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**"Screening root-endophyte diversity in *Musa spp.* to  
manage *Fusarium oxysporum* f. sp. *cubense*, the causal  
agent of Fusarium wilt of banana"**

**Master Thesis**

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## Abstract

Bananas play key roles in food security and income generation worldwide. Fusarium wilt, caused by the soil-borne pathogen *Fusarium oxysporum* f. sp. *cubense* (Foc) is frequently ranked as a major threat mainly for smallholder farming system. Resistant varieties are the best control practice, but are either not available or do not meet market standards. As chemical and cultural control practices are nearly not effective, new strategies such as the use of biocontrol agents are urgently needed. Tissue-culture disease-free planting material is one of the main measures to manage Foc. However, these plants are more susceptible than conventional suckers. The fact that the *in vitro* culture process also removes endophyte microbial community has been highlighted as a possible cause. Due to the different mechanisms associated endophytes provide, inoculation of tissue-culture plants with a set of beneficial endophytic microorganism could improve plant fitness including resistance to Foc. In the assumption that wild species or ancient banana genotypes, which never passed through tissue-culture process, are sources of novel endophytes, a core collection of root-associated endophytic microorganisms from 20 *Musa* spp. genotypes was developed in this study. Further characterization included rDNA sequencing as well as *in vitro* and *in vivo* tests to evaluate antagonistic behaviour against Foc and growth promotion potential. A total of 360 bacterial and 143 fungal isolates were obtained. Twenty representative fungal and 20 representative bacterial isolates were further identified by phenotypic characterization and / or specific genome region sequence analysis. Most frequent bacteria genera found include *Klebsiella*, *Enterobacter*, *Bacillus*, *Acinetobacter* and *Burkholderia* in this order, while *Trichoderma* spp. and *Fusarium oxysporum* prevailed among fungi. Most of the identified isolates were already known to colonise *Musa* spp. However, some genera such as *Sphingobacterium*, *Grimontella*, *Providencia*, *Pleosporaceae* were not reported yet and could be described for the first time in this study. In addition a set of microorganism with not significant similarities in the database analysed were also found and will probably constitute new descriptions. Antagonism *in vitro* assays revealed that some isolates reduced mycelia growth of Foc. YK024 (*Trichoderma asperellum*) inhibited Foc growth by 80.5% and YK037 (*Burkholderia cepacia*) by 37.5%. The bacterial isolate S010 was putatively identified as *Alcaligenes* spp. and increased Foc growth by 20.5%, which constitute a new finding. Preliminary studies in greenhouse conditions showed that some of the selected isolates increased banana growth compared to untreated control plants, but further studies are needed to reach any conclusion. This study generated the first insight on exploring root-associated endophyte microbial diversity from *Musa* spp., which constitute an unique source for identifying and use microorganisms with potential roles on providing ecosystem services on banana.