



**2021 Virtual HBCU-UP/CREST  
PI-PD Meeting**



**Research Initiation Award:  
Search for the Epigenomic  
Mechanisms of Paternal  
Inheritance of Aggression in  
Social Honeybees**

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# Project Overview

- The overall hypothesis is that the m6A RNA methylation may modulate the paternal inheritance of aggression in social honeybees.
- The main **objectives** are to
  - 1) discover and quantify the distribution of m6A and potential paternal influence using colorimetrically quantification analysis in the brain mRNA of different generations (paternity hybrids and their parents);
  - 2) analyze the allele specific (parent-of-origin) gene expressions and gene alternative splicing events by a transcriptomic approach in the brain of Africanized paternity hybrids and their parents; and
  - 3) analyze the role of m6A residues in the allele specific (parent-of-origin) gene expressions via whole genome m6A-seq in the brain of Africanized paternity hybrids and their parents.

# Best Practices/Successes

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- 1. RNA methylation assay
- 2. Sample collection last summer and this summer
- 3. Nanopore sequencing ongoing

# Implications

- There is a significant difference of RNA methylation between honeybee queen and workers.
- Aggression assay from 2019 and 2020 field study showed F1 offspring of Africanized Honey Bees as paternal source are more aggressive than those of the reciprocal crosses.

# Identified Gap(s) for Future Collaboration or Enhancement

## RNA-seq analysis

- How many differentially expression and spliced genes in the F1 offspring?
- How many parent-of-origin genes?

## RNA methylation analysis

- How many differentially methylated genes?
- Do these genes have association with gene expression or splicing events?