

## PhD Research Progress Report (2018-2019)

**TITLE:** Genetic analysis of resistances to *Fusarium oxysporum* f. sp. *cubense* (Foc) race 1 in banana (*Musa* sp.)

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**Timeline of study:** August 2015 – August 2019

**University:** Stellenbosch University, South Africa

### Research Objectives:

- To understand inheritance of banana resistance to Foc race 1
- To construct high-density genetic linkage map with a diploid population
- To map QTLs and identify SNPs markers associated with resistance to Foc race 1

### Objectives or study areas

- Segregation test for Paliama X Borneo mapping population for resistance to Foc race 1
- Phenotyping of Paliama X Borneo mapping population for resistance to Foc race 1
- Phenotyping Malaccensis X Malaccensis mapping population for resistance to Foc race 1
- Genotyping (SNP calling and linkage mapping)
- Marker-trait association (QTL mapping) for resistance to Foc race 1

### Achievements: Highlight significant achievements

#### Paliama X Borneo 190 F<sub>1</sub> genotypes

1. Paliama and Borneo differs in reaction to Foc race 1 with susceptibility and resistance respectively
2. F<sub>1</sub> genotypes showed continuous frequency distribution in reaction to Foc race 1
3. F<sub>1</sub> genotypes fitted 9:7 ratio a deviation from Mendel segregation
4. The phenotypic data for Foc race 1 consists of 162 (85%) Paliama X Borneo F<sub>1</sub> genotypes
5. DNA are extracted for 190 genotypes of Paliama X Borneo population based on CTAB
6. Genotyping were done for 190 genotypes based on DarT platform
7. 3,318 SNPs segregating in the F<sub>1</sub> population were identified

8. Linkage map (“Borneo map”) were constructed with 2778 SNPs mapped into 11 linkage groups
9. QTL analysis were conducted and three QTLs conferring resistance to Foc race 1 were detected (MapQTL software)
10. The SNPs markers flanking the detected QTLs were identified
11. QTLs detected revealed positive and negative additive gene effect to the resistance to Foc race 1

#### Malaccensis X Malaccensis 188 genotypes

12. The phenotypic data for Foc race 1 of 133 (70%) genotypes of Malaccensis X Malaccensis are available
13. The genotypes showed continuous frequency distribution in reaction to Foc race 1 with some skewness toward the resistant parent
14. The genotypes fitted 9:7 ratio a deviation from Mendel segregation

### **Background/introduction**

#### Brief background

Fusarium wilt, caused by *Fusarium oxysporum* f. sp. *cubense* (*Foc*), is a plant disease affecting many banana cultivars grown by smallholder farmers in the Africa Great Lakes Region. Long persistence of *Foc* in the soil and challenging facing fungicides applications complicates the control measures. Therefore, resistance among banana cultivars remain the most effective and sustainable management option. With the exception of the East Africa highland bananas (EAHB), most other banana cultivated in the East Africa region including “Sukari Ndizi” (AAB) and “Mchare” (AA) are susceptible to *Foc* race 1. *Foc* race 1 is thus considered a major banana production constraint in the Africa Great Lakes region.

Banana resistance to *Foc* race 1 has been reported in several wild diploid bananas as *M. acuminata* ssp. *malaccensis* and *burmannica*. However, introgression of resistance into edible cultivars is slow due to sterility and the long banana life cycle. Genetic markers for the early selection of resistance traits will speed up banana breeding for *Foc* resistance and other important traits. The development of genetic markers is currently hindered by the presence of relatively few banana-mapping populations and a lack of dense genetic linkage maps.

The aim of this study is to elucidate the genetics of resistance in banana and identify genetic

markers associated with resistance to *Foc* race 1, with the following objectives:

- To understand inheritance of banana resistance to *Foc* race 1
- To construct high-density genetic linkage map with a diploid banana population
- To map QTLs and identify SNPs markers associated with *Foc* race 1 resistance.

The findings from this study could be of value for marker-assisted selection in banana breeding programs. This will consequently contribute to banana improvement in the African Great Lakes region. This study will be conducted at IITA Arusha station and at the Plant Pathology facilities at Stellenbosch University.

### **Objective / Study 1**

#### **To understand inheritance of banana resistance to *Foc* race 1**

- Evaluation of Paliama x Borneo genotypes for resistance to *Foc* race 1
- Method: Millet seed inoculation technique as described by Viljoen *et al.* (2017)
- Results:
  - Paliama and Borneo differs in reaction to *Foc* race 1 with susceptibility and resistance respectively
  - F<sub>1</sub> genotypes showed continuous frequency distribution in reaction to *Foc* race 1
  - F<sub>1</sub> genotypes fitted 9:7 ratio a deviation from Mendel segregation
  - The phenotypic data for *Foc* race 1 consists of 162 (85%) Paliama X Borneo F<sub>1</sub> genotypes
  - DNA are extracted for 190 genotypes of Paliama X Borneo population based on CTAB

### **Objective / Study 2**

#### **To construct high-density genetic linkage map with a diploid population**

- Methods: SNP calling and linkage mapping analysis with JoinMap version 4.1
- Results:
  - Genotyping were done for 190 genotypes based on DarT platform
  - 3,318 SNPs segregating in the F<sub>1</sub> population were identified
  - Linkage map (“Borneo map”) were constructed with 2778 SNPs mapped into 11 linkage groups

### **Objective / Study 3**

#### **Mapping of QTLs and identifying SNPs markers associated with Foc race 1 resistance in banana**

- Method: QTL mapping will be done with Map QTL
- Results:
  - QTL analysis were conducted and three QTLs conferring resistance to Foc race 1 were detected (MapQTL software)
  - The SNPs marker loci flanking the QTLs were identified
  - QTLs detected revealed positive and negative additive gene effect to the resistance to Foc race 1 in banana

#### **Conclusion / next steps**

- Inheritance of resistance to Foc race 1 in Paliama x Borneo population revealed to fit quantitative models
- The more saturated linkage map than the previously reported were constructed
- Three QTLs were detected an indication that resistance to Foc race 1 is controlled by more than one gene
- Multi environments evaluation of the Paliama x Borneo population for stability of the QTLs
- Validation of the QTLs and the confirmation of the flanking SNPs markers associated with resistance to Foc race 1