Progress Report

TITLE: Genetic analysis of resistance to *Radopholus similis* in Banana

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Timeline of study: 2016-2018

University: Makerere University

Research Objectives

1. To determine the reaction of banana improved diploids (F_1 hybrids) to *R. similis*.
2. To determine the number of genes controlling resistance to *R. similis* in banana.
3. To identify Quantitative Traits Loci (QTLs) associated with resistance to *R. similis* in banana.

Achievements

- MSc thesis was submitted and defended on December 11, 2019 and graduation is scheduled on January 14, 2020.
- The work has been presented in African Plant Breeders Association (APBA) conference, from October 23rd – 25th, 2019, University of Ghana, Accra.
- The work has been presented in NARO-MAK conference, from 12th -15th November 2018 at the Speke Resort Munyonyo, Kampala.
- Paper containing results from the first two objectives is under preparation

Background/introduction

Banana is grown in 135 countries but mostly found in tropical and subtropical regions around the world. Its production is around 145 million metric tons worldwide which values 26.5 billion euro making banana the most important stable food crops and actually, the world's most popular fruit in terms of international trade (Brown *et al.*, 2017) .

R. similis is the most destructive species in banana and so far resistant varieties, a sustainable and cheaper way of managing them, have not yet been developed (Jenny *et al.*, 2009). Breeding for resistance requires, firstly to identify potential parents with resistance that can be used to transfer the genes (Schutter *et al*., 2001). Heritability and mode of inheritance are key elements to be focused on in designing the breeding approach and breeding strategy

(Acqaah, 2012; Roger & Richard, 1992). Resistance to *R. similis* was reported to be both oligogenically (Dochez 2009) and polygenically (Swai 2016) inherited, therefore clear knowledge about heritability and number of loci controlling resistance to *R. similis* is necessary and it will be very helpful in making the choice of the best banana breeding approaches and choice of the parents. Long cycle of banana crop make conventional banana breeding slow and expensive therefore molecular tools to speed up this breeding are necessary (Nyine *et al*., 2018). Molecular marker technology helps to dissect, to characterize complex traits and to identify beneficial allelic variants. Once markers associated with the traits of interest are identified, they can be used in breeding programs to more efficiently and effectively identify desirable plants from a population. One approach to identify such markers is QTL mapping (Sartie, 2006). So far in banana, there was no report about any work done on identifying QTLs associated with resistance to *R. similis* or any other species of nematodes. This research aimed at understanding the nature of inheritance of resistance to *R. similis* and identify genomic regions controlling this resistance in banana.

Summary of the study

Banana is an important crop worldwide mostly grown in tropical and subtropical regions, of annual production is 145 million metric tons valued at 26.5 billion Euros. Banana production is threatened by various constraints including pests and diseases. Among the pests, *Radopholus similis* is the most destructive species. East African Highland Bananas mostly grown in Uganda and other parts of East Africa are highly susceptible to this species with yield reduction reaching 80%. Breeding for resistance is the only sustainable way of controlling this pest. Unfortunately, banana breeding is limited by many factors such as long cycles. Heritability and mode of inheritance are key elements in determining the appropriate breeding approach and strategy, and interventions aiming at speeding up the breeding cycle for this crop are highly needed. The aim of this study was to understand the inheritance pattern of resistance to *R. similis* and determine genomic regions in the banana genome which are responsible for that resistance. The study was conducted in IITA-Uganda in 2017 and 2018 using a multi parent population produced from crosses between two types of Zebrina GF (susceptible) and Calcutta 4 (resistant) with the two Zebrina GF used as male and Calcutta 4 as female. Yangambi Km5 was used as a resistant control, while Valery was used as susceptible control. The study was conducted in 7 series and genotypes were arranged in a randomized complete block design. The single-root nematode screening method was used, and data were collected on total nematodes count and root damage as necrosis. The final

nematode population of each genotype was compared with the final nematode population of each of the controls. The analysis of variance using Genstat 19th edition showed a significant variation of the genotypes for total nematodes count and necrosis damage. The traits had moderate heritability of 56% and 43% (for nematode reproduction and necrosis damage respectively) and they were positively correlated (r= 0.48). Out of 104 genotypes screened, 11 were resistant, 39 partially resistant, 54 susceptible. For the QTLs identification, the same material highlighted above was genotyped using Diversity Array Technology – sequencing (DArTSeq) platform that generated 88,947 SNPs. Genstat 19th edition was used to run the QTL analysis for the two traits with a total of 21,266 filtered SNPs. The analysis revealed 7 putative QTLs associated with *Radopholus similis* in banana located on chromosomes 1, 2, 3 4 and 9.

Conclusion

The improved banana diploid population used in this study was geneticaly diverse with different level of resistance to *R. similis* making this population a useful resource for future banana breeding activities targeting *R. similis* resistance. During screening or selection for banana resistance to *R. similis,* root necrosis damage and nematode reproduction should always be considered together since these two traits were only moderately correlated. The phenotypic and QTLs mapping analyses revealed the quantitative nature of resistance to *R. similis* and its polygenic inheritance contributed by several genes.

Recommendations

Identified QTLs associated with resistance to *R. similis* can be used in banana molecular breeding programs targeted at increasing levels of resistance to *R. similis* after being validated with a larger and preferably different population. Deep candidate gene mapping is necessary to be sure of which genes within identified QTLs are really contributing to this resistance. This will make the banana breeding for *R. similis* resistance more efficient and accurate.