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



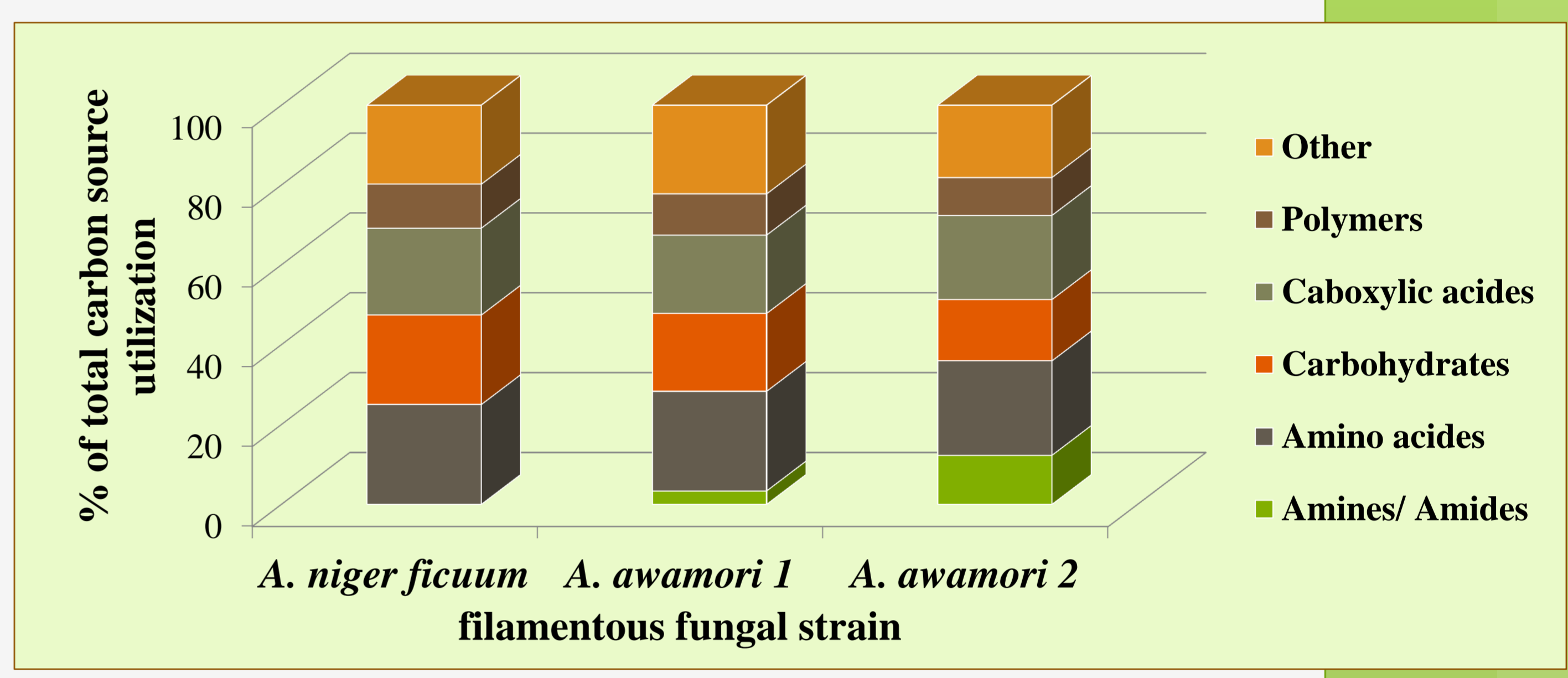
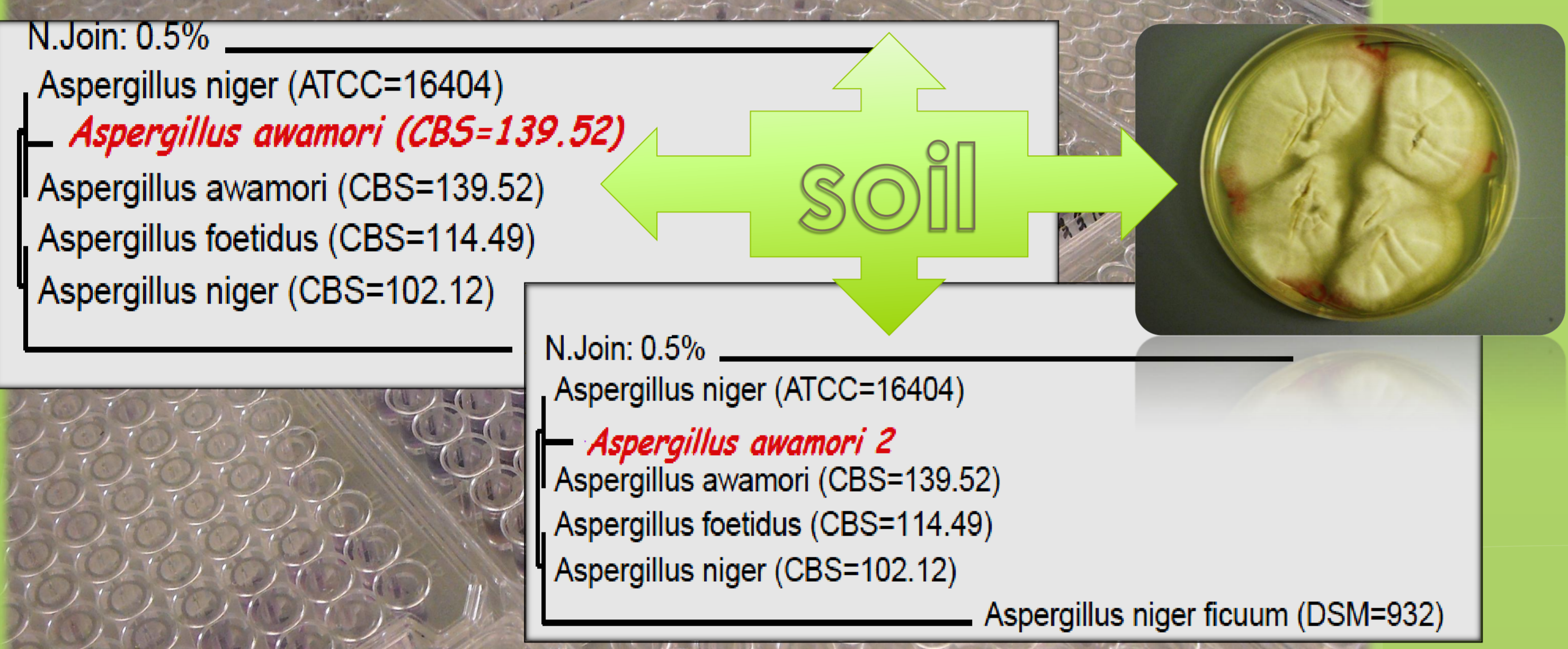
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## INTRODUCTION

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

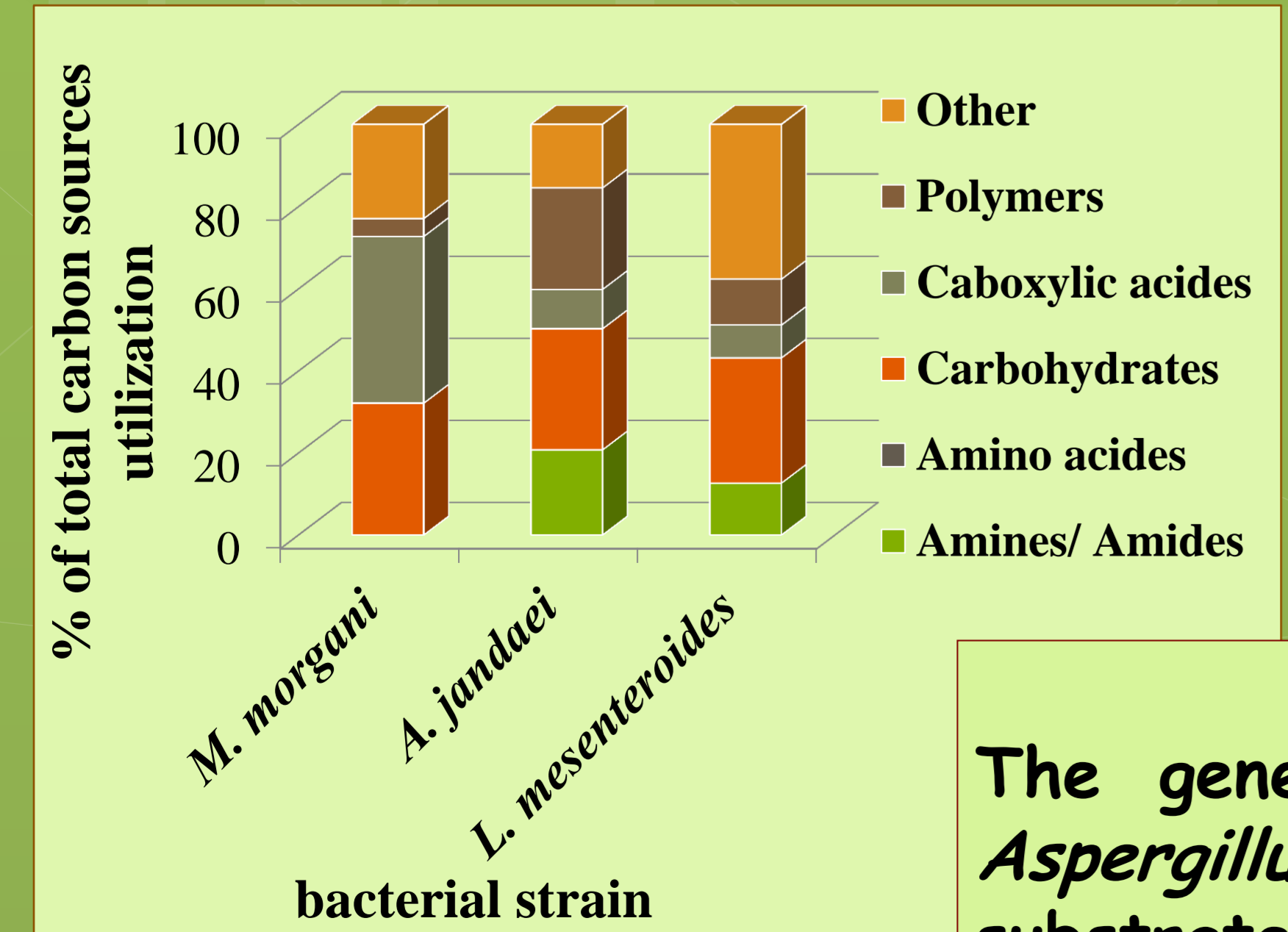
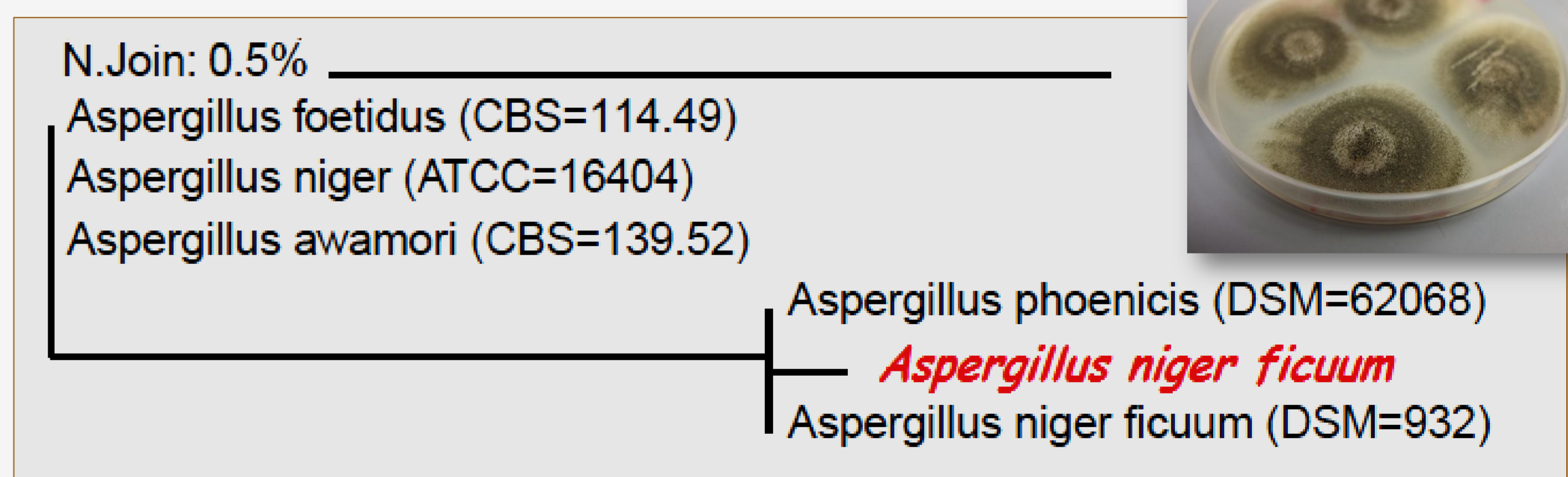
The present research was conducted to find out the utilization effect of microorganism that may be likely adapted for the hydrolysis in first methane fermentation stage.



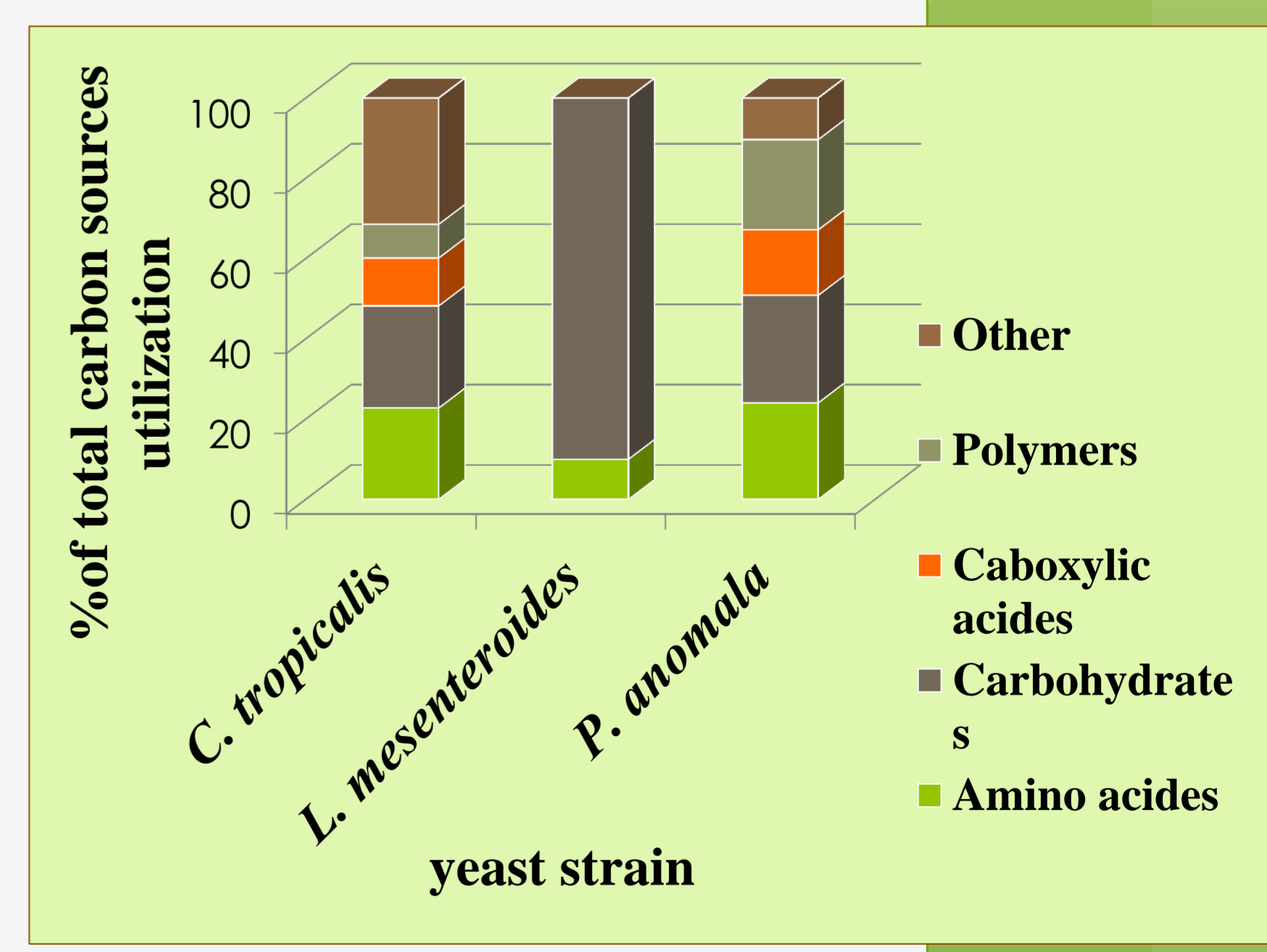
## MATERIAL AND METHODS

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 dextranicum* (ATCC=1925)	100.00	466	496
Bacteria 2 dairy sewage sludge	2	✓	✓	✓	34	Morganella morganii sibirii (Biogroup F) (ATCC=49948)	98.92	488	489
Bacteria 5 dairy sewage sludge	2	✓	✓	✓	29	Aeromonas jandaei (ATCC=49568)	99.78	485	491



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.