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ABSTRACTS



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The Biolog FF and ECO Plates system for evaluation of the catabolic diversity in fungal and bacterial silage's communities

Karolina Oszust, Magdalena Frąc, Agata Gryta, Nina Bilińska

Laboratory of Molecular and Environmental Microbiology, Institute of Agrophysics Polish Academy of Sciences, Doświadczalna 4, 20-290 Lublin, Poland, e-mail: k.oszust@ipan.lublin.pl, frac@ipan.lublin.pl

Grass and corn silage are being recently mentioned in numerous forecasts as material intended to provide in 2020 about 40% of the total production of biogas in Poland, obtained in the process of methane fermentation. The first and one of the key steps in the hydrolysis of complex organic compounds and contaminants, is attributed to microorganisms' catabolic activity – not only filamentous fungi, but also to community of bacteria inherently colonizing organic materials.

The aim of this study was to present the role of the fungal and bacterial grass and corn silage's communities (GS and CS) catabolic abilities, as determined by the selected carbon compounds utilization. Analyses were performed using Biolog Eco and FF Plate® dedicated for bacterial and fungal community, respectively with regard to GS and CS, as environmental samples.

Eco Plate contains 31 different carbon sources, located in separated well, whereas FF – 95. Tetrazolium violet redox dye is used for each well as a color indicator. If added 100 x dilution of environmental sample, inhabiting microorganisms utilize particular substrates. Microbial response in each microplate is expressed by average well-color development (AWCD). In this study we used the following five groups of carbon substrates: 1) carbohydrates, 2) carboxylic and acetic acids, 3) amino acids, 4) polymers and 5) amines and amides to evaluate a percentage of total absorbance value of the plate corresponding to the type of silage, within 168 h of incubation in 27°C. Correlation of individual carbon sources with first (PC1) and second (PC2) principal component and cluster analysis for particular treatments based on catabolic profile were also conducted.

Clear differences were revealed in catabolic abilities of bacterial and fungal communities of both types of silage (GS and CS). Studied objects differed in carbon sources individual types corresponding with PC1 and PC2. Carbohydrates and amino acids were found as the most intense utilized carbon source groups, irrespectively of analyzed plate (Eco and FF), however, differed between GS and GC. Our results may suggest quite probable differences in methane fermentation process efficiency, due to diverse ability for microbial hydrolysis of complex organic compounds.

Preferred presentation: () oral or (X) poster

Session number: (2 Biodegradation of organic contaminants)

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