

ASSESSMENT OF THE FUNGAL DIVERSITY IN ENERGY TRANSMISSION TOWERS BY ITS-rDNA CLONE LIBRARIES

Author(s) Michel Rodrigo Zambrano Passarini¹, André Rodrigues², Lara Durães Sette¹

Institution(s) 1. UNICAMP, Universidade Estadual de Campinas, Rua Alexandre Cazelatto, 999 - Vila Betel, Paulínia, SP - CEP 13140-000, Brazil 2. UESC, Universidade Estadual de Santa Cruz, Rodovia Ilhéus-Itabuna - Ilhéus, BA - CEP 45662-900, Brazil

Abstract:

In the present work we profiled the fungal community associated with Brazilian energy transmission towers using culture-independent techniques. Clone libraries were constructed for two screw samples (A and B) presenting signs of corrosion and/or biofilm associated and two samples (C and D) of corrosion dust from energy transmission towers located in São Paulo state. Prior to DNA extraction, samples were kept in peptone water for 10h (100 rpm, 25°C), followed by a centrifugation step to recover material for DNA isolation. Amplification and DNA sequencing of clone libraries used primers ITS1F and ITS4 for ITS-rDNA gene region. Assembled contigs were compared with sequence data available at NCBI-GenBank using BLASTN. In addition, phylogenetic analyses were conducted in MEGA 4.0 to better resolve taxonomic position of sequences. Community structure comparisons were carried out using species richness diversity indices calculated in DOTUR. A total of 288 clones were obtained (96 clones/library) for samples B, C and D (amplification failed for sample A). However, 160 out of 288 clones generated high-quality sequences used in the diversity analysis (51, 58 and 51 sequences for libraries B, C and D, respectively). Results revealed a total of 30 operational taxonomy units (OTUs) including 20 related to filamentous fungi and 10 related to yeasts. Representatives of phylum Ascomycota (141 clones) included the genera *Capnobotryella*, *Devriesia*, *Fusarium*, *Strelitziana* and *Teratosphaeria*; on the other hand, representatives of phylum Basidiomycota (19 clones) included the genera *Cryptococcus*, *Fellomyces*, *Kockovaella*, *Panaeolus*, *Rhodotorula*, *Sirobasidium*, *Sporobolomyces* and *Tremella*. Fungal communities from samples B and D presented similar species richness according with the diversity indices and rarefaction curves. On the other hand, clone library from sample C showed significant higher species richness when compared with the other libraries and rarefaction curves indicated that more clones would be necessary to cover the original diversity of this fungal community. The fact that fungi are associated with metallic surfaces presenting signs of corrosion point out for future studies on the role of such microorganisms in MIC. Financial Support: Bandeirante Energia S/A and Fapesp

Key words: fungal community structure, microbial corrosion, culture-independent technique