

The Digital Genebank and its contribution in mining alleles in cassava landraces for climate adaptation

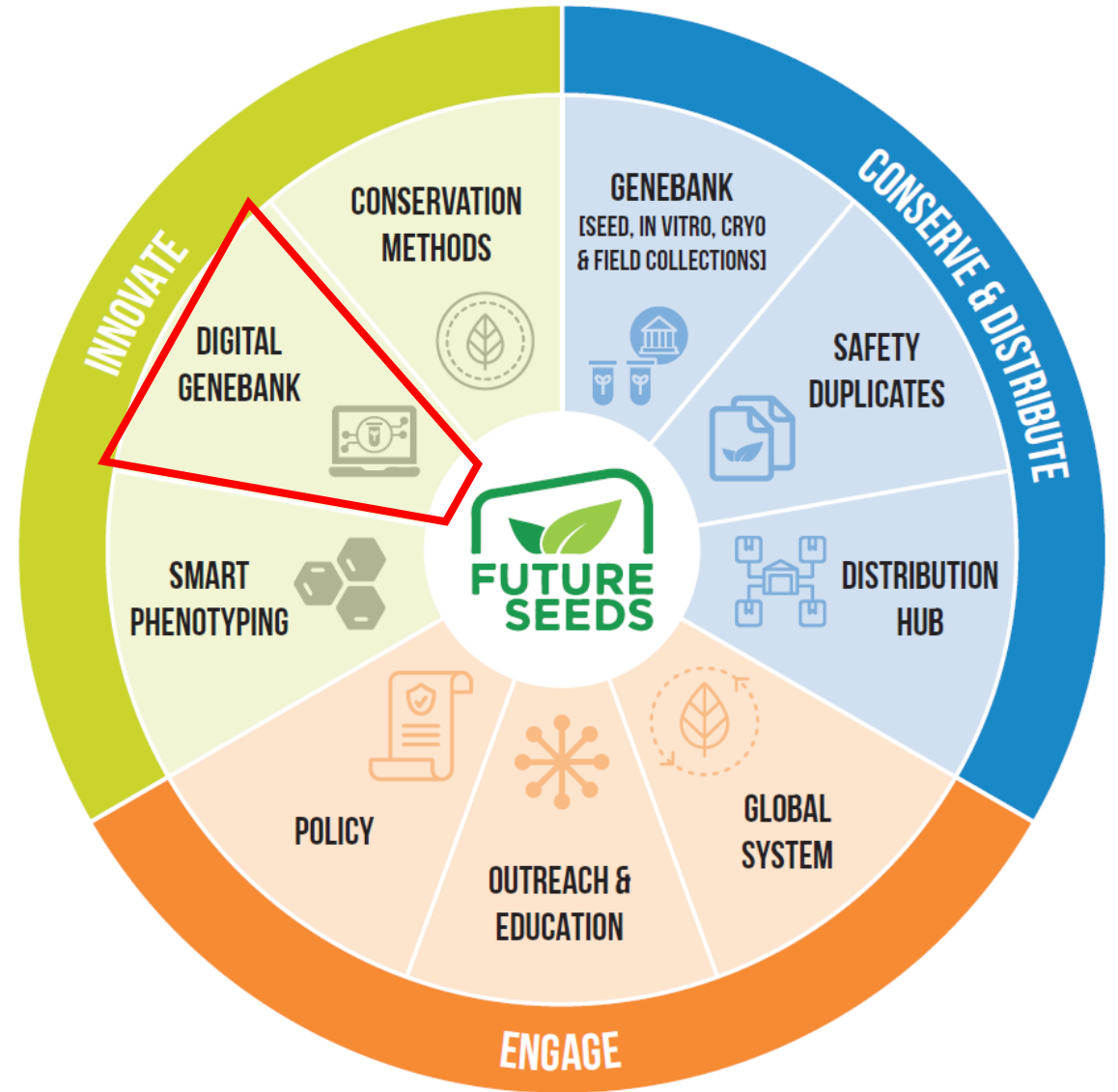
Monica Carvajal-Yepes PhD

Digital Genebank, Future Seeds



Leverage new technologies in genomics, in digital phenotyping and in information technologies to improve the conservation and use of crop diversity

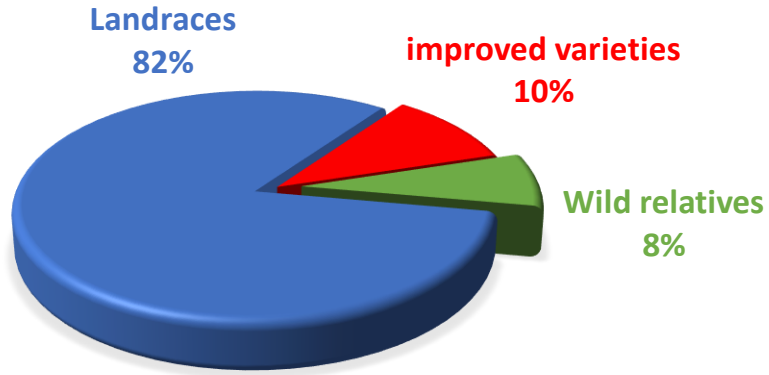
Cassava, Bean and Tropical Forages collections





Future seeds conserves the globally largest Cassava Collection

5,965
accessions



Extracted DNA



97% of the collection was genotyped

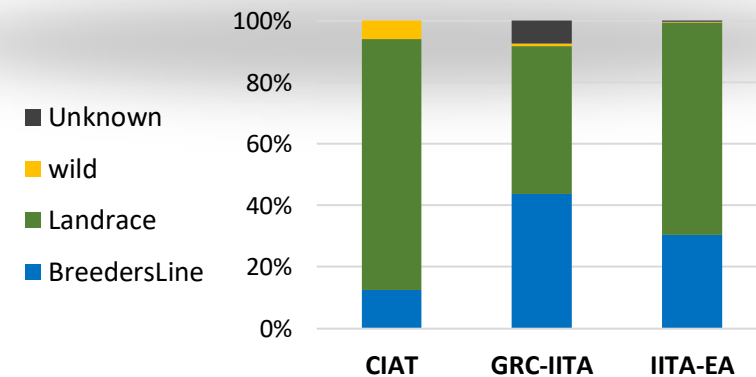
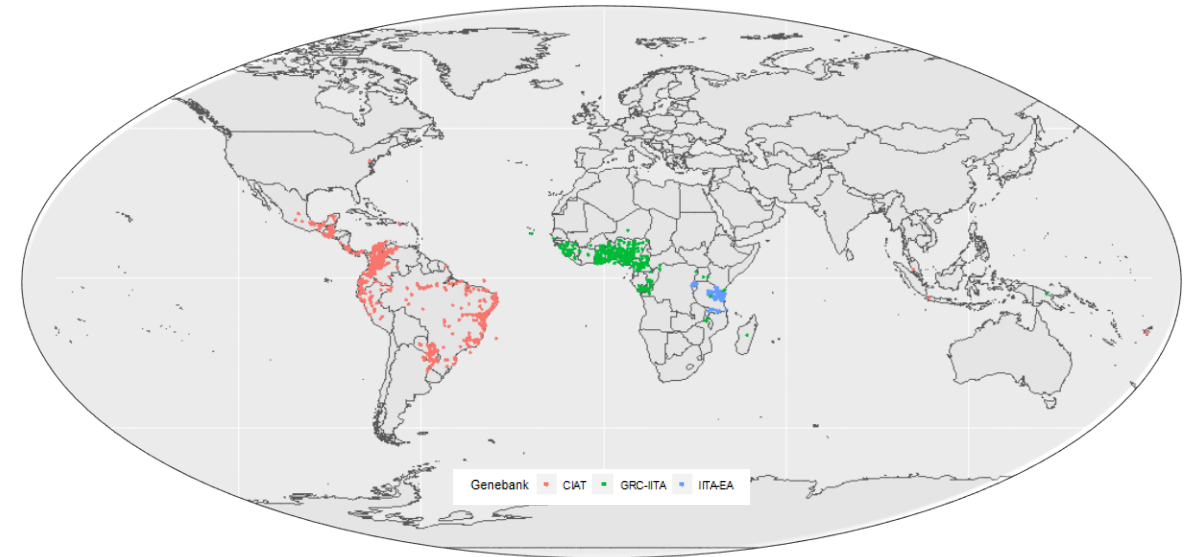
DArTseq
technology



ATT	CGC	CGT	AA		
--	T	CTC	CGT	AA	
ATT	CGC	CGT	CA		

2022: co-analysis of Alliance and IITA International Cassava Genebank Collections

Center / Status	Total	Lat/Lon
CIAT	6002	3826
Breeding Lines	753	478
* Landrace	4896	3120
wild	353	228
GRC-IITA	3222	1852
Breeding/Research material	1409	681
Landrace	1548	1129
Unknown	240	17
Wild relative	25	25
IITA-EA	952	491
Breeding	289	10
Landrace	658	480
Unkown	4	
wild-hybrid	1	1
Total	10176	6169



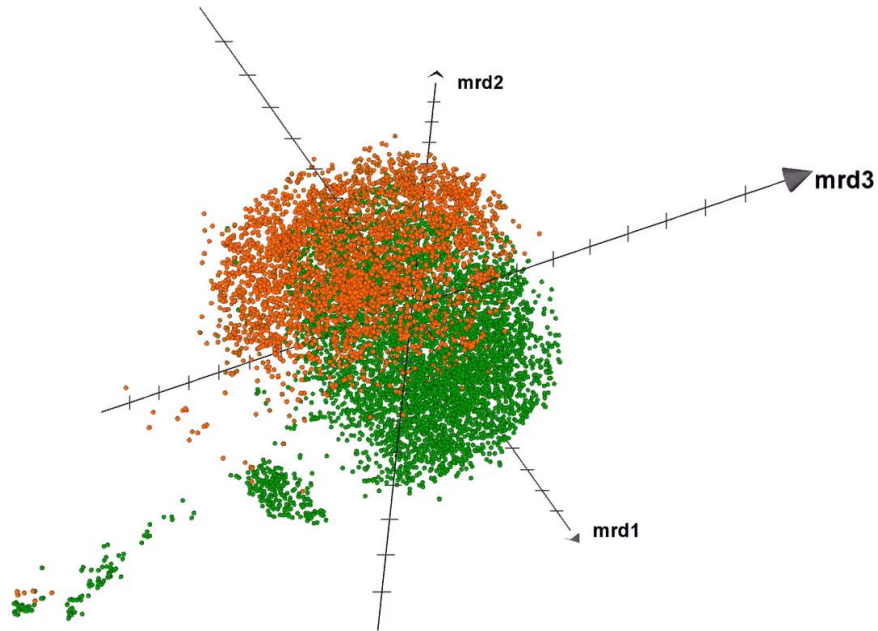


Global Diversity Analysis of Two International Cassava Genebank Collections

● CIAT: 6002 samples
● IITA :4174 samples
Total: 10,176



MDS analysis



Comparison	Number of comparisons	mrd mean	mrd sd
CIAT_CIAT	18009001	0.3301	0.0508
CIAT_IITA	19338444	0.3326	0.0421
IITA-IITA	5189031	0.293	0.0408

4 conservation:

Coordinated stratified curation

- Identify redundancy within and across collections. To:
 - Optimize **conservation costs**
 - Resources for **germplasm evaluation**
 - **Guiding** cry-conservation efforts

4 use:

- Identify collection gaps
- framework for genomics-assisted genebank management
- **Mining useful alleles** for introgression of desired traits into cassava breeding programs.

A remarkable degree of “genetic complementarity” between the two genebank collections

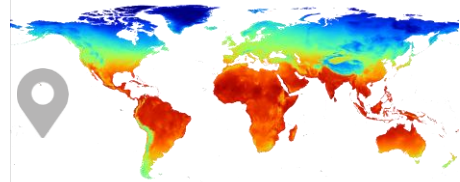


Genebank Platform

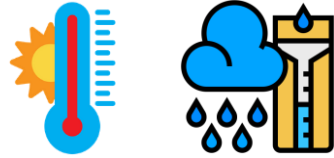


Mining alleles for climate adaptation

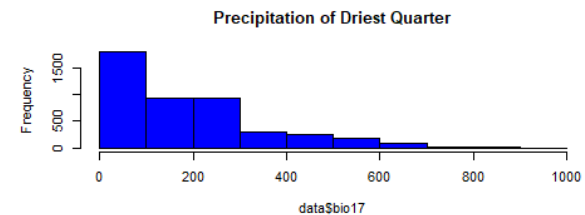
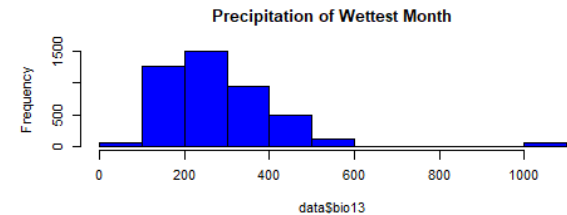
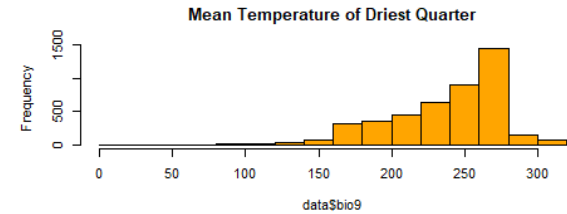
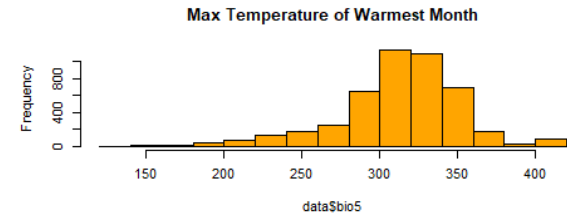
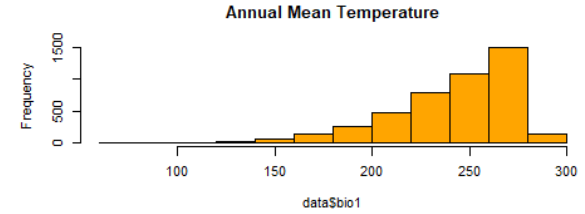
- ✓ Review the passport data
- ✓ 3,112 landrace accessions
- ✓ Geolocation of collection sites
- ✓ Adapted to specific environmental conditions



Lat / Lon



19 bioclimatic variables extracted



11 eVar



8 eVar



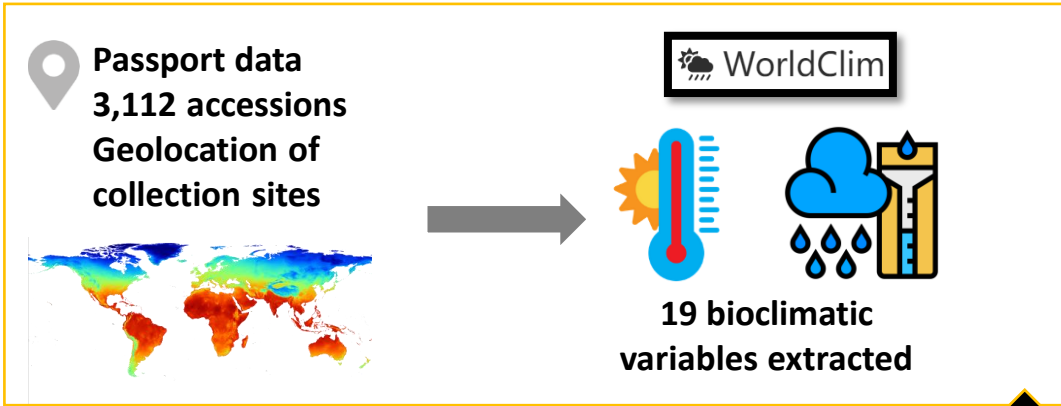
adapted



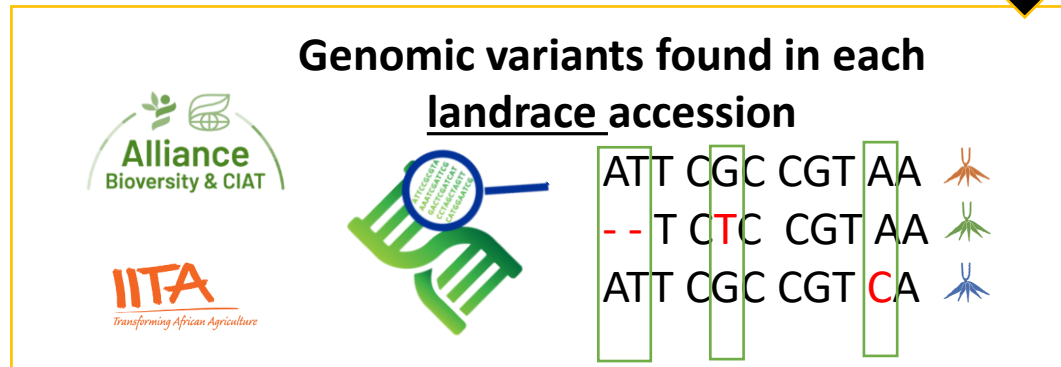
“Landraces are domesticated, locally adapted varieties that has developed overtime through adaptation to is natural and cultural environment”.
(Camacho et al, 2007)



Mining alleles for climate adaptation



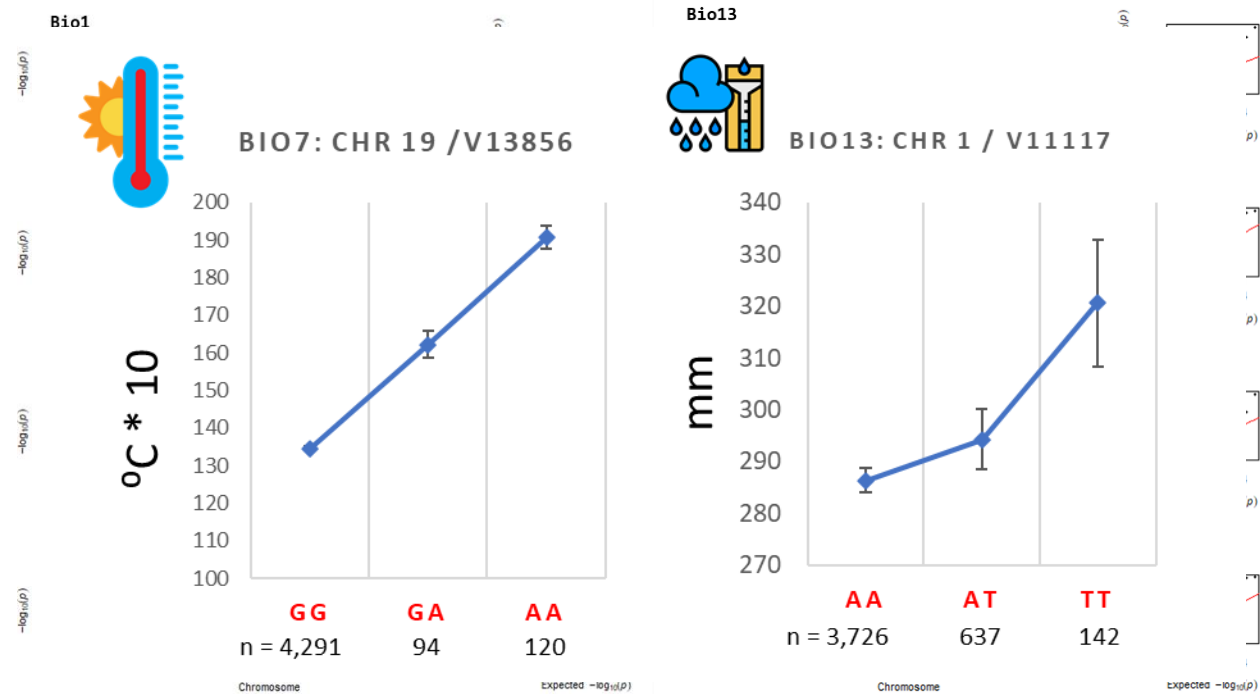
BILL & MELINDA GATES foundation



Environmental association analysis

4,505 samples (3093 CIAT and 1412 IITA)

Mining 18,888 genomic variations to identify those variants associated with climate adaptation



Identify a total of 48 candidate markers distributed across the 18 cassava chromosomes and to one scaffold (9 eVar).

Acknowledgments:

Peter Wenzl
Jorge Franco
Jessica Ospina
Miguel Correa
Monica Velez
Ericson Aranzales
Norma Manrique
Xiaofei Zhang
Ana Maria Leiva
Luis Augusto Becerra

Sarah Dyer, EMBL-EBI, Hinxton, United Kingdom

Rajneesh Paliwal
Michael Abberton
Morag E. Ferguson



Genebank
Platform

