Are we measuring what we think we are measuring? Recent experience in using DNA fingerprinting and implications for tracking varietal adoption and assessing impacts

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Abstract

Varietal adoption based on household surveys has mostly relied on farmers' response to varietal identification. This method can give biased estimates if farmers are unable to identify improved varieties as a group or by name, or give names that do not match with the improved variety list. To tackle these potential problems requires time intensive data collection such as including follow-up questions in the survey instrument, visiting the field to observe plant characteristics, or collecting sample materials (i.e., photos, seeds/plant tissues) from the farmers for later verification by experts. Each of these approaches has implications on the cost of data collection and the accuracy with which they can correctly identify a variety. This paper reports the results of two pilot studies conducted in Ghana and Zambia to test different approaches of collecting variety-specific adoption data, and to validate them against the benchmark of DNA-fingerprinting to determine which method is most effective in measuring varietal adoption. Results suggest large variations in the estimates of adoption rates obtained by these different methods, compared to DNA fingerprinting results. This paper also highlights some potential challenges of varietal identification when multiple released varieties are discovered to be essentially the same based on the DNA fingerprints or when released varieties share the same DNA fingerprint as some landrace materials included in the reference library. The Implications of these results on the effectiveness of alternate methods of varietal identification, including DNA fingerprinting are discussed.

JEL Codes: C81 Methodology for Collecting, Estimating, and Organizing Microeconomic Data, Data Access, C83 Survey Methods, Sampling Methods, O3 Technological Change; Research and Development

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1. Introduction

Since the pioneering research by Griliches (1958) on assessing the impact of hybrid corn adoption in the U.S. almost six decades ago, the interest in measuring the impacts of adoption of improved technology by farmers has expanded to include a gamut of agricultural technologies in both developed and developing country settings. Among the most widely assessed agricultural technologies in the developing country context is the adoption of improved varieties. These assessments have consistently reported that adoption of improved varieties and rapid varietal turnover increases productivity, income and other measures of welfare of farm households (Evenson and Gollin 2003, Zeng et al., 2015, Walker and Alwang, 2015, Mathenge, Smale and Olwande 2014).

Central to these assessments is the identification of improved varieties, estimating the adoption rate, and assessing varietal turnover. Most varietal adoption and impact assessment studies in the past have relied on either the low cost method of expert elicitation (e.g., Walker and Alwang 2015, Alene et al. 2009) or the resource-intensive, but 'gold-standard' method of conducting farm household surveys and eliciting this information directly from farmers (e.g., Zeng et al. 2015, Shiferaw et al. 2014, Kassie et al. 2011). However, despite their wide use, the reliability of these approaches has never been verified, leaving the bias and standard errors of these adoption estimates unknown.

Compared to the expert elicitation method, 'farmer elicitation' method can be fairly accurate in a setting where farmers are mostly planting seeds freshly purchased or acquired from the formal seed system as certified or truthfully labeled seed. In other words, the farm survey method can be effective if the seed system is well-functioning and can effectively monitor the quality and genetic identity of varieties being sold by the seed vendors. However, in settings where the formal seed system is non-existent or ineffective, and farmers mostly rely on harvested grain (either from their own farms or acquired from other farmers or purchased from the market) as the main source of planting material, the reliability of estimating varietal adoption using this method is challenging (Yirga et al. 2014). By implication, it also makes the results of impact assessments based on those survey-based adoption estimates questionable.

The challenges stem from several confounding factors. These include biological factors such as the loss of genetic identity due to cross-pollination when seeds are recycled several seasons, and social factors such as: 1) farmers' inability to identify varieties by names, 2) the inconsistency in the names of the varieties as identified by the farmers and what is in the variety registration list (i.e., varieties may have locally adapted names), and 3) farmers' lack of understanding of what is an 'improved / modern variety' vs. 'unimproved / traditional' variety or inability to distinguish between different types of hybrids and varieties.

DNA fingerprinting, which is routinely used by plant breeders, offers a reliable method to address these challenges and to accurately identify varieties grown by farmers. The use of this method can thus increase the accuracy and credibility in the interpretation of results of

economic analysis based on household surveys that estimate the causal link between the adoption of improved varieties and the impact on crop productivity and income.

Despite the advantages, the use of DNA fingerprinting as part of adoption surveys is non-existent or limited to few recent attempts by some CGIAR centers and NARS partners. These include the use of DNA fingerprinting for rice varietal identification in Bolivia (led by CIAT) and India (led by IRRI), varietal identification of maize and wheat in Ethiopia (led by the Ethiopian NARS and IFPRI with support from the Gates Foundation), and monitoring the efficacy of maize seed system in Uganda (led by Ugandan NARO in partnership with the University of Georgia). There are several issues related to sampling, logistics, and cost-effectiveness of using this innovative method that need to be investigated *vis a vis* other alternate methods before DNA fingerprinting becomes routine for tracking varietal adoption and assessing the impact at the farm level. The objective of this paper is to precisely address these issues. It reports the results of two pilot studies conducted in Ghana and Zambia in 2013 to test different approaches of collecting variety-specific adoption data and to validate them against the benchmark of DNA-fingerprinting to determine which method is most accurate and cost-effective in measuring varietal adoption. Based on these results, the paper draws implications on assessing determinants of technology adoption and impacts based on the traditional method versus the 'truth' as established by DNA fingerprinting (or genotype by sequencing method).

2. Method and approach

Two pilot studies were conducted—one in Ghana for cassava (*Manihot esculenta*) and the other in Zambia for beans (*Phaseolus vulgaris*) to test the effectiveness of alternate methods of tracking varietal adoption using farm household surveys. Both these pilots involved a multi-disciplinary team of experts (i.e., breeders, geneticists, social scientists and economists) from the national agricultural research systems (e.g., the Council for Science and Industrial Research-Crops Research Institute of Ghana, and the Zambia Agricultural Research Institute), the international agricultural research institutes (IITA for cassava and CIAT for beans), and the U.S. universities (Michigan State University and Cornell University).

Methods of varietal identification evaluated

Six methods of tracking varietal adoption using farm household surveys were evaluated across the two crop–country combinations (CCC) (Table 1). These methods can be grouped into two types—farmer elicitation methods (methods A-C) and expert elicitation methods (methods D-F) (Table 1). The protocol followed for each of these methods is as follow:

Method A: As part of the survey instrument, farmers were asked to provide the name(s) and type (improved vs. local) of varieties planted in the current planting season (for cassava) or the last completed season (for beans). In both the cases additional information on the source of the first and current planting materials and number of years a variety was grown by the farmer was collected.

Method B (tested only for cassava): As part of the survey interview, farmers were asked about specific varietal characteristics by showing a series of photographs. In the case of cassava, pictures of cassava plants depicting different morphological characteristics were shown and farmers were asked to identify the characteristic (e.g., color, size, shape) that best match with the characteristics of the variety he/she was growing. Farmer responses were later matched with the variety specific characteristics of all the accessions included in the reference library (as catalogued by the cassava breeder) to identify the variety cultivated by the farmer.

Method C (tested only for beans): This method involved showing the farmer seed samples representing different varieties and asking him/her to identify the seed sample that matched the varieties grown on their farm. To implement this method, all the released bean varieties (plus some popular local varieties) were organized in small pockets of plastic bags that were easy to carry by enumerators. As part of one of the survey modules, farmers were asked whether the variety he/she is growing matched any of the variety in this sample. If the response was yes, the enumerator noted down the sample code and latter matched with the name of the variety corresponding to that sample. If the farmer's response was no, the variety grown by the farmer was interpreted as 'other traditional / local landraces.'

Table 1. Methods of varietal identification tested in the pilot countries

Methods		Ghana (cassava)	Zambia (beans)
V	DNA fingerprinting (used as a benchmark to compare/validate other methods)	X	X
A	Farmer elicitation (name and type of variety)	X	X
B	Farmer elicitation based on series of photographs of plants and / or seeds	X	
C	Farmer response on type of variety he/she had planted that match seed samples presented by the enumerators		X
D	Trained enumerators/experts visiting the field and: 1. Recording observations on varietal characteristics (phenotyping); and 2. Identifying the variety based on observation (phenotyping)	X	
E	Taking photos of the plant in the field or seeds harvested by farmers for latter identification by experts (i.e., breeders, agronomists, etc.)	X	X
F	Collecting harvested seeds from farmers for latter identification by experts (i.e., breeders, agronomists)		X

Method D (tested only for cassava): A trained cassava expert (i.e., field technician from the cassava breeding program) was included as part of the survey team and visited the cassava fields enumerated in the household survey to test two closely related methods of varietal

identification. The first method involved the expert recording his/her observations on 11 morphological characteristics of a representative plant corresponding to each variety planted on that field as identified by the farmer. This information recorded by the expert was later matched with the variety specific characteristics of all the accessions included in the reference library (as catalogued by the cassava breeder) to identify the variety cultivated by the farmer. A second variation of this method was varietal identification recorded by the visiting expert him/herself based on observation of the plant in the field.

Method E: This method consisted of taking photographs of the plant in the field (in the case of cassava) or a sample of harvested seeds (in the case of beans) and later using these pictures for varietal identification by a panel of experts.

Method F (tested only for beans): Consisted for collecting seed samples of varieties grown by the farmer for later identification by breeders or other bean experts. In the case of beans, this method is an extension of the step involved in doing the DNA fingerprinting analysis for varietal identification. The seed samples collected for that purpose were used to seek expert elicitation on varietal identification.

DNA fingerprinting

In both the pilots, DNA fingerprinting was used as a benchmark against which alternate approaches were evaluated / validated (method V). This involved first establishing a reference library of DNA fingerprints, and then collecting samples (plant tissues or seeds) during the farm surveys and genotyping them using the same or a sub-set of markers used to establish the reference library. In the case of cassava, a total of 64 accessions of released varieties (n=18) and popular landraces (n=46) were included in the reference library (see Annex 1A and 1B). Samples of these accessions along with the samples collected from farm surveys were all genotyped at 56,849 single nucleotide polymorphisms (SNP) loci. Genetically identical sets of clones were then identified by using distance-based hierarchical clustering and model-based maximum likelihood admixture analysis (Rabbi et al., 2015).

In the case of beans, 13 accessions specific to Zambia (including 11 released varieties listed in Annex 2 and two landrace Kabulengeti market classes) and 723 accessions from the East/Southern Africa region (that were genotyped as part of another project by CIAT) were included in the reference library as the 'background' materials to compare the samples collected from farm surveys. The farmer samples were genotyped using 66 assays/markers selected as a sub-set of ~800 SNPs used for the reference library. The 66 SNP assays were made up of 4 groups, each of which has more or less the same power to differentiate released varieties from each other and from the background genotypes (Raatz 2015).

Sampling and data collection

In Ghana, the pilot study was conducted in three regions which account for 61% of cassava production in the country in 2010 (Angelucci 2013; FAOSTAT 2014). The three study regions included Brong Ahafo, Ashanti and Eastern. A total of 500 households were targeted for the survey using a multistage cluster sampling method. Only districts with more than 5000 ha under cassava cultivation were identified in the sampling frame. In the first stage, 5-8 districts per region were randomly selected from this sampling frame. In the second stage 5 villages per district were randomly selected. Finally, 5 cassava farmers from each village were selected based on a random start and then skipping x = N/5 (where N = approximate number of households in the village) number of houses until the target number of cassava farmers were reached.

A total of 495 cassava growing households distributed across 100 villages from 20 districts in the three study regions of Ghana were surveyed in October-November 2013. The survey was coordinated by a research team led by the cassava breeder from the Council for Science and Industrial Research-Crops Research Institute of Ghana and a socio-economist from the Agriculture Innovation Consult. The survey team consisted of enumerators who were in-charge of completing the household modules, a cassava expert in-charge of completing the field survey module, and a DNA sampling expert in-charge of collecting, labeling and storing the plant tissue samples as per the protocol established with the help of researchers from IITA. In each household, the field with the most number of cassava varieties grown by the farmer were visited to collect the leaf samples for DNA analysis and to collect information / pictures required to test methods D and E described above. The GPS coordinates of the field were recorded and farmers were asked to identify plants representing each of the varieties grown. During the field visits if the cassava expert found natural variation in the observed characteristics of a variety, they were instructed to collect leaf samples from each variation of a variety observed (and label them as variations of variety x). Apical leaf samples were collected from one plant representing each variety (or its variation) and preserved in silica gel for transportation to a central laboratory at IITA in Ibadan, Nigeria for DNA extraction. The extracted DNA samples were then shipped to Cornell University's Institute of Biotechnology for analysis using the genotyping-by-sequencing (GBS) method. Data interpretation and analysis for varietal identification based on the GBS results was led by researchers at IITA.

In Zambia, the pilot study was designed to take advantage of an already planned bean varietal adoption and impact study by the Zambia Agricultural Research Institute (ZARI) with support from PABRA and CIAT (Hamazakaza et al. 2014). The study was conducted in Muchinga and Northern provinces of Zambia. These provinces were purposively selected because of their importance in bean production, accounting for about 70% of the area under beans in Zambia, and because most of the prior seed dissemination efforts were concentrated in this part of the country.

A total of seven districts were purposively selected (again based on the importance of the bean crop) from the two provinces: four districts (Kasama, Mbala, Mporokoso, Mpulungu) in the Northern Province and three (Chinsali, Mpika, Nakonde) in the Muchinga Province, which together represent 59% of the total bean area in Zambia. After the districts were selected, a two-stage cluster sample selection method was used. In the first stage, villages were randomly selected from each district according to the proportion of villages within the selected districts in each province. In the second stage, six households were systematically selected within each village. A sample of 400 farmers across 67 villages was determined based on the available budget. Thus, 41 and 26 villages were selected in the Northern and Muchinga provinces, respectively and 6 farmers per village were surveyed to get a total sample size of 402 farm households. To select the households, a systematic random sampling procedure was followed. The village register list obtained from the local headman or village secretary served as the sampling frame and each household in this list was numbered sequentially. The first household was selected at random from this list, and the remaining five households were chosen at fixed interval x = N/6 (where N = number of households on the village list) until the target number of bean farmers was reached.

The survey was implemented between August-September 2013 and the information collected refers to the 2012-2013 agricultural season (December 2012-April 2013). The enumerators were trained by a research team from ZARI, MSU and CIAT on how to use the instruments for household- and village-level data collection, how to take photographs of the seed samples, and how to implement the protocol for collecting 10-15 seeds of each variety the farmer had harvested in the 2012-2013 agricultural season and labeling them for proper tracking. Each enumerator received a set of seed samples representing ten different improved varieties that was presented to the farmer to facilitate in variety identification (method C). Each small plastic bag containing these seeds had a code and only the supervisors knew which code belonged to which variety.

For DNA fingerprinting, the seed samples collected from the farmers were germinated by the ZARI bean breeder at the Kasama research station in May-June 2014. With the help of a CIAT technician, leaf tissue samples from young germinated bean plants were collected in a 96 well-plate leaf sampling kits and shipped to LGC Genomics lab in U.K. for genotyping. All the farmer samples were genotyped using 66 SNP markers (or assays) that were identified by the research collaborator (a bean genetics expert) from CIAT specifically for this study.

In both the countries, household level questionnaires collected information on household characteristics, farm characteristics, varietal identification questions corresponding to methods A-C, and variety-level questions on preferences, use, like/dislike characteristics, etc. In both the countries, a community level questionnaire was also completed to collect some community level characteristics that can explain varietal adoption outcomes. In the case of Ghana the household level data were collected using *SurveyBe*, a computer assisted personal interviewing (CAPI) method. In Zambia, the survey was conducted using the paper-based personal interviewing (PAPI) method. Farmers' participation in both the surveys was voluntary and they

were fully informed on the survey objectives and how they were selected to participate in the survey.

Varietal identification using expert elicitation based on photographs and seed samples

After the field survey, the seed samples and photographs collected in Zambia, and photographs of plants taken in Ghana were used in varietal identification (methods D-F) by a panel of crop experts who were familiar with the varieties grown in the study area. For beans, the breeders and extension staff from the study districts were invited to ZARI's Misamfu Research Station in Kasama to participate in the identification of varieties using photos (day 1) and seed samples (day 2). This expert panel meeting in Zambia was conducted in March 2014. For cassava, the expert elicitation panel discussion was organized at CRI in August 2014 and included cassava breeders, experts and field technicians from CSRI-CRI, IITA and the University of Cape Coast. In both the cases, the overall elicitation process was facilitated by a socio-economist either from IITA (in the case of cassava) or from MSU (in the case of beans) who did not participate in varietal identification.

There were some differences in the implementation of expert elicitation method in the two countries. In the case of Zambia, the bean samples were identified by names and if the experts could not name a variety, "no name" was recorded as their answer. On the other hand, in the case of cassava, variety was mostly identified as improved, not improved, mix (a cross between improved and non-improved), or unknown. Also, in the case of cassava the opinion on the type of variety based on the photo identification method was recorded separately by each of the seven experts. However, in the case of beans, after some exchange of opinions a consensus about the name of the variety was reached and only one name corresponding to a sample was recorded. Also, in Zambia, if the experts could not identify a variety by name, "no name" was recorded as their answer. In some instances, when a variety was identified as a "mixture" (which is common in Zambia), each of the varieties within this mixture were evaluated separately (i.e., each was given a name).

3. Results

Table 2 presents a few descriptive statistics of the 402 bean growing households surveyed in Zambia and 495 cassava growing households in Ghana. On average a sampled household in Zambia cultivated beans on 1.4 plots and a sampled household in Ghana cultivated cassava on 2 plots. A typical farmer in the study area of Zambia had cultivated 2 varieties of beans in the 2012-2013 season. This resulted in a total of 831 bean varietal observations (or data points) for which different methods of varietal identification can be applied. In the case of cassava, the average number of cassava plots was reported to be 1.9 per household, resulting in 924 total number of cassava varietal observations across 495 households. Out of these total number of varieties documented, 917 were genotyped. In the case of beans, since the survey was conducted several months after the harvest season, many farmers had no seed stock left to

share with the enumerators. Thus the number of samples genotyped is also less than the total number of varieties documented in the household survey. Moreover, due to technical glitches and quality issues, the database of photographs available for varietal identification for both beans and cassava was substantially lower than the number of seed / plant samples collected (Table 2).

Table 2. Characteristics of the farmer and number of samples collected in Ghana and Zambia to test different methods

Details	Zambia (Beans)	Ghana (Cassava)
Number of farmers surveyed	402	495
Average number of plots on which the crop was planted (range)	1.36 (1-4)	2.05 (1-25)
Average number of varieties planted per household (range)	2.08 (1-6)	1.92 (1-7)
Average number of varieties planted per plot visited (range)	--	1.85 (1-5)
Number of varietal data points reported in farmer survey (for method A and B)	831	924
Number of samples genotyped (DNA fingerprinted) (for method V)	823	917
Number of samples photographed and available for varietal identification (for method E, F)	792	792

Classification of reference library materials and farmer samples into variety groups based on DNA fingerprinting

Tables 3 and 4 present the results of DNA fingerprinting and its implication on the classification of farmer samples and library samples into unique variety groups. The results of varietal identification using methods A to F are compared against this benchmark and will be presented at the conference. The results suggest that there are large differences between the estimates of adoption rates obtained by these different methods, compared to fingerprinting results. Implications of these results on the cost effectiveness of alternate approaches, lessons learned and suggestions for scaling up the best methods will be discussed.

Table 3. Classification of farmer samples and accessions from reference library in to unique variety clusters based on DNA fingerprinting: Results for cassava in Ghana

Unique variety group based on DNA fingerprinting	# of accessions from farmer samples classified under a variety group	Accessions from reference library that fall in the variety group		Classification of farmer samples that fall in this cluster 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	Local variety
Variety 2	158	(2) IFAD; UCC	(7) TUMTUM ; DWA2000_070 ; ELISHA ; WCH2000_020 ; KW_2000_010 ; KWANWOMA ; OFF_2000_134	**IMPROVED VARIETY**
Variety 3	65	(1) NKABOM	(1) DEBOR 2	**IMPROVED VARIETY**
Variety 4	17	(1) AFISIAFI	(3) ABUSUA; MONICA; UCC2001_449	**IMPROVED VARIETY**
Variety 5	57		(2) ADE2000_182 ; DMA2000_031	Local variety
Variety 6	37		(2) KW_2000_148; UCC2001_399	Local variety
Variety 7	20	No match	No match	Local variety
Variety 8	21	(1) BANKYE_BRONI_1	(1) UCC20001_464;	**IMPROVED VARIETY**
Variety 9	13	No match	No match	Local variety
Variety 10	33	No match	No match	Local variety
Variety 11	11	No match	No match	Local variety
Hybrids (or Admixtures)				
50% ancestry from variety 1	17	No match	No match	Local variety
50% ancestry from variety 2	11	No match	No match	Local variety
50% ancestry from variety 3	19	(3) ESSAM_BANKYE; BANKYE_HEMAA ; TEKBANKYE; DOKU_DUADE		**IMPROVED VARIETY**
50% ancestry from variety 4_group 1	8		(2) BRONI; KW2000_181	Local variety
50% ancestry from variety 4_group 2	2	(3) NYERIKOGBA; ABASA_FITAA; OTUHIA		**IMPROVED VARIETY**
50% ancestry from variety 5	12	No match	No match	Local variety
50% ancestry from variety 6	33	No match	No match	Local variety
50% ancestry from variety 8	21		(4) 12_0236; 12_02Y5 ; CONGO_BATIALION; ESIABAYAA	Local variety

Unique variety group based on DNA fingerprinting	# of accessions from farmer samples classified under a variety group	Accessions from reference library that fall in the variety group		Classification of farmer samples that fall in this cluster group
		Released varieties	Landraces / Local varieties	
50% ancestry from variety 9	29	No match	No match	Local variety
50% ancestry from variety 11	5		(2) KW_2000_030; UCC2001_249	Local varieties
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	Local variety
Multi-ancestry clones _group 2	5	(6) BANKYE_BRONI_2; AMPONG; FILINDIAKONIA; BANKYE_BOTAN; SIKABANKYE; AGBELIFIA		**IMPROVED VARIETY**
Total	917	18	46	

Table 4. Classification of farmer samples and accessions from reference library in to unique variety clusters based on DNA fingerprinting: Results for beans in Zambia

Unique variety group based on DNA fingerprinting	# of accessions from farmer samples classified under a variety group	Accessions from reference library that fall in the variety group		Classification of farmer samples that fall in this cluster group
		Released varieties	Landraces / Local varieties	
Variety 1	0	Chambeshi		**IMPROVED VARIETY**
Variety 2	0	Kabale		**IMPROVED VARIETY**
Variety 3	192	Kabulangeti_set 3 Kabulangeti_10004		**IMPROVED VARIETY**
Variety 4	0	Kalambo		**IMPROVED VARIETY**
Variety 5	0	Kalungu		**IMPROVED VARIETY**
Variety 6	0	Kapisha		**IMPROVED VARIETY**
Variety 7	21	Lukupa		**IMPROVED VARIETY**
Variety 8	4	Lwangeni		**IMPROVED VARIETY**
Variety 9	2	Lyambai		**IMPROVED VARIETY**
Variety 10	0	Mbereshi		**IMPROVED VARIETY**
Variety 11	0	Sadzu		**IMPROVED VARIETY**
Variety 12	6		KABLANKETI	Local variety
Other	602	No MATCH	NO MATCH	Local variety

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Annex 1A: List of cassava released varieties included in the reference library for Ghana

s/n	Variety Name \a	Year released	Institutional Origin/Final Cross/Country	Variety Attributes/Pedigree
1	Abasafitaa	1991	IITA/CRI	Yield, pest & disease resistant
2	Afisiafi	1993	IITA/CRI	Yield, pest & disease resistant
3	Tek Bankye	1997	IITA/KNUST	High yield, good cooking quality
4	Nyerikobga	2002	SARI	Lower gari swelling power
5	Filindiakong	2002	IITA/CRI	Considered early, high DM
6	IFAD	2004	KNUST	High yield, good cooking quality
7	Nkabom	2004	KNUST	Poundability, high yield
8	UCC (Capevars bankye)	2005	UNIV OF CAPE COAST	Poundability, high yield
9	Bankye botan	2005	UNIV OF CAPE COAST	Poundability, high yield
10	Bankyehemaa	2005	IITA/CRI	Poundability, high yield
11	Esam bankye	2005	IITA/CRI	High yield/dry matter, flour
12	Dokuduade	2005	IITA/CRI	High yield, starch content
13	Agbelifia	2005	IITA/CRI	High yield/dry matter, flour
14	Otuhia	2009	IITA/CRI	High yield disease/pest tolerance
15	Sikabankye (Sika)	2009	IITA/CRI	High yield, starch content
16	Bankye broni \b	2009	IITA/CRI	High yield disease/pest tolerance
17	Ampong	2009	IITA/CRI	High yield disease/pest tolerance

\a two released varieties – Gblemoduade, released in 1993 and Eskamaye, released in 2002 were not included in the reference library as they were not physically available at the CRI research station for sample collection.
\b Two copies of Bankye _broni were included in the reference library, which makes the total number of released variety samples = 18

Annex 1B: List of cassava landraces included in the reference library for Ghana

1	12_0197	13	AW3_10_011	25	DMA2000_66	37	OFF_2000_023
2	12_0236	14	BNSIA_TUMTUM	26	DWA2000_069	38	OFF_2000_037
3	12_02Y5	15	BOSOMENSIA_1	27	ELISHA	39	OFF_2000_133
4	ABUSUA	16	BOSOMENSIA_2	28	ESIABAYAA	40	UCC2000_110
5	ADE2000_182	17	BRONI	29	KSI2000_125	41	UCC20001_464
6	ADW2000_002	18	CONGO_BATIALION	30	KW_2000_009	42	UCC2001_249
7	ADW2000_003	19	DEBOR_1	31	KW_2000_030	43	UCC2001_399
8	ADW2001_051	20	DEBOR_3	32	KW_2000_148	44	UCC2001_448
9	AFS_2000_050	21	DEBOR_BEPOSO	33	KW2000_181	45	WCH2000_010
10	ANKRA	22	DEBOR_KAAN	34	KWANWOMA	46	WCH2000_019
11	ANKRA_10_003	23	DMA2000_002	35	MONICA		
12	AW3_10_008	24	DMA2000_031	36	OFF_2000_018		

Annex 2: List of bean released varieties included in the reference library for Zambia

Variety name	Year of release	Seed color	Seed size	Growing Habit	Color of flowers	Color of immature pods	Color of mature pods (before drying)
Chambeshi	1998	Khaki / cream	Large	Bush	White	Green	Cream
Lukupa	1999	Cream mottled	Medium	Indeterminate bush	White	Green	Cream with stripes
Lyambai	1999	Red mottled	Medium	Bush	Pinkish	Green	Cream
Kalungu	2004	White	Medium	Indeterminate bush	White	Green	Cream
Kabulangeti	2007	Purple	Medium	Indeterminate (semi-climber)	White	Green	Cream with purplish stripes
Kapisha	2007	Cream	Medium	Indeterminate (semi-climber)	White	Green	Cream
Kabale	2007	Pinkish	Medium	Bush	Pinkish	Green	Cream
Lwangeni	2009	White	Small	Indeterminate bush	White	Green	Cream
Kalambo	2011	Cream mottled	Large	Indeterminate Dwarf	White	Green with speckles	Cream with speckles
Sadzu	2011	Red mottled	Large	Climber	White	Green	Cream
Mbereshi	2012						