Description of Bacterial and Archaeal Consortia from the Gut of the South American Termite *Cornitermes cumulans*

Grieco,M.A.B.[a]; Cavalcante,J.J.V.[a]; Cardoso,A.M.[a]; Medeiros,M.N.[a] Vieira,R.P.[b£], Machado, E.A [b¶].; Clementino,M.B.M[c]; Albano,R.M [d]; Garcia,E.S[c]*; Souza,W.[b¶]; Constantino,R.[e] and Martins,O.B.[b]

[a] Diretoria de Programas (DIPRO), Instituto Nacional de Metrologia, Normalização e Qualidade Industruial (INMETRO) Duque de Caxias – RJ. Brasil

[b] Instituto de Bioquímica Médica (IBqM) and [¶] Instituto de Biofísica Carlos Chagas Filho (IBCCF) - Universidade Federal do Rio de Janeiro (UFRJ) rio de Janeiro RJ Brasil

[c] Instituto Nacional de Controle de Qualidade em Saúde (INCQS) and *Instituto Oswaldo Cruz (IOC) – Fundação Oswaldo Cruz (FIOCRUZ) Rio de Janeiro RJ Brasil;

[d] Departamento do Bioquímica. Universidade do Estado do Rio de Janeiro, Rio de Janeiro, RJ, Brasil

[e] Departamento do Zoologia- IB -Universidade de Brasília – Brasília, DF, Brasil

Cellulose is the most abundant biomass in the world and there is great interest both for basic and biotechnological research to further understand the mechanisms employed by different organisms to extract energy and survive using exclusively lignocellulose degradation. Termites are the major decomposers in the detritus food chain and the microbiota from their gut is responsible for most of the biomass degradation. These Isoptera are excellent research subjects for studying the interactions among microbial species and the numerous biochemical functions they perform to benefit their host. However, culture independent molecular studies have revealed that most of these microbial gut symbionts have not yet been identified. Accordingly, the aim of this study was to analyze the Bacteria and Archaea gut associated microbiota of the South American termite *Cornitermes cumulans* collected at Juiz de Fora, Minas Gerais, Brazil to increase our knowledge on the diversity of these microorganisms. Total genomic gut DNA was extracted and amplified using 16S rRNA specific primers for Bacteria and Archaea. The amplicons were ligated into the pGMT vector and grown in *Escherichia coli* for sequencing. Analysis of the bacterial clone library showed a remarkable high diversity of lineages within the Bacteria. We identified predominantly members of the phyla *Spirochetes*, followed by *Bacteriodetes*, *Firmicutes*, *Actinobacteria*, *Fibrobacteres* and *Planctomycetes*. In the Archaea clone library we observed new phylotypes (clones sharing > 97% sequence identity were grouped in the same phylotype). Most Archaea clones belonged to divergent lineages more related with the Crenarcheota than with Euryarcheota phylum although a few clones were related to this later group, including one clone related to methanogenic Archaea. To describe this group, DNA samples were PCR amplified using methyl coenzyme M-reductase specific primers and the amplicons were cloned as described above.

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