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Analysis of yeast conservative nucleotide sequences by genomic bioinformatic methods

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 protential 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.

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