Testing the effectiveness of different approaches of collecting variety-specific adoption data against the benchmark of DNA fingerprinting: The case of cassava in Ghana

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DNA fingerprinting

- DNA fingerprinting was used as a benchmark against which 5 alternate approaches were evaluated / validated.
- Sampling and logistics:
  - Leaf tissues from one plant representing each variety on one most diverse plot per HH (total HHs = 495, total samples = 917)
  - Samples collected in a small screw-capped plastic jar with silica gel (logistics)
  - DNA extraction done at IITA and sequencing done at Cornell (logistics)
- Method—Genotype by sequencing (GBS)
  - This involved collecting / assembling samples of 64 accessions for the reference library (by CRI)
  - Samples of these accessions along with the samples collected from farm surveys were all genotyped at 56,849 single nucleotide polymorphisms (SNP) loci. (at Cornell)
  - Genetically identical sets of clones were then identified by using distance-based hierarchical clustering and model-based maximum likelihood admixture analysis (by IITA)

Results: Genotyping data used to classify the reference library and farmer samples into 11 unique varietal clusters
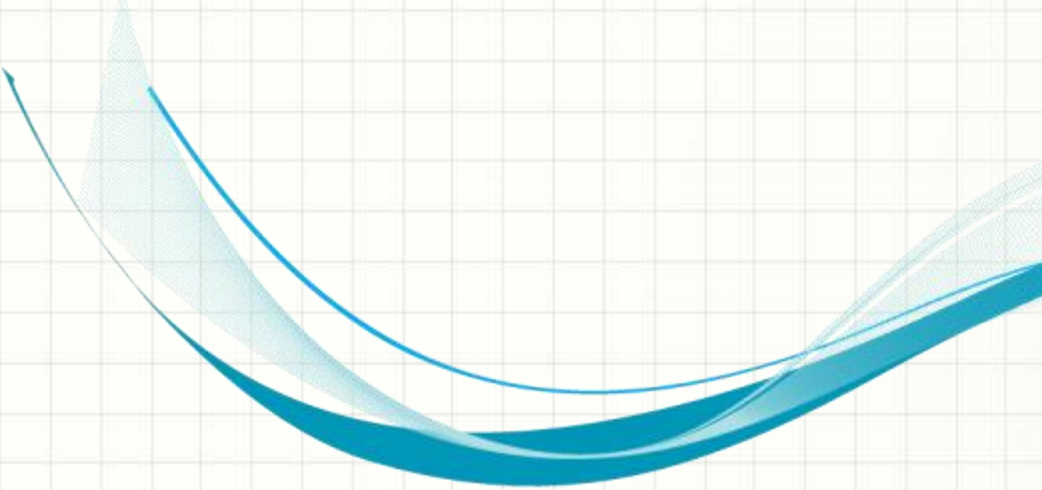
Unique variety group	# of accessions from farmer samples	Accessions from reference library that fall in the variety group	
		Released varieties	**Landraces / Local varieties**
Variety 1	208		(12) ADW2000_003; ADW2000_004; ANKRA; BOSOMENSIA_1; DEBOR 1; DEBOR_KAAN ; DMA2000_002 ; DMA2000_66 ; KSI2000_126 ; OFF_2000_019 ; OFF_2000_023 ; UCC2000_111
Variety 2	158	(2) IFAD; UCC	(7) TUMTUM ; DWA2000_070 ; ELISHA ; WCH2000_020 ; KW_2000_010 ; KWANWOMA ; OFF_2000_134
Variety 3	65	(1) NKABOM	(1) DEBOR 2
Variety 4	17	(1) AFISIAFI	(3) ABUSUA; MONICA; UCC2001_449
Variety 5	57		(2) ADE2000_182 ; DMA2000_031
Variety 6	37		(2) KW_2000_148; UCC2001_399
Variety 7	20	No match	No match
Variety 8	21	(1) BANKYE_BRONI_1	(1) UCC20001_464;
Variety 9	13	No match	No match
Variety 10	33	No match	No match
Variety 11	11	No match	No match

Results for cassava in Ghana (cont'd): **several hybrids or admixtures**

Unique variety group	# of accessions from farmer samples	Accessions from reference library that fall in the variety group	
		Released varieties	**Landraces / Local varieties**
50% ancestry from variety 1	17	No match	No match
50% ancestry from variety 2	11	No match	No match
50% ancestry from variety 3	19	(3) ESSAM_BANKYE; BANKYE_HEMAA; TEKBANKYE; DOKU_DUADE	
50% ancestry from variety 4_group 1	8		(2) BRONI; KW2000_181
50% ancestry from variety 4_group 2	2	(3) NYERIKOGBA; ABASA_FITAA; OTUHIA	
50% ancestry from variety 5	12	No match	No match
50% ancestry from variety 6	33	No match	No match
50% ancestry from variety 8	21		(4) 12_0236; 12_02Y5 ; CONGO_BATIALION; ESIABAYAA
50% ancestry from variety 9	29	No match	No match
50% ancestry from variety 11	5		(2) KW_2000_030; UCC2001_249
Multi-ancestry clones _group 1	115		(11) 12_0197; ADW2001_051; AFS_2000_050; ANKRA_10_003; AW3_10_008; AW3_10_011; BOSOMENSIA_2; CONGO_BATIALION; DEBOR_BEPOSO; OFF_2000_037 WCH2000_011
Multi-ancestry clones _group 2	2	(6) BANKYE_BRONI_2; AMPONG; FILINDIAKONIA; BANKYE_BOTAN; SIKABANKYE; AGBELIFIA	
Total	914	18	46

DNA results for cassava in Ghana

- Several interesting findings
    1. Some improved varieties are genetically identical (e.g., IFAD and UCC)
    2. Many released varieties are hybrids or admixtures
    3. **Library accessions representing both 'released varieties' and 'landraces' fall under the same varietal cluster groups (e.g., variety group 2, 3, 4)**
- The last bullet point (#3) especially poses a challenge for tracking adoption of released varieties
- The problem is: How to classify farmer samples that fall in these variety cluster groups? Should they be classified as 'improved/released' varieties or local/landrace varieties?
- The difference in adoption estimates is significant (4% vs. 31%) and no methods come closer to the 'truth' in adoption estimates under the liberal (31%) scenario

Implications and Key Insights from this Study…

- **Confirmation:** Identifying cassava varieties accurately by NAME in a setting where hundreds of variety names exist is a challenge across all the methods tested (type I and type II errors across all methods)

- **Surprise:** Genotyping provides a 'true picture' of what is in farmers' fields. But the implication of this 'truth' in estimating adoption of 'improved varieties' can be ambiguous if the 'released varieties' share the same DNA fingerprints as other released varieties or accessions considered to be landraces

  – Implication: Identification of farmer adopted varieties by name or by type with 100% certainty remains inconclusive

  – A thorough analysis of the reference library needs to be done prior to scaling up to ensure unique identities of released varieties; If released varieties cannot be distinguishable from one another or from landraces, then DNA fingerprinting for the purpose of tracking adoption of 'released varieties' is meaningless