

APPLIED MICROBIOLOGY, ANTIBIOTICS, ANTIMICROBIALS AND BENEFICIAL MICROBES

May 20-21, 2019 Tokyo, Japan

Identification of microbial diversity in grape must by whole metagenome sequencing

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Wine is a complex beverage, which consist of hundreds of metabolites through the action of bacteria and yeasts. These microbial communities play an important role during the winemaking process, as they metabolize sugars from grapes and produce secondary metabolites that influence aromatic quality of wine. However, there is not enough knowledge about these microbial communities. The aim of the study is to accurately identify bacteria, yeasts and especially bacteriophages, the most abundant organisms in biosphere, in grape must from Small Carpathian wine-producing region through the whole metagenomic sequencing method. Total DNA has been extracted from the grape must and performed whole metagenome sequencing approach using Illumina NextSeq platform. Data obtained were analyzed with several bioinformatic methods. MetaSPAdes have been used to assembly reads. The likely taxonomic source of each contig was estimated using BLAST. VirFinder was used to identify bacteriophage sequences from unidentified bacterial contigs. Reads were then classified with Clark using bacterial, viral and fungi database. Taxonomic labels have been recognized to the form of Krona graphs. The whole metagenome sequencing approach allowed the identification of complex microbial community. A good amount of microbial diversity has been identified and also some potential bacteriophage sequences. Wine has a very diverse community of microorganisms. This study allowed for a better characterization of grape must microbiome and helped to understand specificity of wine in this region.

Biography

Miroslav Böhmer has completed his Master's degree from Comenius University, Faculty of Natural Sciences in Bratislava. He is currently working on many projects associated with microbiology, microbiome, metagenomics and bioinformatics.

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