

**MOLECULAR ANALYSIS OF ENDOPHYTIC BACTERIA ISOLATED FROM
TROPICAL MAIZE (*Zea mays* L.)**

Figueiredo, J.E.F.¹, Coelho, V.T.S.², Zuccherato, L.W.², Marra, L.M.³, Neves, N.A.³,
Silva, H.P.⁴, Luciano, E.S.⁵.

¹Embrapa, Minas Gerais, Brazil; ²Departamento de Bioquímica, UFMG, Minas
Gerais, Brazil; ³UFVJM, Minas Gerais, Brazil; ⁴UFMG, Minas Gerais, Brazil;
⁵UNIFENAS, Alfenas, Minas Gerais, Brazil.

Endophytic bacteria play important roles in agriculture by improving plant performance and adaptation against biotic and abiotic stresses. Nevertheless, studies on endophytic communities in tropical ecosystems are still limited. Molecular methods were used for identifying endophytic bacteria from tropical maize (*Zea mays* L.). Electrophoretic profile (SDS-PAGE) of total protein extract revealed a high level of polymorphism with a high number of scrutinable bands. Among twenty-five colonies, six were identified as duplicates. Partial sequencing of 16S ribosomal gene was performed in attempt to verify the authenticity of SDS-PAGE. Among isolates with similar protein profile, four were confirmed as replicates and two were different strains. 16S rDNA sequences comparison in Genbank revealed nine unidentified species of bacteria, nine *Bacillus subtilis*, five *B. pumilus*, one *B. licheniformis* and one *B. amyloliquefaciens*. RAPD analysis using twenty random primers showed a high degree of polymorphism within and among species. Phylogenetic relationship applying RAPD markers was in accordance with rDNA sequencing results. According to the present study SDS-PAGE may be used as a fast and cheap first step method for identifying inter-specific variation in maize endophytic bacteria, rDNA sequencing may be applied for identifying strains with similar protein profile and RAPD may be useful for phylogenetic studies.

Key words: endophytic bacteria, maize, SDS-PAGE, RAPD, rDNA sequencing