## PS3-12 Metabolic diversity of diazotrophic bacteria isolates from Brazilian maize and sorghum cultivars by the biolog system

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Brazil is an emerging agricultural power potential of millions of hectares available for agricultural expansion. The main challenge of the Brazilians is to keep the high productivity of the agrobusiness, and still keep the environmental, economic, and social pressures under control. Biological nitrogen fixation in association with maize and sorghum plants offers an economically attractive and ecologically sound means for sustainability agriculture. The present study was conducted to evaluate the variability among diazotrophic bacteria from maize (M) and sorghum (S) grown under different edafoclimatic conditions. Diversity of 47 isolates of diazotrophic bacteria, with variable morphological characteristics obtained from roots (R), sap (S), silk (E), and from immature maize grains (G), was determined based on differential carbon substrate utilization profile by the Biolog system with GN2 Microplates. The resulting differences were analyzed using Jaccard's similarity coefficient and UPMG clustering. Diversity was calculated using the Shannon index. Dendrograms of metabolic diversity data (presence or absence of growth in different carbon substrates) revealed that the isolates are classified into nine apparent clusters. Cluster A comprises 31 isolates; cluster B includes one isolate; cluster C, two isolates (MR10 and SR6); cluster D, two isolates (SS2 and SS3); cluster E, three isolates (MR6, MG1, and MR7); cluster F, four isolates (MG2, MR8, AI1, and AI2); cluster G, one isolate (MS9), and cluster H with three isolates (MR1, ME, and MR9). In a comparative analysis with standard species, 66% of the strains were similar with *Azospirillum brasilense* (cluster A) and only 4% were more similar to *Azospirillum lipoferum* (cluster F). Results showed a high biodiversity among the different strains, but no correlation between the phenotypic groups and the origin of the strains was observed. Selected strains were subcultured for identification by 16s rDNA sequencing.