



International Journal of Environment and Health Sciences

(IJEHS) 2020, VOL. 2, NO. 1

<http://www.stenvironment.org/>

Genomics and proteomics of *Saccharomyces cerevisiae* used for biofuel production

Sumit Sharma¹, Saurabh Jyoti Sarma^{1,*}, Satinder Kaur Brar^{2,3}

¹Department of Biotechnology, Bennett University, Greater Noida (UP), India

²INRS-ETE, Université du Québec, 490, de la Couronne, Québec, Canada

³Department of Civil Engineering, Lassonde School of Engineering, York University, North York (Toronto), Canada

Received on: 10.01.2020

Revised on: 29.01.2020

Accepted on: 05.02.2020

ABSTRACT

Saccharomyces cerevisiae is the first eukaryotic organism whose genome was sequenced with genomic information of a total of 16 chromosomes. It is being used as a model organism to study the molecular structure and functional characterization of higher eukaryotes. The genomic, proteomic, transcript and metabolic resources are the best platforms to provide information regarding genome, proteins, transcripts and metabolic pathways. The evolution of simple genetics of yeast to genome editing and utilization of genomic resources are summarized in this review. It will give a general overview of various database resources and tools for gathering and generating computational information of yeast. SGD (*Saccharomyces* Genome Database) is an open resource for comprehensive biological integrated information for *Saccharomyces cerevisiae* and helps in finding the target gene such as ADH (alcohol dehydrogenase) for improving biofuel production enhancement. Genome-wide homology annotation also helps in identifying genes and ORFs and also in assigning functions. The potential utilization of these resources may overcome the findings of a target for gene discovery and their use in industrially relevant gene modifications.

Keywords: *Saccharomyces cerevisiae*, Genetics, Genomics, Proteomics, Transcriptomics, Metabolomics.