



## GROWTH AND ENDOGLUCANASE ACTIVITY OF MICROORGANISMS INHABIT THE TERMITE (*Zootermopsis angusticollis*) GUT

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**Introduction.** Cellulose represents the most abundant carbon source of the earth. However, it is a remarkably stable biopolymer that consist of glucose units linked by  $\beta$ -1,4 glycosidic bonds (1). An enzyme family commonly called cellulases carries out the hydrolysis of this molecule to release free sugars. The most important cellulases are Endoglucanase (endo- $\beta$ -1,4-glucanase, EC 3.2.1.4), Celobiohydrolase (exo- $\beta$ -1,4-glucanase, EC 3.2.1.91) y  $\beta$ -Glucosidase (EC 3.2.1.21). All of them are used in a wide range of biotechnological process including textile, paper industry, animal feeds (2), and also, the biofuel industry (3). The biofuel production represents a novel clean energy source. However, at present the high cost of the enzymes limits their massive use. The objective of this experiment was to screen the termite gut to look for novel bacteria encoding for cellulases with potential to be used in biotechnological process.

**Methods.** Bacteria were isolated from the gut of termite (*Zootermopsis angusticollis*). Cellulase activity was determined using plate-based assays containing carboxymethyl cellulase (CMC) as substrate (20mg CMC/plate). RAPD-PCR was used do differentiate colonies purified. Bacteria possessing high cellulase activity were selected for analysis of partially sequenced 16S rDNA genes.

**Results.** 29 potentially different colonies were isolated. However, RAPD-PCR reveled only nine different strains. Sequence comparison of obtained partial 16S rDNA sequences with BLAST database (Table 1) indicate low identity with reported sequences for some of the isolated colonies. The CMC assay showed that the strains C-1.1, C-2.10, C-2.7, C-2.3, C-7.12 and C-2.11 had the best behavior consuming 39.06, 39.06, 34.14, 27.3, 25.22 and 21.05 mg CMC at 72 h of incubation, respectively (Figure 1). The

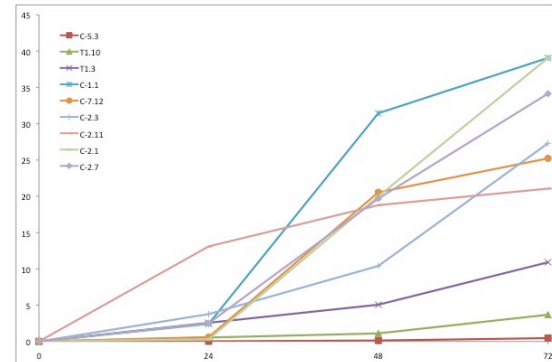


Fig.1 Degradation of CMC by nine strains of bacteria isolated from the termite gut.

Table 1. Sequence comparison of the obtained partial 16S rDNA sequences with the BLAST database.

Strain	GenBank reference	% Identity
C-1.1	HQ008633	79
	EU464477	80
C-2.10	DQ466089.1 <i>Bacillus cereus</i>	77
C-2.7	JX575993.1 <i>Rummeliibacillus</i>	98
	sp.	
C-2.3	JQ607776.1	97
C-7.12	JX575993.1	98
C-2.11	KC236752.1 <i>Bacillus</i> spp.	96
T1.3	JQ271583.1 <i>Rummeliibacillus</i>	99
	sp.	
T1.10	EU464477.1	96
C-5.3	NR_043860 <i>Trabulsiella odontotermis</i>	99

**Conclusions.** The strains C-1.1, C-2.10, C-2.7, C-2.3, C-7.12 and C-2.11 had the best potential to be used as gene donors.

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