

Population Genomics of the Coffee Berry Borer (CBB) Localities: Unveiling its Introduction, History and Genetic Variation in Jamaica

Ameka Myrie^{1*}, Errbii Mohammed², Lukas Schrader², Eva Schultner¹, Jan Oettler¹

¹ Zoology/Evolutionary Biology, Universität Regensburg, Universitätsstrasse 31, 93053 Regensburg, Germany

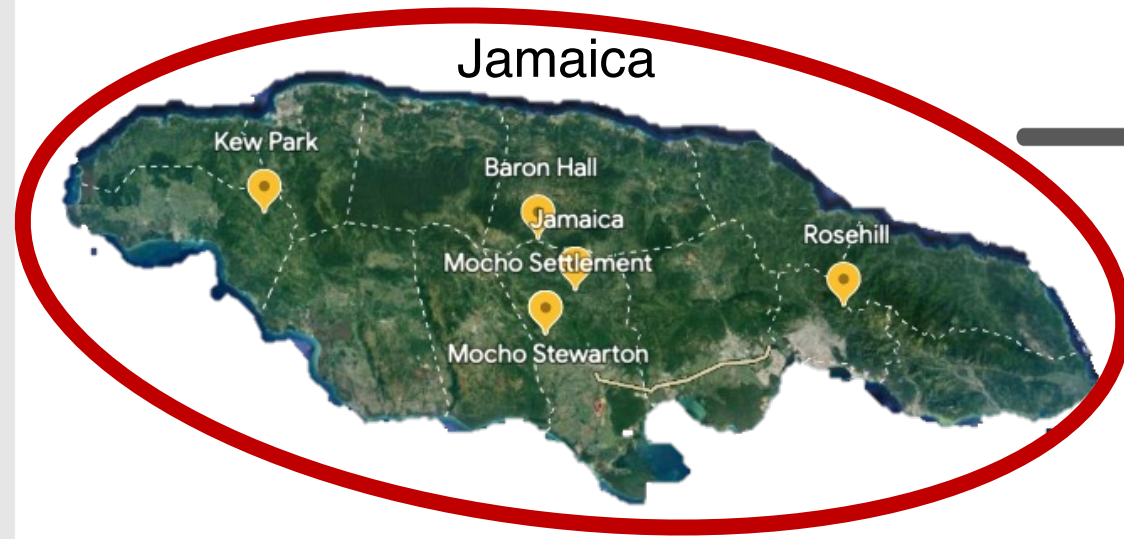
² Institute for Evolution and Biodiversity, University of Münster, Molecular Evolution and Social Biology Group

Rationale

- The Coffee Berry Borer (*Hypothenemus hampei*, Scolytinae, Curculionidae) has invaded all major coffee-producing areas in the world.
- The beetle is a model organism for studying rapid adaptation as it is a highly successful pest species.
- Females mate with their flightless brothers inside the coffee berry, before flying off to infest new berries, limiting gene flow.
- The CBB was discovered in Jamaica in 1978 and there is limited information about its evolutionary dynamics.
- We aimed to determine if Jamaican CBB populations originated from a single or multiple introduction events and to describe their genome-wide patterns of variation and differentiation ~40 years after their initial discovery.

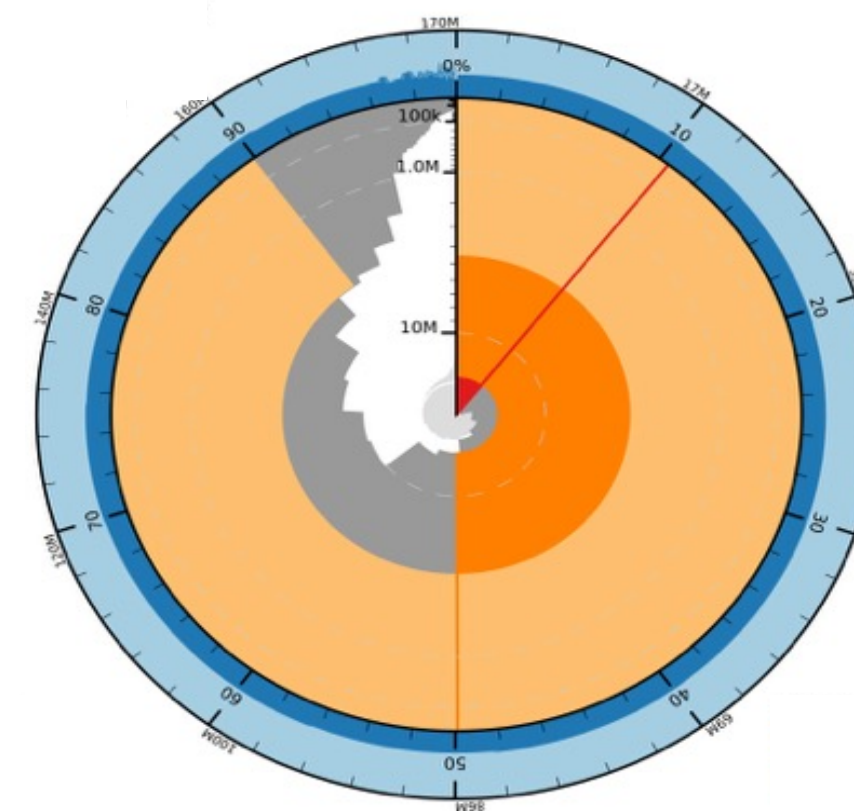
Methodology

Study Sites



Reference Genome via MinION Sequencing

Genome Assembly
BUSCO scores (against Endopterygota) based on 2124 genes:
Complete 98.9%
(Fragmented:0.3%, Missing:0.8%)



Protein annotation:
BUSCO scores (against Endopterygota) based on 2124 genes:
Complete 97.3%
(Fragmented:0.3%, Missing:2.4%)

Whole-Genome Sequencing

2 Pools of 40 CBBs from RH and BH, coverage 62x & 58x

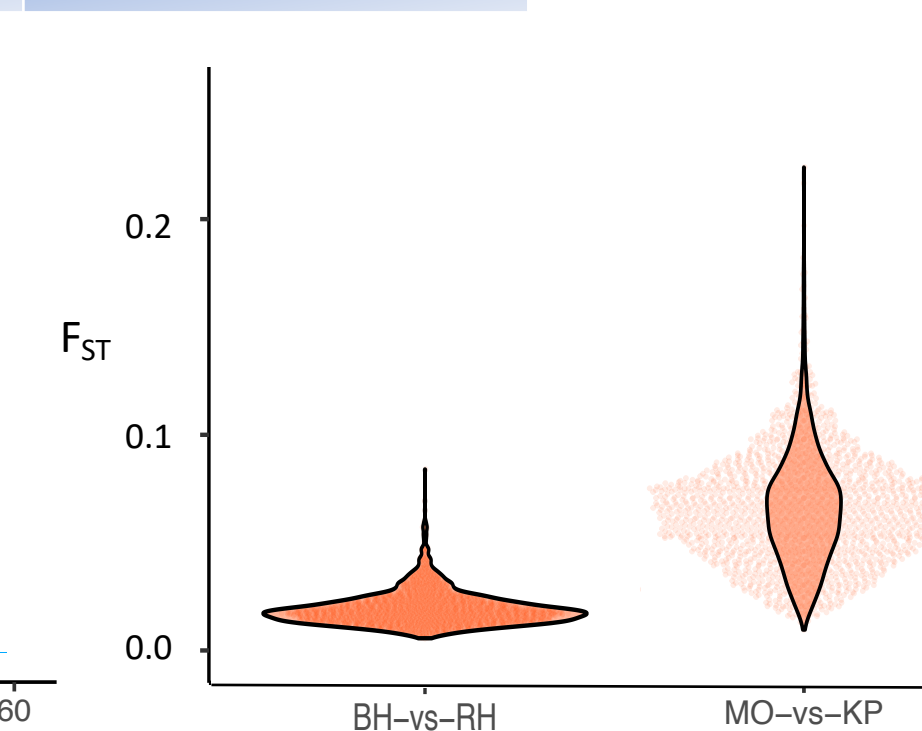
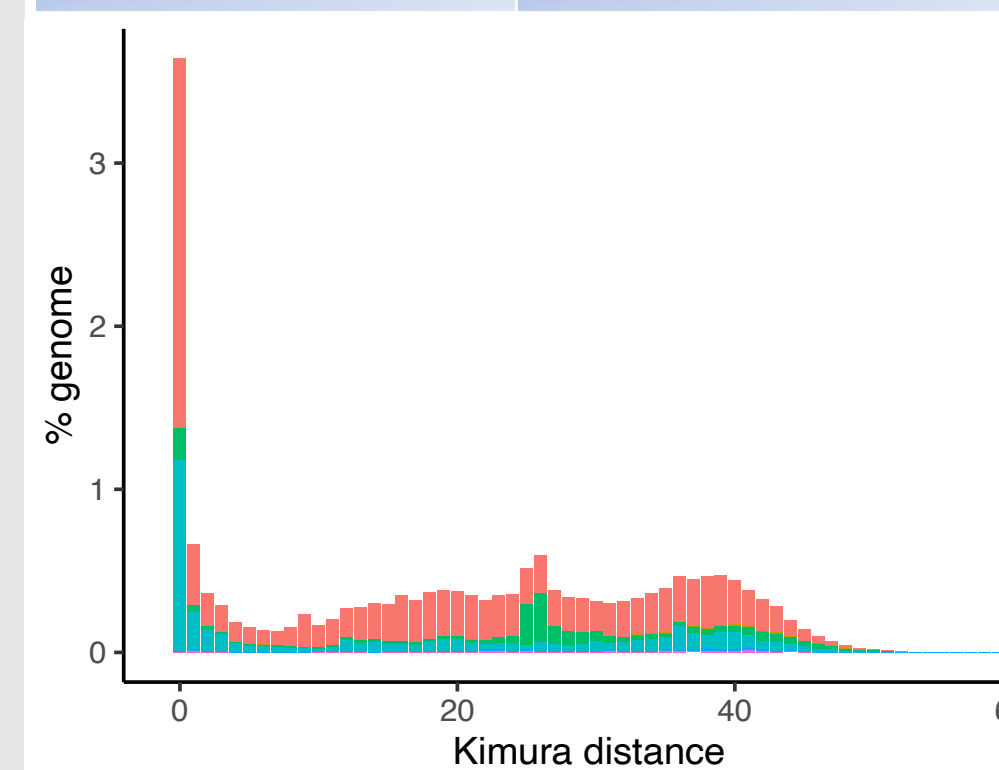
1 Pool of 33 CBBs from MO, coverage 40x

1 Pool of 21 CBBs from KP, coverage 55x

Genomic Analyses of seq data using Popoolation 1 and 2.

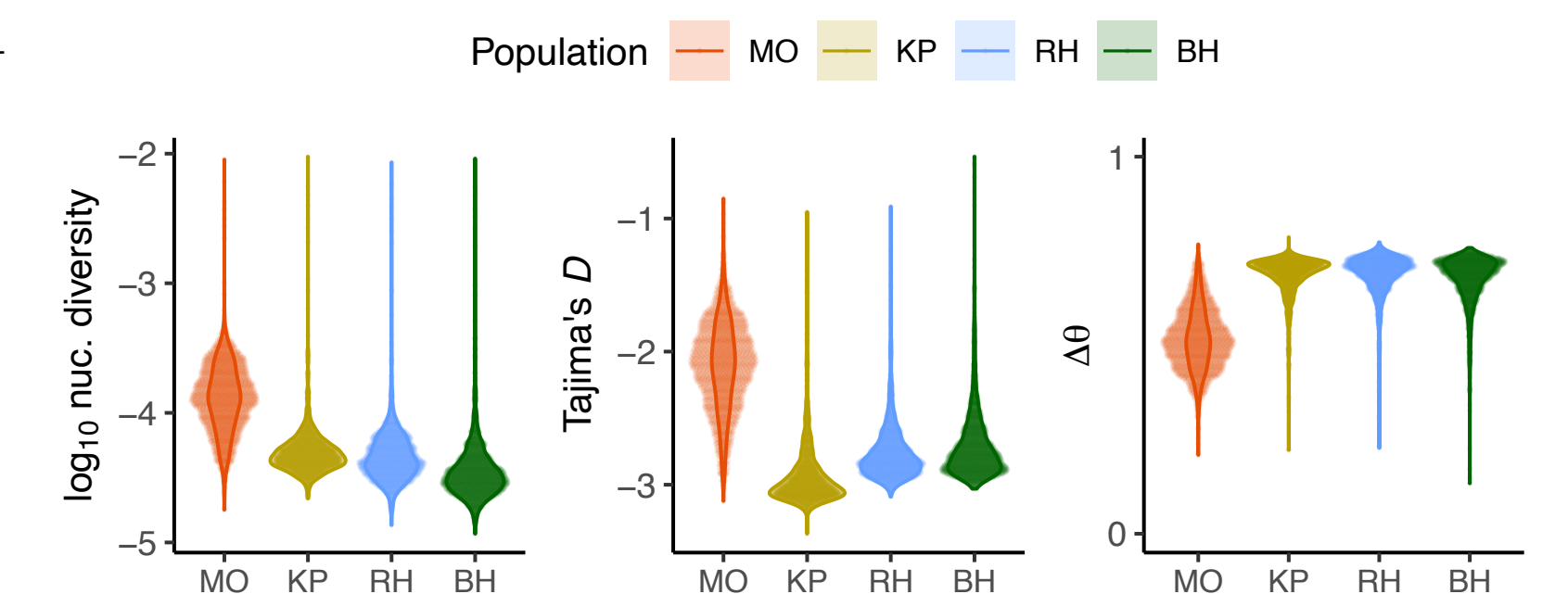
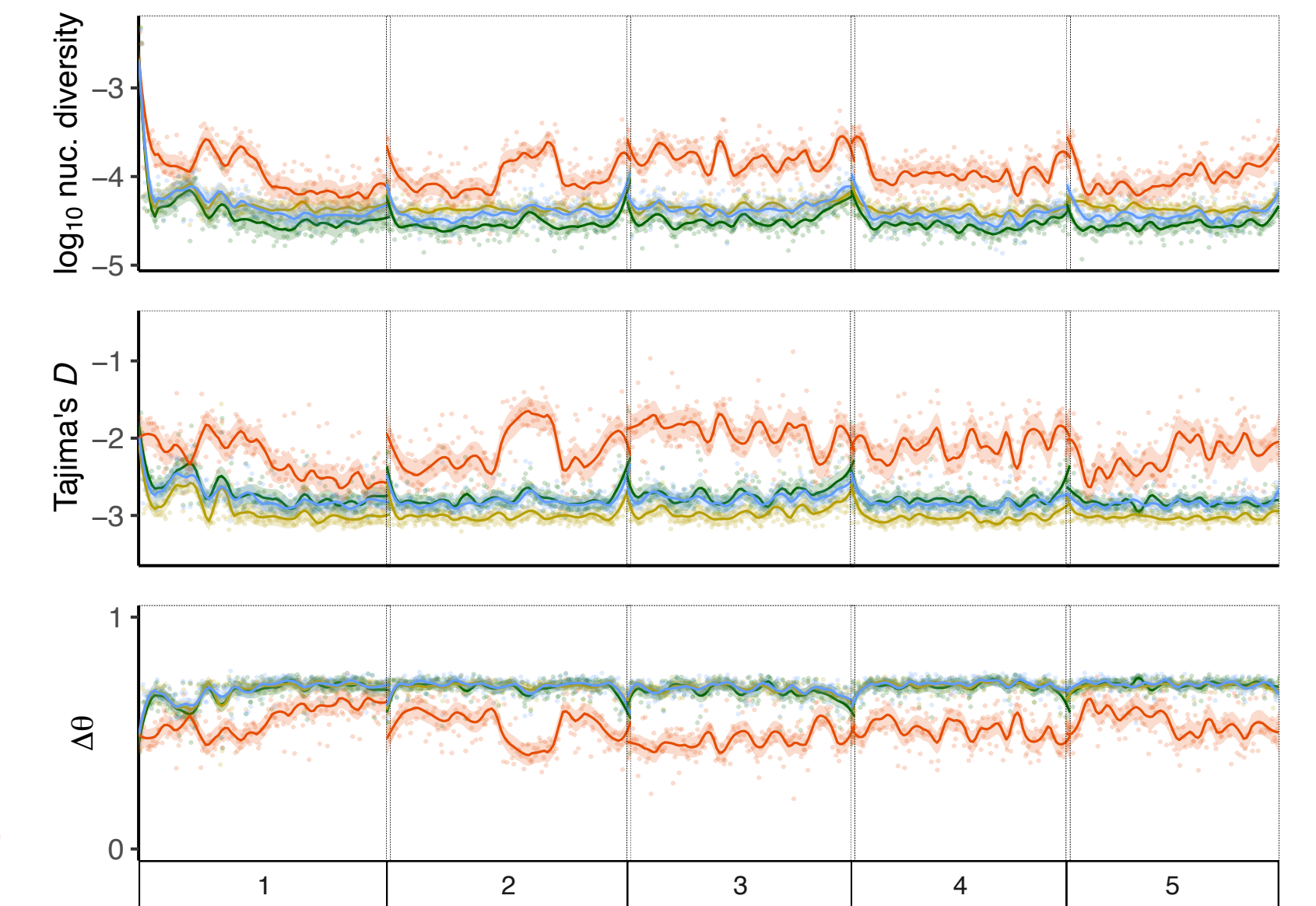
Results

Genome Assembly Statistics	Previous Genome	Our Reference genome
Size	163 Mb	170Mb
Longest scaffold	0.440 Mb	18 Mb
GC content	32.46%	32.6%
N50 contigs	0.011 Mb	14 Mb
TE Content	8.2%	28.89%



Genetic Differentiation between CBB localities across Jamaica

Active TEs found among the CBB localities across Jamaica



Nucleotide diversity, Tajima's D, and DeltaTheta (rare variants) among CBB localities in Jamaica

Conclusion and Perspectives

- The CBBs in Jamaica stem from one major introduction event.
- After 44 years and over ~250 generations after the CBB was first recorded in Jamaica, there is some genetic differentiation between the Jamaican localities.
- Transposable elements (TEs) exhibit activity throughout various locations and could potentially be responsible for generating genetic variation among the localities.
- This finding lays the basis for future studies of rapid adaptation of this important insect pest.