

**COST Action:** FA1103

**STSM title:** Endophytic microbial communities associated with the cocoyam (*Xanthosoma sagittifolium*) crop

**Reference:** ECOST-STSM-FA1103-140915-063721

**STSM dates:** from 14-09-2015 to 25-09-2015

**STSM Host Institution:** Fondazione Edmund Mach (FEM), San Michele all'Adige, Italy

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**Activities:**

Automated ribosomal intergenic spacer analysis (ARISA), DNA-dependent fingerprinting approach was employed to assess the diversity of endophytic microbial communities associated with the cocoyam crop. Capillary electrophoresis was conducted on a ABI Prism 3130xl Genetic analyzer, equipped with a 50 cm capillary array filled with POP 7™ polymer. The electropherograms obtained from preliminary capillary runs were analyzed by employing the Gene Mapper 4.0 software and peaks normalization was done inside the experiment. The fluorescence threshold was set to 50 relative fluorescence units (RFU). More so, peak binning was set to 1.5 bp and manual correction was applied where peak shifts occurred. Data obtained was exported as an excel file following which operational taxonomic units (OTU) frequencies were scored as 0 or 1 indicating presence or absence respectively, in each of the treatments. Data was analyzed using the Past3 statistical software. The rest of the samples will be analyzed after capillary runs have been completed.

Following the ARISA analysis, a Next Generation Sequencing – NGS – approach was designed to facilitate an in depth understanding into how soil, environmental and genetic variables may be linked to the presence and the abundance of fluorescent *Pseudomonas* spp on the cocoyam rhizosphere. To do this, an Illumina library will be prepared comprising about 10 million reads for 80 DNA samples. The housekeeping genes for *Pseudomonas* spp, *rpoB* and *rpoD* will be employed for Illumina sequencing. The characteristic of the samples are as described below:

<b>Location/Precipitation</b>	<b>White-Healthy</b>	<b>White-Diseased</b>	<b>Red-Healthy</b>	<b>Red-Diseased</b>
Ado-Ekiti (1200 mm/yr)	10	10	10	10
Umudike (3000 mm/yr)	10	10	10	10

It is anticipated that the results obtained will contribute to our understanding of the different drivers of bacterial community composition in the tropical cocoyam crop thereby enabling better choices to enhance beneficial bacterial populations and overall plant health against the cocoyam root rot disease.