TITLE: BIOCHEMICAL PROFILE AS A TOOL-HELPING FOR IDENTIFICATION OF ENVIRONMENTAL AEROBIC ENDOSPORE-FORMING BACTERIA

AUTHORS: MARTINS, P.H.R.¹; RABINOVITCH, L.²; VIVONI, A.M.²; BRITO, J. T.¹; CAVALCANTE, D.A.¹; OREM, J.C.¹; MAGALHÃES, M.I.A.¹; ARAUJO, A.S.¹; DINIZ, C.C.¹; DE-SOUZA, M.T.¹

INSTITUTION: 1. UNIVERSIDADE DE BRASÍLIA, DISTRITO FEDERAL, DF (CAMPUS UNIVERSITÁRIO DARCY RIBEIRO, BRASÍLIA – DF. CEP 70.910-900) - BRASIL; 2. FUNDAÇÃO OSWALDO CRUZ – INSTITUTO OSWALDO CRUZ, RIO DE JANEIRO, RJ (Av. Brasil, 4365, MANGUINHOS – RJ. CEP 21040-900) – BRASIL.

ABSTRACT:

Aerobic endospore-forming bacteria (AEFB) embrace species from the genus Bacillus and related genera, allocated on phylum Firmicutes, within the class Bacilli, order Bacillales which encompass seven out of nine families assigning endospore-forming members. AEFB are widely distributed in natural environments being soil the main repository. Though Bacillus spp. were some of the first bacteria ever characterized, the wide range in physiological and genetical diversity makes the demarcation of genus and species a very difficult task. The traditional biochemical, morphological and physiological characteristics are essential tools for identifying aerobic endospore-formers. These features include growth at different temperatures, pH values, salt concentrations, growth in the presence of various substances such as antimicrobial agents, and data on the presence or activity of various enzymes and metabolites. The diverse physiology of AEFB requires elaborate biochemical tests for identification. The aerobic endospore-forming bacteria Collection (CBafes)/UnB houses 312 environmental (SDF) strains isolated by heat-shocking soil from the Federal District, Brazil. As part of a polyphasic carachterization approach, 24 biochemical tests of 57 randomicallyselected strains were performed. The results obtained were analyzed using the ABIS online identification platform. The genus Bacillus was predominant (87,72%) and the remaining 12,28% was distributed among genera Lysinibacillus (5,26%), Brevibacillus (3,51%), and Paenibacillus (3,51%). B. pumilus (75,43%), B. amyloliquefaciens (3,51%), L. sphaericus (3,51%), and P. validus (3,51%) were the most prevalent species. These results are being compared to 16S rDNA sequence-based phylogeny, 23 complete genome sequences among other polyphasic taxonomy approaches aiming a consistent identification and classification of the SDF strains.

Keywords: Firmicutes; Sporulation; Polyphasic Characterization; Bacillus Phenotype

Development Agency: Universidade de Brasília, Fundação de Apoio a Pesquisa do Distrito Federal (FAP-DF) and Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq).