

Phylogenetic Study of Tuber Endophyte

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Abstract—Tuber crops are the second most important group of crop plants and among them tropical root and tuber crops which include cassava, sweet potato, yams and aroids are essential as staple food (FAOSTAT, 2013) and are utmost important for world food security. Aroids like *Amorphophalluspaeoniifolius* (Elephant foot yam). Plant roots comprise more than 50% of the plant's biomass. Endophytic microorganisms (both bacteria and fungi) are excellent sources of bioactive natural products which remain asymptotically inside plants have the potential of being exploited for their beneficial properties as well as application in agriculture, health, food sectors. We have isolated seven different endophytic colonies from three different tuber crop like *Amorphophalluspaeoniifolius*, *Colocasia esculenta*, *Ipomea batatas*. Following sequencing of 16S rRNA and phylogenetic analysis, the bacteria identified were: *Staphylococcus sciuri*, *Exiguobacteriumacetylicum*, *Achromobactermucicisolens*, *Bacillus subtilis*, *Bacillus xiamenensis*, *Exiguobacteriumindicum*, *Bacillus stratosphericus*. The Molecular Evolutionary Genetics Analysis version X (MEGA X) was used to construct phylogenetic tree, Nucleotide Similarity and Distance. These results will provide important knowledge on the diversity of endophytic bacteria inhabiting tuber crops and a better understanding of the microbiome can be exploited for future applications in areas of agriculture, medicine, and the environment.

Keywords: Endophytes, 16SrRNA, phylogenetic tree, tuber.