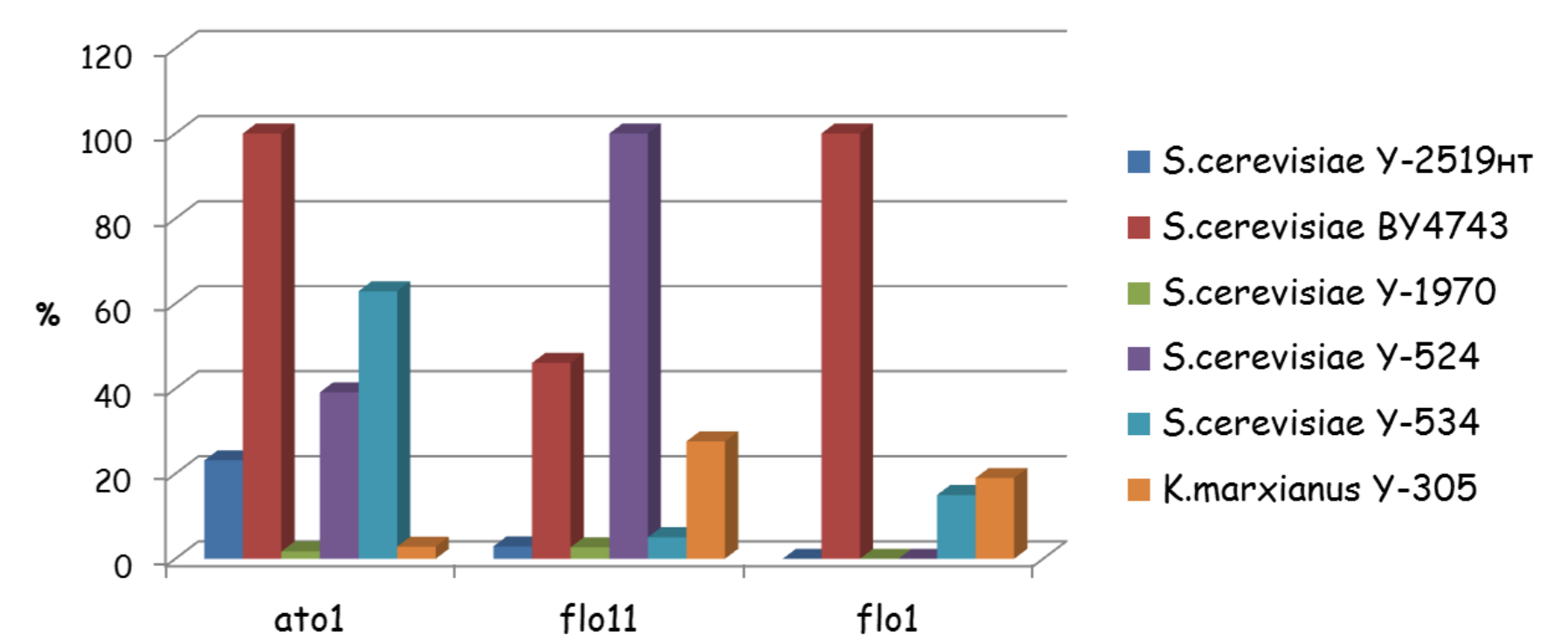


Figure 2. Variability of *ato1*, *flo1*, *flo11* genes expression among yeasts