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Analysis of yeast conservative nucleotide sequences by genomic bioinformatic methods

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One of the first microorganisms used by humans to meet food and beverage needs was yeast. Yeasts are the simple eukaryotic microorganism that has a wide range of applications in various industries [1]. Due to their ability to synthesize many products, such as ethanol, enzymes, vitamins, yeasts are extensively used as a model for the production of different metabolic products beneficial for human health. Besides yeasts are also used for genetic construction of the producers of recombinant proteins and metabolites. It has been defined three fields of yeast application in modern biotechnology: production of metabolites, production of recombinant proteins, and *in vivo* biotransformations [2].

The development of genomic, proteomic and bioinformatic methods has introduced into the biotechnological processes the new instruments to explore the industrial potential of organisms and deeper understanding of yeast metabolic pathways and their genetic basis.

The purpose of the present study was the bioinformatic analysis of conservative nucleotide sequences, their variability between different yeast species and genus. To meet this aim 18S rRNA and 26S rRNA genes sequences of 10 strains of *Saccharomyces cerevisiae*, 3 strains of *S. boulardii*, 8 strains of *Kluyveromyces lactis* 6 strains of *K. marxianus*, 12 strains of *Rhodotorula mucilaginosa*, 7 strains of *R. hordea* and 7 strains of *R. glutinis* were analyzed using Molecular Evolutionary Genetics Analysis (MEGA) software [3].

The results of bioinformatic analysis showed that the highest percent of variable and parsimony-informative sites were detected when sequences of 26S rRNA gene were compared: 74% and 31%, respectively. Opposite data were revealed for the intragenus genetic variability value, the highest meaning was observed at the comparison of 18S rRNA gene sequences: 0.776 (*Saccharomyces*), 0.710 (*Kluyveromyces*) and 0.012 (*Rhodotorula*).

The results obtained in the study can facilitate the selection of yeast phylogenetic biomarkers and promote the establishment of yeast sequences database.

1. Nandy S.K., Srivastava R.K. A review on sustainable yeast biotechnological processes and applications // Microbiological research. — 2018. — 207. — P.83–90.

2. Mattanovich D., Sauer M., Gasser B. Yeast biotechnology: teaching the old dog new tricks // *Microbial cell factories*. — 2014. — 13(1). — P.1-5.
3. Tamura K., Stecher G., Peterson D., Filipski A., Kumar S. MEGA6: molecular evolutionary genetics analysis version 6.0 // *Molecular biology and evolution*. — 2013. — 30(12). — P.2725-2729.

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Sample analyses for *Vaccinium vitis-idaea* bioactive compounds extraction

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Plants of the genus *Vaccinium* have great biological value as sources of food, medicinal and cosmetic products. One of the representatives of this genus, *Vaccinium vitis-idaea* or lingonberry, has large amount of biologically active compounds, especially arbutin, ascorbic, benzoic and ursolic acids, tannins, betain, flavonols, etc. Those components of lingonberry improve state of blood and vessels, have the antiinflammatory, antiatherosclerotic, lipotropic, antihelminthic and similar to adrenal hormones action [1]. Leaves of *V. vitis-idaea* are considered to be much richer in biologically active compounds than fruits. Extracts of the plant are widely used not only for medicinal purposes but for cosmetics additives. For example, arbutin is applied as a natural skin brightener for reduction of melanin production and getting rid of age spots. Preparations and cosmetic products from the lingonberry and its components are enough rare on the market of Ukraine. Thus, the study of technology for bioactive compounds of *V. vitis-idaea* extraction is rather relevant.

Samples from two experimental plots located in different regions of Ukraine were analyzed. The first plot was in the Carpathians, Zakarpattia oblast, Rakhiv district and the second one was in Polissya, Zhytomyr oblast, Radomyshl district. The samples of *V. vitis-idaea* plants were collected during the flowering stage in June and later, in August 2021. All analyses were carried out according standard methods. The standard procedure for the isolation and analysis of substances was based on extractions with the subsequent titration. The assay of arbutin was fulfilled by the iodometric titration or by titration of acids extracted with water with an alkali solution, or by the titrometric assay of the vitamin C with the Tillman's reagent [2]. Received results are represented in the table 1.

The fulfilled analyses demonstrated that lingonberry material collected in Zakarpattia oblast was much better quality, with higher content of vitamin C and arbutin, and lower level of radioactivity.

It should be noted that plants of *V. vitis-idaea*, like the other representatives of the family Ericaceae, has symbiotic relationships with ericoid