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

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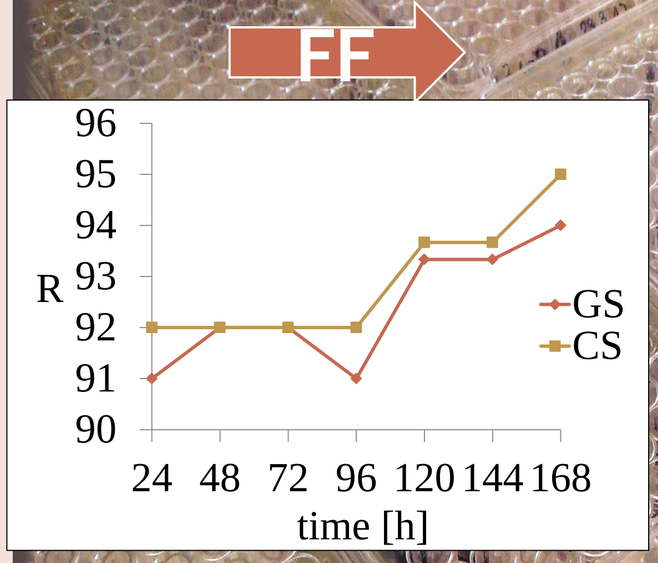
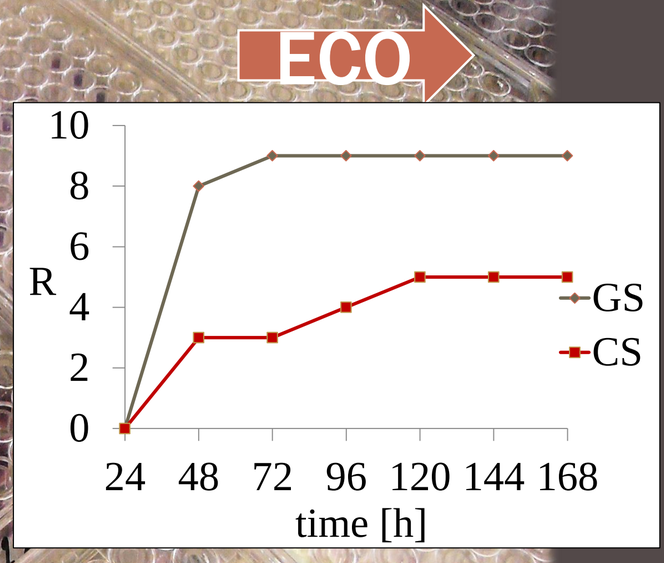
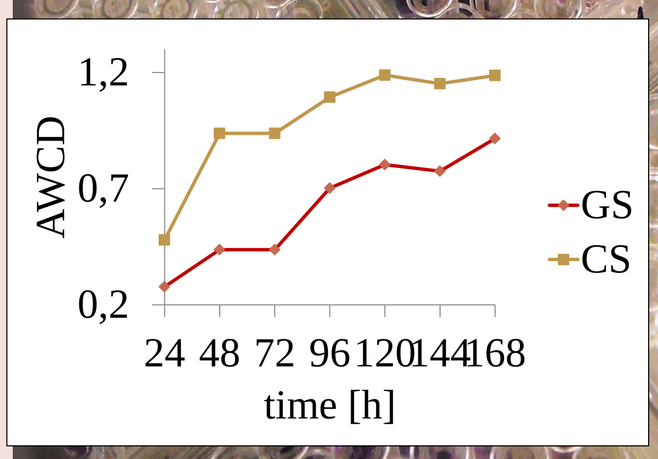
Results

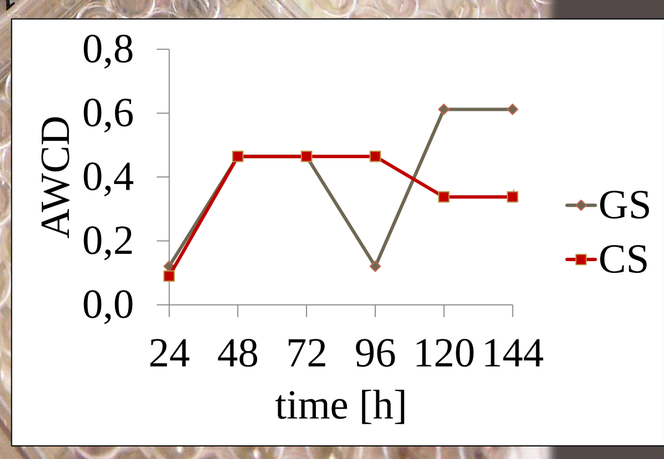
FF

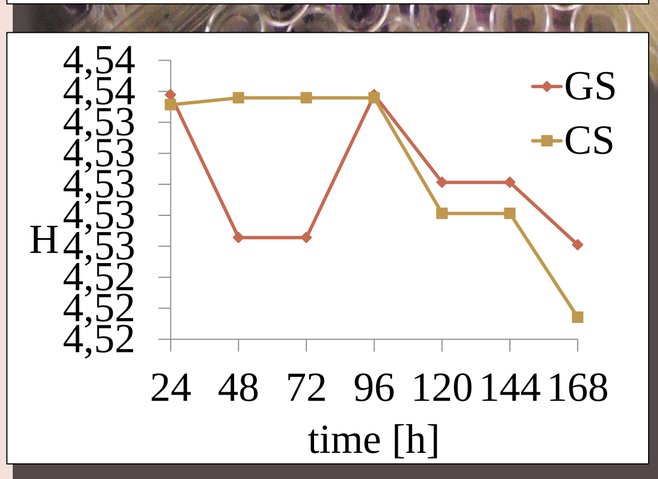


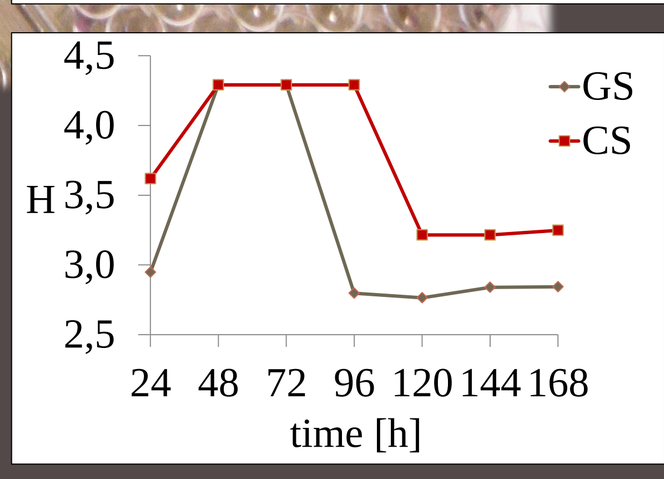
ECO

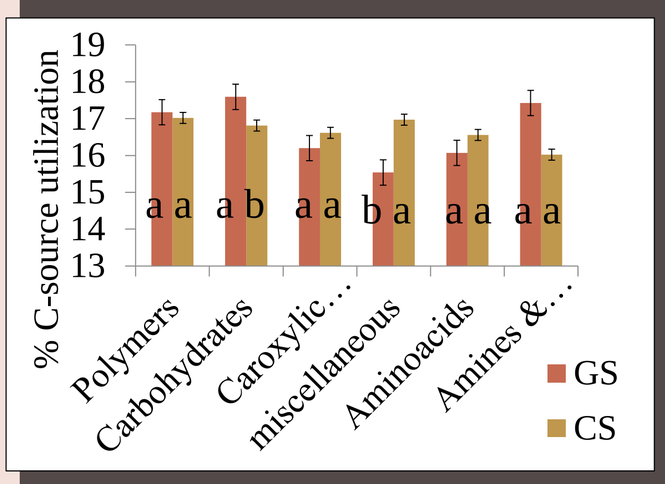


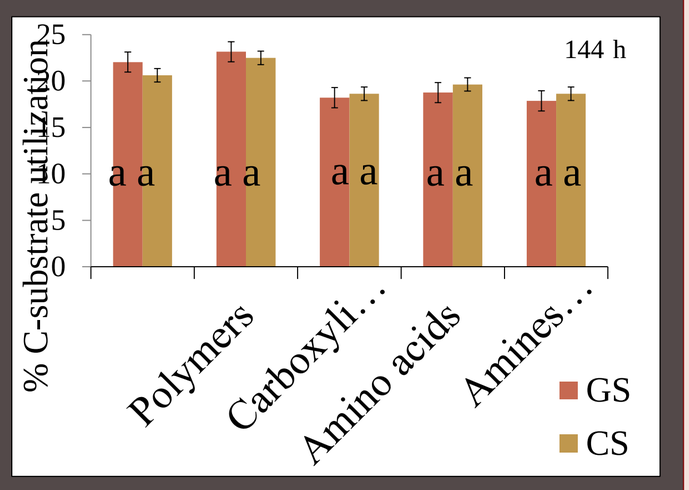


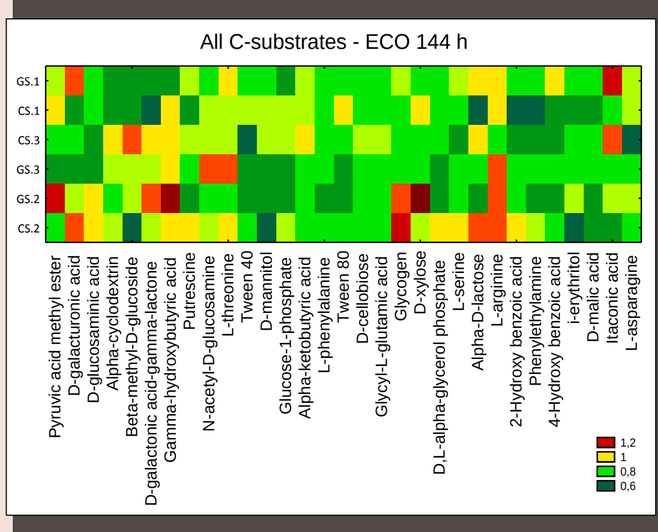




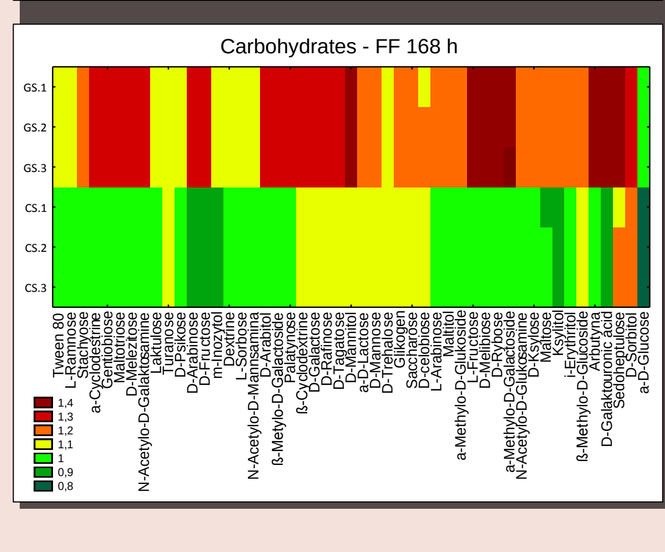








CS			GS		
	PC1	PC2		PC1	PC2
Pyruvic acid methyl ester		0,968	Pyruvic acid methyl ester		0,932
Tween 40		0,952	Tween 40		0,830
Tween 80		0,956	Tween 80		0,742
Alpha-cyclodextrin		-0,986	Alpha-cyclodextrin		-0,814
Glycogen	0,971		Glycogen	-0,859	
D-cellobiose		-0,834	Beta-methyl-D-glucoside	0,952	
Alpha-D-lactose		-0,955	i-erythritol	0,785	
Beta-methyl-D-glucoside	-0,903		D-mannitol	0,725	
D-xylose		0,758	D-glucosaminic acid	-0,881	
i-erythritol	-0,987		D-galactonic acid-gamma-lactone		-0,899
D-mannitol	-0,934		D-galacturonic acid	-0,729	
N-acetyl-D-glucosamine	0,959		2-Hydroxy benzoic acid	-0,737	
D-glucosaminic acid	0,997		L-arginine	-0,743	
Glucose-1-phosphate		-0,778	L-asparagine	-0,738	
D,L-alpha-glycerol phospl	0,994		L-phenylalanine	0,761	
D-galactonic acid-gamma-lactone		-0,984	L-serine	-0,988	
D-galacturonic acid	0,844				
2-Hydroxy benzoic acid	0,817				
4-Hydroxy benzoic acid		-0,740			
Gamma-hydroxybutyric acid		0,995			
Itaconic acid	-0,978				
Alpha-ketobutyric acid	-0,983				
D-malic acid	-1,000				
L-arginine	0,902				
L-asparagine		0,802			
L-phenylalanine	-0,927				
L-serine	0,994				
L-threonine	0,869				
Glycyl-L-glutamic acid		-0,715			
Phenylethylamine	0,705	-0,709			
Putrescine		-0,920			



Introduction

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.

Research objective

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.

Materials and methods

Eco Plate contains 31 different carbon sources, located in separated well, whereas FF - 95.

Tetrazolium violet redox dye in 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.

Key findings

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.