



"Scientific work funded from the budget for science by National Center of Research and Development"



Biochemical potential and molecular identification of microorganisms isolated from soil and different organic wastes



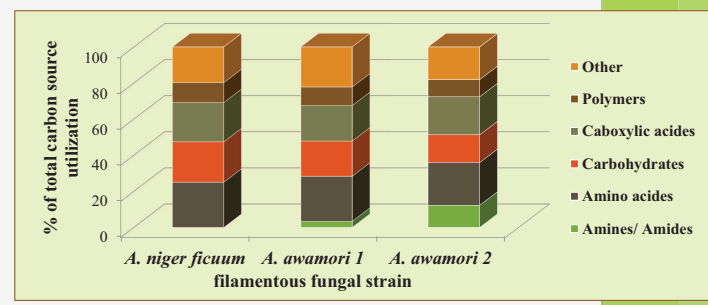
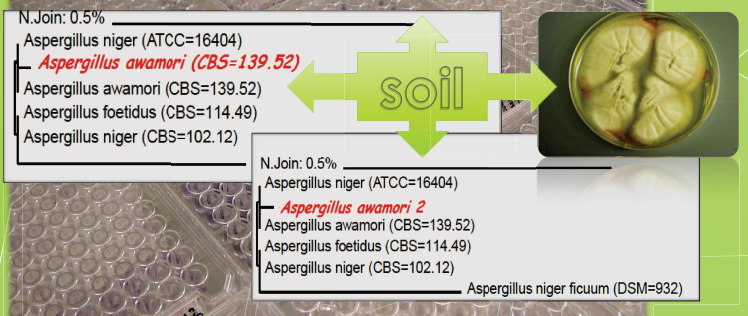
Karolina Oszust, Magdalena Frąc, Anna Siczek,
¹Institute of Agrophysics Polish Academy of Sciences in Lublin,
 ul. Doświadczalna 4, 20-290 Lublin 27, Poland
 e-mail: m.frac@ipan.lublin.pl

INTRODUCTION

Different habitats like soil, dairy sewage sludge and fruit wastes were screened, using selective media. Our aim was to isolate microorganisms that are capable of complex organic compounds decomposition into simple ones with production of such enzymes as: amylase, protease, pectinase and cellulase. Followed the most numerous c.f.u.'s nine hydrolytically effective strains of bacteria, moulds and yeast were tested.

OBJECTIVE

The present research was conducted to find out the utilization effect of microorganism that may be likely adapted for the hydrolysis in first methane fermentation stage.



MATERIAL AND METHODS

A rapid method for the microbial cellulases detection was conducted on agar plates medium (2% cellulose) using Gram's iodine during five days culture. Biochemical potential using BIOLOG™ System was evaluated with FF plates for fungi, YT and GEN-III for yeast and bacteria species, respectively. Molecular identification using comparative rDNA sequencing was carried out, comparing the LSU-D2 region for fungi and 16S rDNA fragments for bacterial strains. The Microseq-ID software was used for performing sequence matching and creating Neighbor-Joining trees.

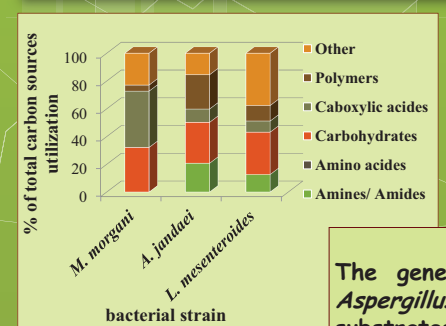
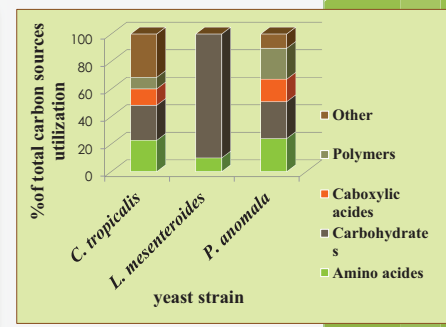
Specimen	# Samples	Base calling	Filter	Assembly	Specimen Score	Top Match	% Match	Consensus Length	Library Entry Length
Bacteria 1 fruit industry wastes	2	✓	✓	✓	33	Leuconostoc mesenteroides dextranum* (ATCC=1925)	100.00	466	496
Bacteria 2 dairy sewage sludge	2	✓	✓	✓	34	Morganella morganii sibirica (Biogroup F) (ATCC=49948)	98.92	488	489
Bacteria 5 dairy sewage sludge	2	✓	✓	✓	29	Aeromonas jandaei (ATCC=49568)	99.78	485	491



N.Join: 0.5%
 Aspergillus foetidus (CBS=114.49)
 Aspergillus niger (ATCC=16404)
 Aspergillus awamori (CBS=139.52)

Aspergillus phoenicis (DSM=62068)
Aspergillus niger ficum
 Aspergillus niger ficum (DSM=932)

Specimen	# Samples	Base calling	Filter	Assembly	Specimen Score	Top Match	% Match	Consensus Length	Library Entry Length
YT 1 fruit industry wastes	2	✓	✓	✓	35	Kloeckera apiculata (ATCC=32856)	99.40	282	282
YT 2 dairy sewage sludge	2	✓	✓	✓	39	Candida tropicalis (ATCC=750)	97.22	280	278
YT 3 fruit industry wastes	2	✓	✓	✓	39	Pichia anomala (ATCC=8168)	99.41	281	282



RESULTS

The genetically identified strains belonged to the genus: *Aeromonas*, *Morganella*, *Leuconostoc*, *Aspergillus*, *Candida* and *Pichia*. Individual strains varied in their ability to attack various C-source substrates in appropriate Biolog Plates, and presented potential efficiency in decaying cellulose. Its biochemical characterisation indicated that all of presented strains may play a role as a decomposers of different materials, and may be useful in organic wastes degradation process.