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High Resolution Melting (HRM) Method for Brettanomyces Yeast Identification

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Keywords:

Brettanomyces yeast, RT-PCR method,

Relevance

In brewing, **Brettanomyces** are generally considered contaminant. However, some types of beer, such as traditional Belgian ales, lambic, gez, as well as Flanders brown ale and Flanders red ale, owe their unique flavors to this yeast. In addition, with the development of resource-saving technologies, researchers became interested in residual brewer's **Brettanomyces** yeast as a source of biologically active substance — a polysaccharide of the yeast cell walls - beta-glucan.

Brettanomyces identification is difficult. Today, molecular biology microbiology methods are widely used for their identification. The polymerase chain reaction method (PCR) was used in this research.







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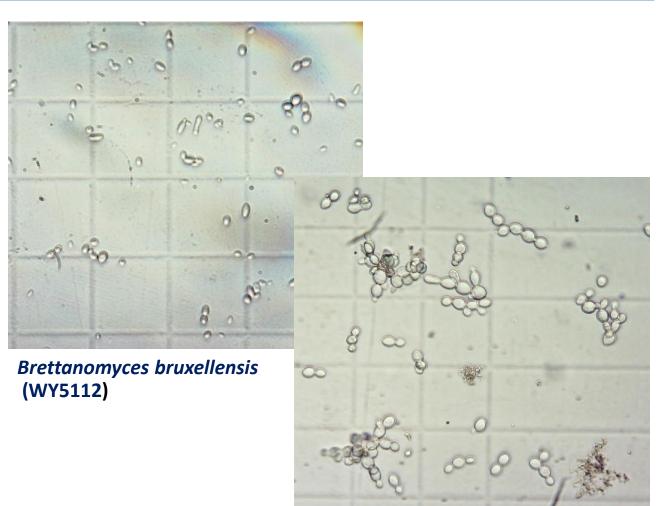
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Research Objective:

the objects of this study were Brettanomyces and Saccharomyces yeast strains, obtained from the collections of brewing yeast cultures.



Saccharomyces cerevisiae (WLP300)









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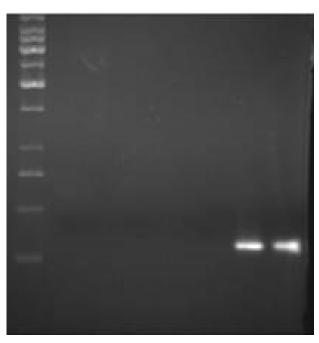
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Results

M 1 2 3 4 5



Results of PCR analysis of 26S RNA fragments obtained using primers DB90F and DB384R specific to *Brettanomyces* yeast.

Figure shows clear bands of a specific PCR product.

Therefore, the nucleotide samples on tracks 4 and 5 belong to *Brettanomyces* yeast.

Figure – bands of a specific PCR product:

M – DNA molecular weight marker;

1-5 - PCR products.





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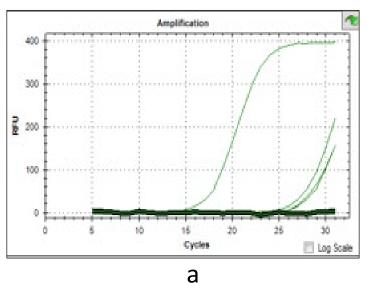
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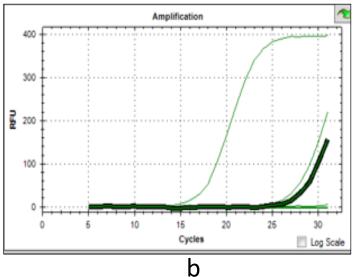
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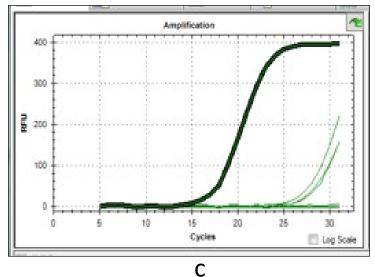


Figure – Results of RT-PCR analysis of 26S RNA fragments obtained using primers DB90F and DB384R, specific for *Brettanomyces*

a – negative control; b – Saccharomyces cerevisiae; c – Brettanomyces bruxellensis

As can be seen from Figure when analyzing *Brettanomyces bruxellensis* yeast DNA amplification curve started to rise already at the 16th cycle. However, a non-specific rise in the amplification curve was also observed in the case of *Saccharomyces cerevisiae*.







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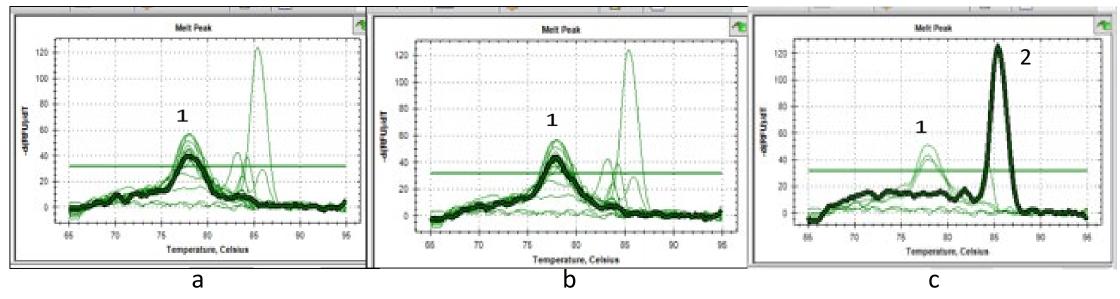


Figure – Results of HRM analysis of 26S RNA fragments obtained using primers DB90F and DB384R, specific for *Brettanomyces*

a – negative control; b – Saccharomyces cerevisiae; c – Brettanomyces bruxellensis

Figure shows non-specific peak №1 in all samples, and only the graph "c" clearly shows the peak №2 of fine melting of the amplified *Brettanomyces* DNA fragment.







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Conclusions

As can be seen from the presented data, the use of HRM analysis allows to identify peaks of amplified specific DNA fragments and to ignore non-specific peaks. So, modern methods of molecular biology allow to identify microorganisms most accurately and in the shortest possible time. This undoubtedly distinguishes them from the traditionally used microbiological and biochemical methods of detection and identification. Moreover, the approaches of molecular biology and molecular genetic methods in particular, help researchers not only in identification issues, but also for the effective management of directed biosynthetic processes.

References

1. Meledina, T.V. Prospects of the Yeast Genus Brettanomyces Using in Brewing / T.V. Meledina, V.A. Ivanova, S.G. Davydenko // Almanac of Young Scientists' Scientific Works of ITMO University. - 2017. - Vol. 1. - Pp. 193-196.

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Thank you for your attention!

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