MSC Research Progress Report

TITLE: Development and application of transcriptome simple sequence repeat markers in genotyping banana weevils (cosmopolite's sordidus) in Uganda

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Timeline of study: 2017-2019

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Research Objectives

i. To develop C. sordidus transcriptome-based SSR markers

ii. To genotype banana weevil populations from different Uganda banana growing agro-ecological zones using the newly developed C. sordidus transcriptome-based SSR markers

Achievements

- MSc thesis was submitted and to defended 21st January, 2020
- Manuscript under review by co- authors

Background/introduction

Banana weevils *(Cosmopolites sordidus)* have been reported to cause significant yield losses and reduced banana plantation lives throughout different Uganda banana growing agro-ecological zones (Twesigye *et al.,* 2018b). In spite of the economic importance of *C. sordidus* very little genomic and transcriptomic information exists of this banana pest (Valencia *et al.*, 2016). Molecular markers such as RAPDs, AFLPs, internal transcribed rDNA (ITS1+ITS2) and the mitochondrial COI $tRNA^{Leu}$-COII region have been applied to study genetic diversity of banana weevils. With these markers, only significant genetic diversity was observed within banana weevil populations but not among populations (De Graaf, 2006; Kumar & Singh, 2018; Magaña *et al.*, 2007; Ochieng, 2002; Twesigye *et al.*, 2018a). As well, these markers are dominant and thus not all the genetic variation can be captured by them, as heterozygotes cannot be separately identified (Burow & Blake, 2019). There is currently very little *C. sordidus* genomic and transcriptomic information available (Valencia *et al.*, 2016). As a

result, Simple Sequence Repeat (SSR) markers which offer high information content, co-dominance, high polymorphism, high number of alleles per locus , locus –specific and readily amplified (Souza *et al.*, 2018; Wang *et al.*, 2019a) have not been developed and applied to study genetic diversity of banana weevils.

Summary of the study

Banana weevils *(Cosmopolites sordidus)* have been reported to cause yield losses of up to 100% and reduced banana plantation lives in Uganda. In spite of the economic importance of this insect pest, no genomic and transcriptomic simple sequence repeat markers have been developed to study its genetic diversity. This study was therefore carried out to develop and apply banana weevil transcriptome-derived SSR markers to genotype *C. sordidus* populations from different banana agro ecological zones (AEZs) of Uganda. Banana weevil populations were collected from 12 representative bananas growing districts of Uganda using pseudo stem traps and maintained in the laboratory for genotyping. *C. sordidus* transcriptome was obtained from the on-going RNAi work at the National Agricultural Research Laboratories Kawanda and assembled *de novo* in CLC genomic workbench 11 platform. A total of 2,089 potential microsatellites, 904 unique markers and 882 polymorphic SSRs were identified using GMATA software. Out of these, 27 microsatellites were selected and amplified in 12 *C. sordidus* populations. Six highly polymorphic SSR markers were able to successfully genotype within and among banana weevil population genetic diversity. These broad "within and among" weevil population genetic diversity could be explained by many factors including bottlenecks, founder effect due to banana weevil population segregation, inbreeding, natural and artificial barriers that regulate rate of gene flow, level of transportation of infected plantlets between different AEZs among others.

Conclusion

The study identified 6 highly polymorphic SSR markers which were used to successfully genotype within and among banana weevil population genetic diversity of 12 banana weevil populations taken from four Uganda banana growing AEZs. These markers identified a broad "within and among" weevil population genetic diversity which could be explained by many factors including bottlenecks, founder effect due to banana weevil population segregation, inbreeding, natural and artificial barriers that regulate rate of gene flow, level of transportation of infected plantlets between different AEZs among others.