

## Goal .....

To contribute to the genetic improvement of cassava through the development and application of molecular biology and bioinformatics tools, supporting pre-breeding and genetic characterization processes.



## Where we work .....

Latin America and the Caribbean (LAC), Sub-Saharan Africa (SSA)  
South East Asia (SEA).



The boundaries and names shown on this map do not imply official endorsement or acceptance by the Alliance of Bioversity International and CIAT.

## How we do it .....

Through experimental research and data analysis focused on omics sciences.



### Cassava Genetics Lab

We conduct sequencing studies, high-throughput genotyping, molecular marker development, and bioinformatic analysis to create tools that enhance genetic characterization and marker-assisted selection in cassava.

## The impact .....



### DNA fingerprinting library

Use of this to enhance the accuracy in CIAT and NARs breeding programs; discovery redundancy in genebanks and field collections and understand varietal adoption in different market segments.



### Significant QTL

Was identified for whitefly resistance and new high-throughput phenotyping methods are being tested for this trait.



### Significant SNPs

Were identified for whitefly resistance, CBSD resistance, and small granule size. The markers associated with these QTLs have the potential to significantly enhance the efficiency of cassava breeding programs, offering a promising path for future research and applications. This potential impact on breeding programs is a key aspect of our results.

## Technologies



**Nucleic Acid Extraction Platform:** The lab offers both manual and automated methods for extracting DNA and RNA. Manual protocols yield high-quality, high-concentration nucleic acids, while the automated oKtopure system can process up to 768 samples per run, providing high-purity DNA for large-scale analyses.



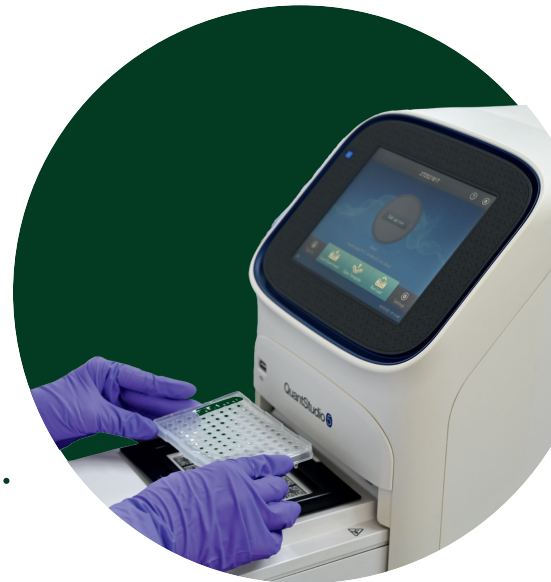
**Genotyping Platform:** Using Fluidigm’s SNPY-Chip technology, the lab conducts high-throughput genotyping to generate DNA fingerprints for cassava. Over 17,000 samples have been processed—the largest cassava genotyped collection globally—enabling varietal ID, duplicate detection, and genetic diversity assessments. The lab also uses KASP technology for small-scale genotyping and marker development to support cassava breeding.



**Flow Cytometry Platform:** The CyFlow Space system is used for ploidy analysis and genome size estimation in cassava and other plant species, supporting various research programs.



**Bioinformatics Platform:** This platform houses over 25,000 cassava sequences from diverse origins, generated using NGS methods like WGS, RADseq, Nanopore, DartSeq, and RNAseq. It provides workflows for genetic analysis (e.g., linkage mapping, QTL, GWAS, genomic prediction, phylogenetics) and is supported by a powerful server cluster with 400 cores and 2,000 GB RAM.



## Our Partnerships



**Leibniz-Institut**  
DSMZ-Deutsche Sammlung  
von Mikroorganismen  
und Zellkulturen GmbH

To know more about  
the program, visit us:



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