Standing
Panel on
Impact
Assessment

# SPIA Uganda Report 2025: Agricultural Diversity Under Stress

John Ilukor, Emmanuel Letaa, Amit Khanal, Julio Barros, Lemi Taye, Davis Gimode, Giulia Ponzini, Godfrey Asea, Vincent Ssennono, James Stevenson, Travis Lybbert, Karen Macours

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Cover Photo: A local woman sells vegetables in Uganda. Diversified agricultural systems can produce multiple crops leading to improved livelihoods for women.
Credit: Neil Palmer/CIAT

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# Abbreviations and Acronyms

| | |
|---|---|
| **3WH** | Three-Way Hybrid |
| **AAS** | Annual Agricultural Survey |
| **APS** | Annual Panel Sample |
| **ACDP** | Agriculture Cluster Development Project |
| **ATAAS** | Agricultural Technology and Agribusiness Advisory Services |
| **BCS** | Biennial Cross-Sectional Sample |
| **BXW** | Banana Xanthomonas Wilt |
| **CAPI** | Computer-Assisted Personal Interviews |
| **CBSME** | Community-Based Seed Multiplication Enterprise |
| **CBSD** | Cassava Brown Streak Disease |
| **CIAT** | International Center for Tropical Agriculture |
| **CIFOR/ICRAF** | Center for International Forestry Research and World Agroforestry |
| **CIP** | International Potato Center |
| **CIMMYT** | International Maize and Wheat Improvement Center |
| **CMD** | Cassava Mosaic Disease |
| **DCIC** | Department for Crop Inspection and Certification |
| **DDA** | Dairy Development Authority |
| **DIIVA** | Diffusion and Impact of Improved Varieties in Africa |
| **EA** | Enumeration Area |
| **EADD** | East African Dairy Development Project |
| **EAHB** | East African Highland Banana |
| **EAAPP** | East African Agricultural Productivity Program |
| **FAO** | Food and Agriculture Organization of the United Nations |
| **GAIN** | Global Alliance for Improved Nutrition |
| **GM** | Genetic Modification |
| **FMNR** | Farmer Managed Natural Regeneration |
| **ICRISAT** | International Crops Research Institute for the Semi-Arid Tropics |
| **IFAD** | International Fund for Agricultural Development |
| **IFPRI** | International Food Policy Research Institute |
| **IITA** | International Institute of Tropical Agriculture |
| **ILRI** | International Livestock Research Institute |
| **IP** | Innovation Platform |

| | |
|---|---|
| **ISSD** | Integrated Seed Systems Development |
| **LSB** | Local Seed Business |
| **LSMS-ISA** | World Bank Living Standards Measurement Study – Integrated Surveys on Agriculture |
| **M&E** | Monitoring and Evaluation |
| **MAAIF** | Ministry of Agriculture, Animal Industry and Fisheries |
| **MCC** | Milk Collection Center |
| **NAADS** | National Agricultural Advisory Delivery System |
| **NaCRRI** | National Crops Resources Research Institute |
| **NaSAARI** | National Semi-Arid Resources and Research Institute |
| **NARS** | National Agricultural Research Systems |
| **NARO** | National Agricultural Research Organization |
| **NPHC** | National Population and Housing Census |
| **NSDS** | National Service Delivery Survey |
| **OFSP** | Orange-Fleshed Sweetpotato |
| **OPV** | Open-Pollinated Variety |
| **OWC** | Operation Wealth Creation |
| **PDM** | Parish Development Model |
| **PMA** | Uganda Plan for Modernization of Agriculture |
| **PPS** | Probability Proportional to Size |
| **QDS** | Quality Declared Seed |
| **SACCOS** | Savings and Credit Cooperative Organizations |
| **SDSR** | Single Diseased Stem Removal |
| **SPVD** | Sweetpotato Virus Disease |
| **UBOS** | Uganda Bureau of Statistics |
| **UDHS** | Ugandan Demographic and Health Survey |
| **UHIS** | Uganda Harmonized Integrated Survey |
| **UNOMA** | Uganda National Study on Objective Measurement in Agriculture |
| **UNPS** | Uganda National Panel Survey |
| **ZARDI** | Zonal Agricultural Research and Development Institute |

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# Executive Summary

Agriculture is central to Uganda’s economy. In support of agricultural development in Uganda, the sustained research collaboration between the National Agricultural Research Organization (NARO) and CGIAR – a global research partnership for a food-secure future - has resulted in numerous innovations related to crops, livestock, and the management of natural resources. This report examines the reach and policy influence of the past two decades of this collaborative research in Uganda.

We draw on an extensive, sustained collaboration among partners: CGIAR Standing Panel on Impact Assessment (SPIA), World Bank Living Standards Measurement Study team (LSMS), the Uganda Bureau of Statistics (UBOS), NARO, the Ministry of Agriculture, Animal Industry and Fisheries (MAIFF), and CGIAR researchers. The partnership for nationally representative data collection was formed under the auspices of the Uganda Household Integrated Surveys (UHIS), a large-scale panel survey implemented by UBOS with support from the World Bank LSMS team.

SPIA integrated plant tissue collection for six major crops (maize, cassava, banana, beans, sweetpotato, and groundnut) into the Uganda Harmonized Integrated Survey (UHIS) 2021/22. This unprecedented effort enables DNA fingerprinting of crop samples collected from farmers’ fields to understand whether farmers are obtaining access to improved varieties that originate from the NARO-CGIAR research partnership.

The first step was identifying the universe of CGIAR-related innovations in Uganda and recording the information in a stocktake. The second step involved identifying ways to collect data with UBOS regarding these innovations. The SPIA-LSMS-UBOS partnership selected a subsample of the UHIS to implement objective measurement approaches like crop-cutting for maize yield estimation and plant tissue sampling for varietal identification using DNA fingerprinting for six crops, as well as an expanded innovation module related to sustainable land management, seed use, varietal mixing, and agricultural practices. Agriculture questions were integrated into Uganda’s National Service Delivery Survey (NSDS), covering extension services, technology adoption, market access, climate change, and disease management. The third step, in collaboration with NARO for maize, cassava, sweetpotato, and groundnut, the International Center for Tropical Agriculture (CIAT) for beans, and the International Institute of Tropical Agriculture (IITA) for banana, involved compiling a comprehensive reference library for the six crops.

We also draw on the results of two related projects that spun off from the main data collection effort and that complement our understanding. The first, with the International Potato Center (CIP) and the Paris School of Economics, revisits households that were part of an earlier 2011 survey in areas where biofortified beans and orange-fleshed sweetpotatoes had been disseminated, aiming to assess the impact of orange-fleshed sweetpotato on child growth outcomes. The second, with the Alliance of Bioversity International and CIAT, UC Davis, and the Ministry of Agriculture, Animal Industry, and Fisheries (MAAIF) Department of Crop Inspection and Certification (DCIC), examines Uganda’s maize and bean seed systems, aiming to quantify declines in genetic purity and germination through testing at different points in the supply chain.

While the samples selected for DNA fingerprinting were designed to be nationally representative, several logistical challenges during data collection resulted in plant samples only being taken from non-randomly selected subsamples. We therefore caution against over-interpretation of any of the quantitative results. However, we believe the orders of magnitude of different types of varieties found in the sample to be informative on the approximate diffusion (or lack thereof) of different types of varieties and offer the following key insights.

Improved maize varieties bred by the National Crops Resources Research Institute (NaCRRI) with support from the International Maize and Wheat Improvement Center (CIMMYT) and IITA, particularly the OPV LONGE 5/5D, are reaching large shares of the households in Uganda, offering the potential for farmers to benefit from important traits such as drought tolerance. We estimate that **57.8% of maize-growing households have at least one plot sample that has a CGIAR-related variety.** However, DNA tests show that farmers’ fields are very mixed, with farmers both recycling their seed (including hybrids) from season to season and drawing heavily on informal sources of seed. The intended traits introduced by plant breeding therefore, do not necessarily materialize in farmers' fields.

Diseases are a major problem constraining cassava production in Uganda. Disease-resistant varieties from NaCRRI, with support from IITA, are reaching around **one third of cassava-growing households in our sample**, particularly the relatively recent (2015) releases NAROCASS 1 and NASE 19. Most banana-cultivating households (71.1%) grow only “matooke” landraces that are very genetically similar to each other, making the banana sector in Uganda highly vulnerable to disease outbreaks. Improved, disease-resistant matooke bananas released by NARO in collaboration with IITA have not yet been taken up by farmers (0.4% adoption of CGIAR-related cultivars). Farmers plant genetically mixed plots of beans, in line with the informality of the seed system for beans, with most farmers buying grain from the market to use as seed. While breeding efforts have focused on varieties high in iron and zinc, adoption of these biofortified beans is limited. We find **only 6% of bean-producing households having DNA related to one of the biofortified bean varieties** (NAROBEAN 1-7) in their plots, while DNA related to CGIAR-related bean varieties was found in plots belonging to 26.5% of households, largely in genetically mixed plots.

Of the sweetpotato-growing households, **around one in ten cultivate a NARO-released variety.** Only 3% of sweetpotato-growing households cultivate orange-fleshed sweetpotato, despite its demonstrated nutritional and health benefits and evidence of earlier widespread dissemination in a number of CGIAR-supported projects under the HarvestPlus initiative. Estimations building on combining the sub-country level roll-out data from those national dissemination efforts with a targeted panel survey in 106 communities across all regions of the country show that children's exposure to orange flesh sweetpotato during the earliest years of life leads to long-term gains in linear growth (height-for-age), with evidence also showing lower morbidity at the age of five. Results hence show that the health benefits of OFSP can be obtained at scale and are suggestive of potential large gains if higher adoption levels could be maintained.

Improved varieties of groundnut were found on farmers' fields, particularly in Eastern Uganda. Overall, **more than one third (37.1%) of groundnut-producing households in our sample are cultivating a variety that was released by NaSARRI** after 1995 with support from ICRISAT, possibly giving access to disease-resistant traits for farmers adopting them.

**Artificial insemination** for cattle is starting to be made available, particularly in Central Uganda, **where one third of communities** report having the service available (national average of 14.2% of communities).

Fruit trees are being planted by households across large parts of Uganda. Overall, **13.5% of rural households across Uganda have planted tropical fruit trees**, of which 11% report having planted an improved variety of fruit.

**Banana and coffee inter-cropping**, a traditional practice that has been researched by CGIAR agronomists over the past 20 years, is very widely practiced (**43.3% of the households that grow either coffee or banana**).

The DNA data show that CGIAR-related crop varieties are reaching households with a broad range of socio-economic characteristics, with cassava and groundnut varieties reaching poor households in particular. In contrast, the NRM and livestock innovations we were able to measure are more likely to reach richer households with higher education levels, while they are less likely to reach younger and female farmers.

**Adoption of CGIAR-related maize varieties is relatively high in most regions**, with the highest rates observed in the Northern region, where virtually all the surveyed communities have some farmers with CGIAR-related maize. For the other crops, **CGIAR-related varieties were found in at most half of the sampled communities, and often much less.** There are notable regional differences: while CGIAR-related varieties of beans and sweetpotato are the strongest in the Central region, we found more CGIAR-related germplasm for cassava and groundnut in the Eastern region, consistent with the focus of some of the regional research stations. Finally, in Western Uganda, adoption of CGIAR-related varieties is low for all crops other than maize. Livestock and Natural Resource Management (NRM) innovations are more frequently observed in the Central region, and are largely absent in the Northern region.

**Half of district-level veterinary officer posts, and over a third of agricultural officer posts, were vacant nationally in 2021.** Agricultural extension officers that were in post report providing information on improved varieties, but this varies by crop, with maize being the most common (97% of respondents) and sweetpotato the least common (57%).

**29% of bean samples obtained from grain markets retained a distinct varietal identity, compared to 79% from Quality Declared Seed (QDS) outlets and 50% in agro-input stores.** This is likely a major limiting factor for the adoption of varieties, given that most bean seed purchases are from the grain market. In maize, when compared to samples taken from in-house seed company fields, seed genetic purity is lower at all subsequent stages (out-grower fields, aggregation, distribution). Mystery shoppers visiting agro-input dealers receive lower quality seed than those obtained through formal DCIC audits.

This comprehensive report highlights both the opportunities and challenges of the diffusion of agricultural innovations in Uganda. The findings show an innovation system that manages to reach a relatively large share of farmers, but with large variation between innovations and relatively large socio-economic and regional inequalities. While some of the results clearly point to the potential of innovations to contribute to improving resilience and addressing hidden hunger, they also clearly show that farmers may not be deriving all the intended benefits from the different innovations. This points to both challenges and opportunities around seed systems, extension, and other complementary investments that, when addressed, could contribute to augmenting and scaling the intended benefits from the AR4D investments. As environmental pressures continue to grow, such investments, together with renewed efforts in breeding, could potentially have large returns.

Checking for bush bean pests and diseases in southwestern Uganda.
Credit: CIAT/NeilPalmer

Bean plant assessments in Kisolo, SW Uganda.
Credit: CIAT/NeilPalmer

# 1. Introduction

What happens in agricultural fields has ripple effects across human development and nutrition, biodiversity and ecological functioning, climate change, and economic growth. As in other low-income countries in Sub-Saharan Africa, agriculture is central to daily life in Uganda. Historically, fertile soils and regular rainfall supported the development of centralized kingdoms, including Buganda (from which the country derives its name), many centuries before the Egyptian, Asian, and British influences of the nineteenth century. Agriculture employs nearly 70% of the labor force in Uganda and is the first job for three-quarters of those between the ages of 15 and 24 years. Almost 73% of the Ugandan population lives in areas defined as rural, where farming is the major economic activity (UBOS, 2019).

Given the importance of the agrifood sector, agricultural research and development has the potential to make a first-order difference for Uganda's economy and livelihoods. CGIAR has been, and still is, at the forefront of developing agricultural innovations globally and across Africa[1]. CGIAR's Standing Panel on Impact Assessment (SPIA) is an independent and impartial panel of experts in impact assessment appointed by the CGIAR System Council with a mandate to expand and deepen evidence on the reach and impact of innovations resulting from CGIAR research investments. Working with a wide range of partners inside and outside CGIAR including the World Bank, national statistical offices, and national agricultural research systems, SPIA has been working to institutionalize the collection of data on the diffusion and use of agricultural innovations by embedding new approaches within nationally representative data collection efforts (Stevenson, Gollin and Macours, 2023). In 2020, SPIA produced the first report in a series that built on years of such partnerships, documenting the diffusion of agricultural technologies at a national scale for Ethiopia (Kosmowski et al, 2020). This report similarly aims to provide a comprehensive overview of the reach of agricultural innovations and policy influences that can be directly linked to stemming from the last two decades of collaborative research between CGIAR and its national research partners in Uganda.

Two broad criteria make Uganda an appropriate focus of SPIA's country study series. First, Uganda has been a high-priority country for CGIAR for many years – reflected in the presence of research staff from numerous CGIAR Research Centers (the Alliance of Bioversity International and CIAT, the Center for International Forestry Research and World Agroforestry (CIFOR-ICRAF), the International Potato Center (CIP), the International Livestock Research Institute (ILRI), the International Institute of Tropical Agriculture (IITA), and the International Food Policy Research Institute (IFPRI)[2]. There are also strong links with the International Maize and Wheat Improvement

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[1] CGIAR is a global agricultural innovation network of CGIAR Research Centers and Alliances employing more than 9,000 scientists, researchers, technicians, and staff working in over 85 countries. It seeks to use agricultural research for development (AR4D) to transform food, land, and water systems for a more sustainable and resilient future in the face of the climate crisis.

[2] Following the One CGIAR transition, from the original 15 CGIAR Research Centers, the Center for International Forestry Research and the World Agroforestry Centre (CIFOR-ICRAF) no longer participate in CGIAR Initiatives but retain offices in Uganda. In 2019, the two centers merged to become the Center for International Forestry Research and World Agroforestry, as did the International Center for Tropical Agriculture (CIAT) and Bioversity International in 2020, becoming the Alliance of Bioversity International and CIAT. As this report includes research carried out before these mergers, we refer to all these CGIAR Research Centers as separate entities where applicable.

Center (CIMMYT) and the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), two CGIAR Research Centers that provide technical support to the national agricultural research system from outside the country's borders. And yet, as with Ethiopia (and Vietnam and Bangladesh – the focus of the other two reports in the initial SPIA series), Uganda is not home to the headquarters of any individual CGIAR Research Center. Thus, Uganda is a strong candidate for looking at the idea of CGIAR in practice as a single system.

Second, there was a strong opportunity through SPIA's partnership with the World Bank Living Standards Measurement Study – Integrated Surveys on Agriculture (LSMS-ISA), to work closely with the Uganda Bureau of Statistics (UBOS) and the Food and Agriculture Organization of the United Nations (FAO) in the design of several national-level surveys. This partnership culminated in the implementation of the Uganda National Study on Objective Measurement in Agriculture (UNOMA) – a joint venture between SPIA, the World Bank, the Uganda Bureau of Statistics (UBOS), and Uganda's National Agricultural Research Organization (NARO) – with all three institutions contributing authors to this report. UNOMA embedded plant tissue collection protocols for six crops (banana, beans, cassava, groundnut, maize, and sweetpotato), and a maize crop cutting experiment into a sub-sample of the 2021/22 round of the Uganda National Panel Survey (UNPS). DNA fingerprinting for crop variety identification was financed by SPIA, while the maize production and yield experiment was financed by the World Bank with support from the 50x2030 Initiative - a multi-partner effort that seeks to bridge the global agricultural data gap by transforming country data systems across 50 countries in Africa, Asia, the Middle East, and Latin America by 2030.

The empirical analysis in this synthesis draws on UNOMA and several other strands of work that SPIA has been pursuing in Uganda since 2016, including a collaboration with UBOS and the Ministry of Agriculture, Animal Industry and Fisheries (MAAIF) to integrate relevant measures of agricultural, livestock and natural resource innovations into the National Service Delivery Survey (NSDS). It has also collaborated with various CGIAR Research Centers, NARO, and MAAIF to disentangle seed market constraints for key crops and worked independently to construct a comprehensive database of the national diffusion efforts for biofortified crops over more than a decade and to trace their long-term adoption and impact. As such, the analysis presented in this report draws on years of strong partnership between SPIA and the World Bank LSMS-ISA team, UBOS, NARO, and MAAIF, researchers from various CGIAR Research Centers, and FAO. The overall direction of the Uganda country work was informed by a consultation workshop in Munyonyo, Uganda, in October 2019, attended by all these partners, as well as senior staff from other Ugandan ministries, donors, and numerous CGIAR and NARO scientists.

To our knowledge, this is the first time that varietal identification for six different crops (covering cereals, root crops, fruit, and legumes) was integrated into one nationally representative sample. This was purposely designed to provide a unique, comprehensive picture of crop and varietal diversity in Uganda. To further ensure that varietal diversity was adequately captured, sampling of each crop was designed to account for the presence of multiple varieties within the same plot. In addition to the analysis presented in this report, a further important output from this effort includes the constitution of the comprehensive reference libraries for each crop available for further research. Additionally, it has created new databases that make available information on the unique combination of objectively verified crop varieties and their DNA information, together with self-reported data from farmers regarding practices and outcomes at the variety-plot level. Added to the highly detailed analysis of crop genetics offered in this report, we also integrate these data with modules on livestock innovations, and household and community-level data on extension and seed systems. Having all these features together in a single, overarching study creates important opportunities for a more detailed analysis of each of the six crops.

The report is organized as follows: Section 2 introduces the context of the Ugandan agrifood system over the last two decades, including various stressors, major policy evolutions, and key dynamic changes that provide the setting for interpretation of the results presented in the rest of the report. Section 3 presents the country-level framework, methods used and the different data sets on which the empirical analysis draws. Section 4 presents a comprehensive stocktake of innovations resulting from the last two decades of CGIAR-related research in Uganda. Section 5 sheds light on the adoption of innovations thought to have scaled, for which measures were built into nationally representative surveys and hence primarily drawing from the most recent waves of the UNPS and NSDS surveys. Section 6 asks, “Who and where are the adopters?” to determine whether innovations reach sub-populations that are of particular interest to CGIAR. Section 7 discusses insights from complementary data sources on extension, impacts of biofortified crops, and seed systems. It also further highlights the value of the DNA fingerprinting data by demonstrating the issue of misclassification when using farmer self-reported data and how it has the potential to skew our understanding of the true picture. Section 8 discusses the overall findings, leading to the conclusion presented in Section 9.

# 2. Uganda’s Agriculture Sector: Diversity Under Stress

## 2.1 Characterization of the Agricultural Sector and the Broad Trends Affecting It

The agricultural sector in Uganda continues to play an important role in the economy, creating approximately 24% of GDP in 2022. It is estimated that seven out of ten Ugandans are either subsistence farmers or working in low-value-added agriculture jobs (African Development Bank, 2024). Investments in the sector are guided by the Agricultural Sector Strategic Plan II, and the agro-industrialization program of the Third National Development Plan (NDP III), which aims to raise the sector's productivity to help contribute to economic growth. The strategy prioritizes ten agricultural products (beef, dairy, cassava, cocoa, coffee, cotton, fisheries, maize, tea, and vegetable oil) with a clear emphasis on crops with current or expected export potential[3].

Uganda is considered among the most diverse countries on Earth (Alesina et al., 2003). There are 56 distinct tribes, and at least eight indigenous minority groups, with small populations of people of European, Asian, or Arabian descent. The country has at least 40 different languages. Diversity is also a defining characteristic of the agricultural system in the country, reflecting the wide range of different agroecologies, with households operating crops and livestock farming in complex combinations. The Uganda Bureau of Statistics (UBOS) recognizes ten distinct agroecological zones[4] (UBOS, 2019). Figure 1 shows a map of the country indicating the regions and sub-regions.

Agricultural biodiversity in the Ugandan context includes both the diversity of genetic resources (crops, varieties, livestock breeds) and species used directly in production, as well as the biodiversity of non-harvested species that directly support or hamper production (soil micro-organisms, predators, pests and pollinators) and the wider environment that indirectly supports agroecosystems. These two sides of agricultural biodiversity are of interest in this report because CGIAR researchers in Uganda have been working on crop and animal breeding to produce crop varieties or select breeds that will increase agricultural productivity and augment resistance or tolerance to pests and diseases; promote crop diversity to enhance nutrient use efficiency, protect soils and improve nutrition; and promote sustainable land management and climate-smart practices to ensure farmers can be resilient in the face of increasing weather shocks.

Uganda’s agricultural biodiversity is under threat from climate change (Kansiime & Mastenbroek, 2016; Mulumba et al., 2012), while population growth increases pressure on land (Mwesigye &

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[3] There was a very interesting discussion in the SPIA-convened consultation in 2019 about the appropriateness of an export-oriented agricultural sector in a land-locked, ecologically sensitive country.

[4] Officially, Uganda has nine agroecological zones (Lake Victoria Crescent, Lake Albert Crescent, Western Rangelands, Eastern Highlands, Northern Moist Farmlands, West Nile Farmlands, Southwestern Highlands, Southern Rangelands, and the Northern Farming System), but UBOS uses ten as there is a widely-held view that the nine do not represent the distinct vegetation type, elevation and climatic conditions sufficiently (e.g. Kabi et al., 2014).

Matsumoto, 2016)[5]. At the same time, the processes of change within the agricultural sector via commercialization and intensification open both new challenges and new opportunities (Phelps et al., 2013).

**Figure 1: Map of Uganda showing regions and sub-regions**

Source: Uganda Bureau of Statistics, 2024.

Climate change and environmental degradation are diminishing the quantity and quality of yield for a number of crops and affecting livestock systems. The informality of the seed system in the country, with reliance on informal community seedbanks, a weak private seed sector, and a reduced government role in genetic conservation, is believed to have hampered agricultural development (Kiwanuka & Kintu, 2004; Nankya et al., 2022). The agriculture sector experiences high rates of harvest loss from pests and diseases (PARM, 2017), with banana (USD 35 - 200 million annually[6]) and cassava (USD 60-80 million annually) particularly affected, owing to

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[5] Over the period between 2000 and 2020, the population almost doubled, from 24.0 million in 2000 to 44.4 million in 2020. World Bank Data Catalog accessed 6th Sept 2023.

[6] The wide range for this estimate reflects the high degree of uncertainty given multiple data constraints.

widespread cultivation of landraces that lack resistance to the main viral, bacterial and insect pests. Furthermore, there is evidence that climate change affects farmers' ability to sustain their livelihood in the face of sustained climate anomalies (Call et al, 2019).

Subjective reporting by district officers on the environmental conditions in their district supports a picture of worsening environmental conditions. A majority (54%) of district officers report a deterioration since 2000 (see Appendix A). There is remarkable geographical heterogeneity. A larger share of officers reported an improvement since 2000 in parts of Western Uganda and Abi (West Nile). On the other hand, a large majority of officers reported degrading conditions across the other regions of Uganda, notably in Serere (Teso), Mukono (Buganda), and Bulindi (Bunyoro), and strikingly, all officers in Nabuin (Karamoja) do so.

There have been increasing concerns about conflicts over land for agriculture, particularly for grazing livestock. Mwesigye and Matsumoto (2016) find that yields in parcels of land that are subjected to land conflict are lower by 22% relative to those not under conflict, for the same households. Parcels with conflicts over tenure rights that possibly result in evictions have 45% lower yields relative to those without eviction conflicts.

Away from areas of outright conflict, population pressure could increase the value of land, leading to increased intensification on existing parcels and changes in production systems (Ali, 2007). Agricultural intensification often involves the gradual replacement of integrated farming systems with more specialized enterprises, thereby reducing agricultural biodiversity (Pingali & Rosegrant, 1995). In Uganda, there are concerns about the loss of important plants from agricultural systems, and thereby the diets of rural people, including cowpea, soya bean, Bambara groundnut, and finger millet (Mwavu et al., 2016, 2018).

Commercialization of livestock production has progressed with the promotion of communal breeding schemes, often using exotic breeds which, along with their resulting crosses, are not always suitable for local production systems. However, indigenous goats and cattle may be more resilient to local weather conditions and diseases. Kabi et al. (2016) suggest that breed improvement goals can also be achieved through a positive selection of desired traits amongst the indigenous breeds.

## 2.2 Policy Context

The National Agricultural Research Act of 2005 provides for the development of an agricultural research system for Uganda to improve the delivery of agricultural research services. The act promotes the development of modern or improved technologies to increase productivity, efficiency, profitability, and sustainable growth of the agricultural sector. There is no mention of the conservation of biodiversity or the maintenance of genetic diversity[7].

The past two decades of government intervention in the agricultural sector have seen several policy reversals, particularly regarding the system for agricultural extension. Nkonya et al (2020) describe the twentieth-century experience of agricultural extension in Uganda, both

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[7] Indeed, during the compilation of the reference library for cassava, sweetpotatoes, maize, and groundnut, it was difficult to get local reference varieties except for bananas, whose local materials are conserved by CGIAR's Alliance of Bioversity International and CIAT at the International Musa Germplasm Transit Center in Belgium.

before and after independence, as being a centrally controlled public system. By the late 1990s, extension was decentralized to make it more locally accountable to farmers' needs. In 2001, the Ugandan government shifted extension delivery to the private sector but with public funding, underwritten by significant external budgetary support from the World Bank, the International Fund for Agricultural Development (IFAD), and several bilateral donors. The National Agricultural Advisory Delivery System (NAADS) was operated by developing farmer groups, contracting with private agents to provide extension services, and conducting demand-driven monitoring and evaluation (Benin et al, 2007; Nkonya et al, 2020).

NAADS was initially supported by the highest levels of the Ugandan government. An impact evaluation carried out by the International Food Policy Institute (IFPRI) (Benin et al, 2007) reinforced the perception that the program was effective in improving farmers' ability to access improved agricultural technologies. Kjaer and Joughin (2012) argue, however, that political interference increased over time, leading donors to gradually abandon support after the conclusion of the first phase at the end of 2009.

Reforms in the early 2010s – notably at a conference convened by MAAIF in mid-2013 – transferred NAADS back to the MAAIF. A new Single Spine Extension System aimed to rebuild and revitalize the public extension system, effectively re-centralizing it under a new Directorate of Agricultural Extension Services. In mid-2014, President Museveni announced that procuring and distributing agricultural inputs and carrying out strategic interventions would be carried out through a program entitled Operation Wealth Creation (OWC), which leveraged the power of the army to distribute planting materials for crops with a high degree of central oversight. Initially, after receiving induction agriculture training, 300 army veterans were sent out to deliver materials[8].

In November 2022, the government announced that OWC would no longer distribute agricultural inputs after farmers complained about low-quality inputs, planting materials arriving at the wrong time, and mismatches between what farmers wanted to grow and the planting materials provided (Robert and Mesharch 2018).

Instead, funds are now sent via the OWC to Savings and Credit Cooperative Organizations (SACCOs) at the local level, under the Parish Development Model (PDM) – a "multi-sectoral strategy for transforming subsistence households into the money economy" (Government of Uganda, 2022). The PDM embeds agricultural transition towards commercially viable production within a wider process of transformation for the poorest regions of the country. Possibly in part as a reaction to these institutional challenges that constrain effective agricultural extension, the large research for development programs such as the East African Agricultural Productivity Program (EAAPP), Agricultural Technology and Agribusiness Advisory Services (ATAAS) Program, and the Agriculture Cluster Development Project (ACDP) – all funded by the World Bank and other partners – have focused on development and promotion of new improved technologies. Promotion of conservation agriculture technologies, terraces, and rehabilitation of degraded watersheds with contour/grass bunds, agroforestry, and sustainable land management practices such as mulching, intercropping, and crop rotations have all come under the purview of these

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[8] Kjaer and Joughin (2019) provide a comprehensive account of this period of reform in extension services and the political motivations underlying them.

programs. They span 40 districts and 77 sub-counties, and have the goal of improving the health of systems that support agricultural production (see also Section 4.5.2).

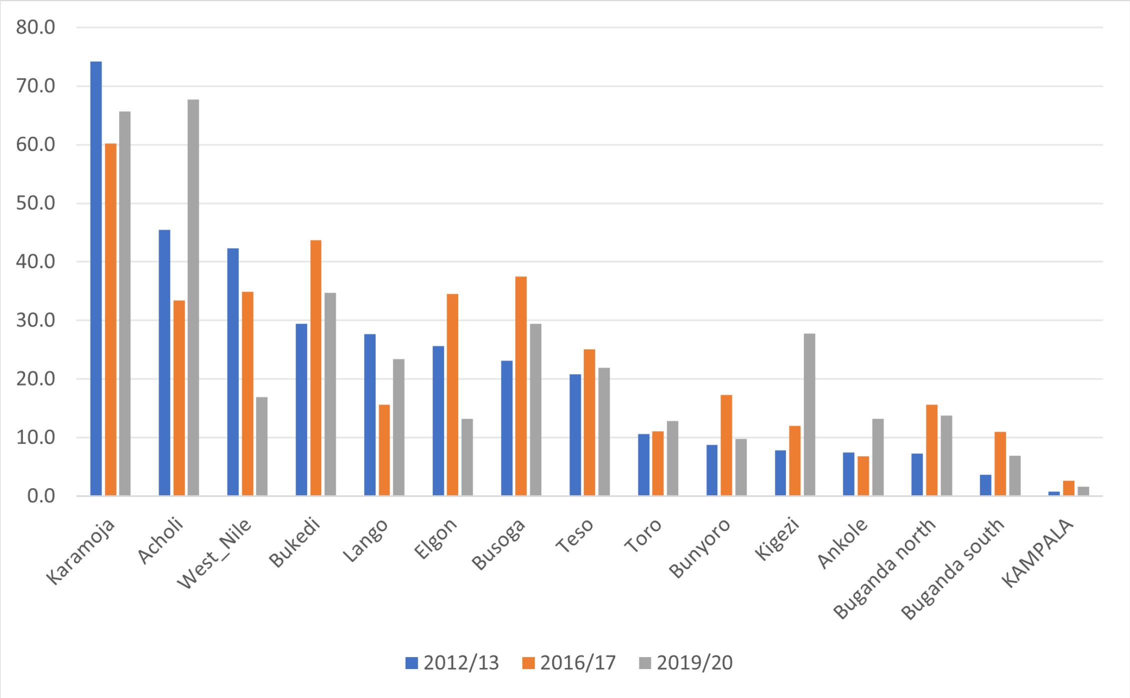
## 2.3 A System Under Stress

Agricultural production and productivity have remained low, and there is a wide gap between yields observed on research stations and in farmers' fields. Productivity per agricultural worker has similarly remained low compared to other countries in the region (World Bank, 2018). It is estimated that Uganda's post-harvest losses range from 30% to 40% for grains and other staples, and 30% to 80% for fresh fruits and vegetables (NPA, 2020). Taken together, progress towards tackling food insecurity, under-nourishment, and poverty would appear to be slow or stagnant in Uganda. A World Bank report identified a significant gap between Uganda's agricultural potential and its current performance (World Bank, 2018). Natural resource degradation has contributed to economic losses and exacerbated poverty. Between 1990 and 2019, forest cover reduced significantly by 44.7%, and woodland cover declined to 17,399 sq km in the year 2019 from 28,347 km$^2$ in 2000. Soil nutrient loss, primarily due to erosion, is estimated to account for USD 625 million per year (World Bank, 2021).

Micronutrient deficiency – the lack of intake, absorption, or use of essential vitamins or minerals the body needs for healthy development – is widespread among children and women of reproductive age in Uganda (WHO, 2013). The Global Alliance for Improved Nutrition (GAIN) supported early projects to fortify widely consumed foods in the country, and in 2011, the Government of Uganda made food fortification mandatory for edible salt (iodine), edible oils and fats (vitamin A), and wheat flour (premix of vitamins and minerals). However, the relatively low share of such processed commercial products in the diets of most Ugandans means that the most vulnerable are unlikely to be reached through this pathway.

There is a notable degree of heterogeneity in poverty across different sub-regions of the country. As Figure 2 shows, the share of households living in poverty in sub-regions like Karamoja, Acholi, and Bukedi has remained persistently high. While there are some subregions with declines in poverty (markedly so in West Nile), others, such as Kigezi, have exhibited increasing trends in poverty. Kigezi sub-region, which has long been an area with a temperate climate, has recently registered increases in temperatures, resulting in rising numbers of cases of malaria (Talisuna et al, 2015) which some researchers have linked to land degradation from increased population pressure and land fragmentation (Himeidan and Kweka, 2012; Lindblade et al, 2000).

**Figure 2: Poverty rates by sub-region 2012-13 to 2019-20**



Source: Uganda National Panel Survey data 2012-13, 2016-17, and 2019-20. Uganda Bureau of Statistics.

## 2.4 Dynamics of Agricultural Change in Uganda: Evidence from Prior Waves of the Uganda National Panel Survey

Here we examine data from eight prior rounds of the Uganda National Panel Survey (UNPS) survey, administered between 2009 and 2021[9]. This gives us a good insight into the dynamics and spatial patterns of agricultural changes over the period leading up to the current study, with a focus on the pressures for land in the country. Livestock numbers and spatial concentration have been dynamic over this period. Figure 3 shows the average share of households holding livestock. There is a marked gradient of livestock becoming less dominant in the livelihoods of Ugandan households as one goes down from north to south. This average picture, however, masks significant movements in livestock numbers that have taken place over the period. Figure 4 shows the percentage point changes between 2009 and 2019 in the share of households that have livestock. This shows large reductions in some regions that were historically part of the cattle belt (Ankole and Buganda), while numbers stayed more stable in the Eastern parts of the cattle belt (Karamoja, Lango, Elgon), and notably increased in Acholi.

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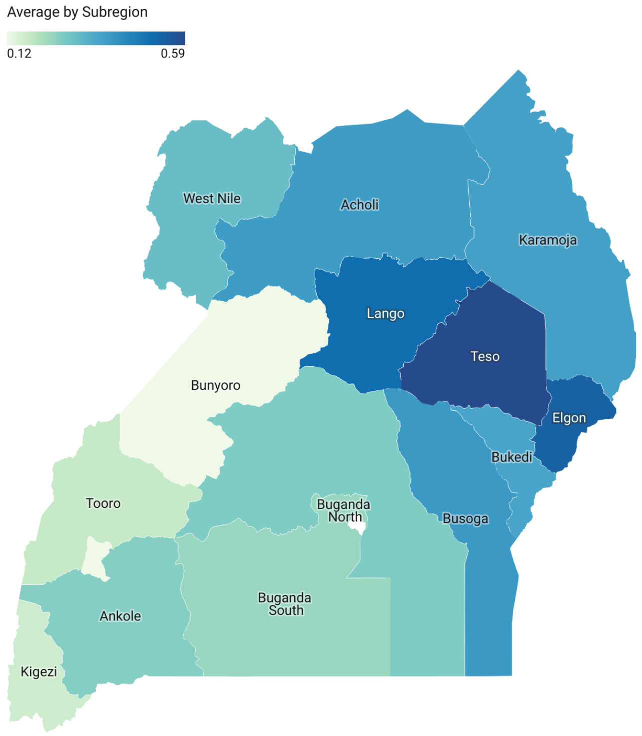
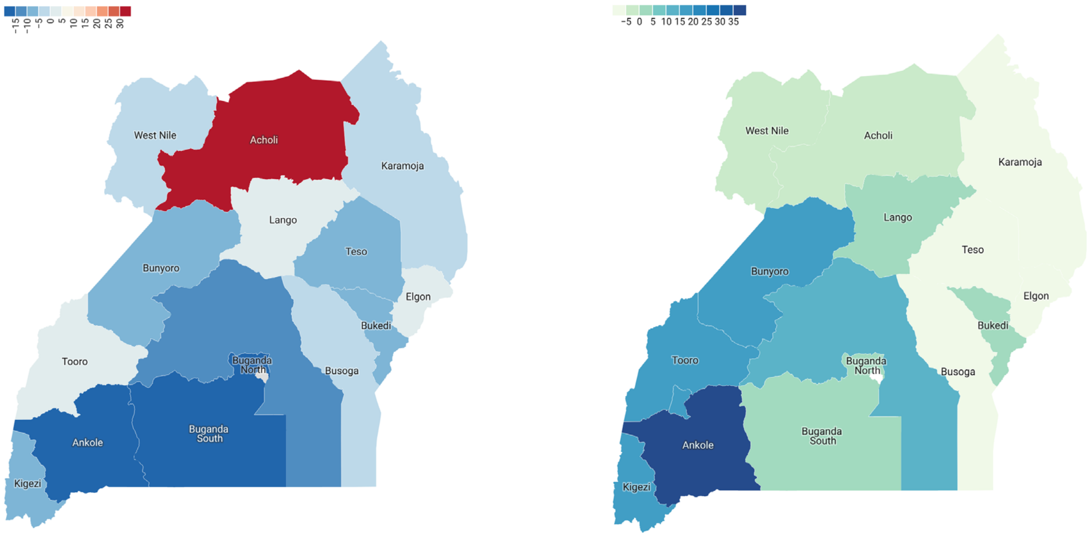
[9] The description of the dynamics by sub-region is meant to be illustrative to provide the dynamic context for the interpretation of the results on the diffusion of agricultural and livestock innovation that are the focus of this report. While the availability of the long-term UNPS panel is of particular value to illustrate these long-term changes, the UNPS is not representative at the sub-region level so sub-region changes should be interpreted as approximative only.

**Figure 3: Share of livestock farmers, Uganda, by sub-region (2009-2019)**



Source: Authors. Uganda National Panel Survey data 2009-2019.

**Figure 4: Dynamic change in livestock farming (percentage point change between 2009 and 2019)**



**(A) Change in share livestock farmers among all farmers**

**(B) Change in the share of livestock farmers without access to pastures**

Source: Authors. Uganda National Panel Survey data 2009-2019.

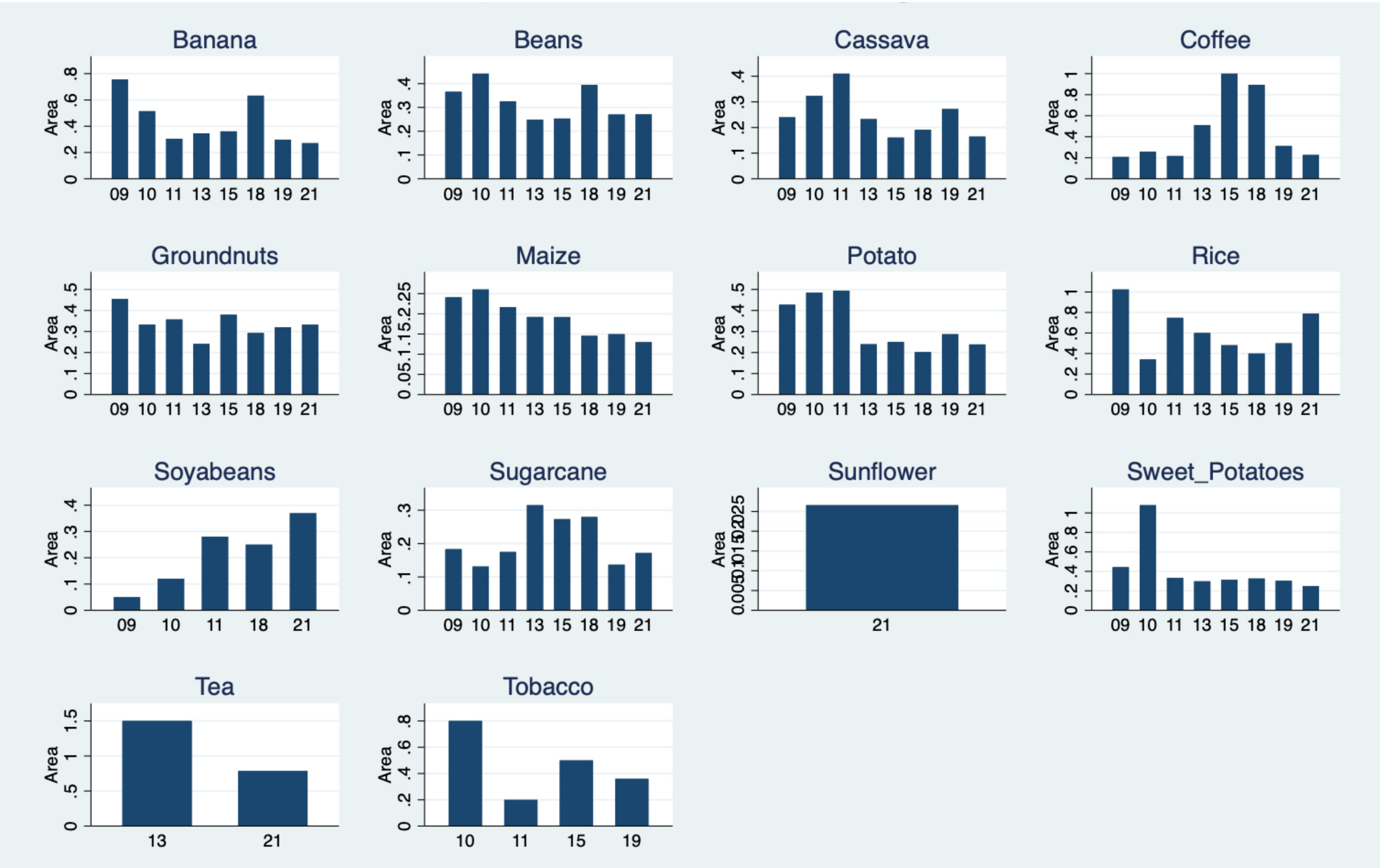
Note: Color codes indicate the intensity of the change between 2009 and 2019.

Figure 4B shows that the falling share of households having livestock in the Western sub-regions of Ankole and Kigezi, compared to previously shown in Figure 4A, goes together with a marked increase in the share of livestock-holding households without access to pastures all across the South West of the country. Pastureland individualization and other land pressures may have led to cattle movements to the East, where common pastures remain common.

We see this same land pressure reflected in crop agriculture in multiple ways. Take the Kigezi sub-region, for example, in the far southwest of the country. Figure 5 shows crop area trends across the survey waves for each of the major crops in Uganda. For most crops, particularly the major staples of maize, cassava, and banana, there appears to be a negative trend over this period, although with important variations between years. Figure 6 shows on a national scale that the size of individual plots is also, on average, smaller over time. All else equal, this picture of extra pressure on land should increase its value, providing households with further incentives to intensify their production on the land they do have, motivating them to obtain improved planting materials and higher-quality agricultural inputs, and giving the land greater managerial attention.

Inter-cropping – planting multiple crops together in a single plot – is one way of deepening the exploitation of the limited land resources that Ugandan farmers have by providing more intensive management to the plot. Two different crops can occupy non-rival, or even potentially complementary, ecological niches within the same plot. Figure 7 provides no clear trend at a household level in terms of the diversity of different crops cultivated. When we look at Figure 8, we see a consistent trend at the plot level wherein farmers are increasingly inter-cropping – fewer and fewer farmers have a single crop on any given plot.

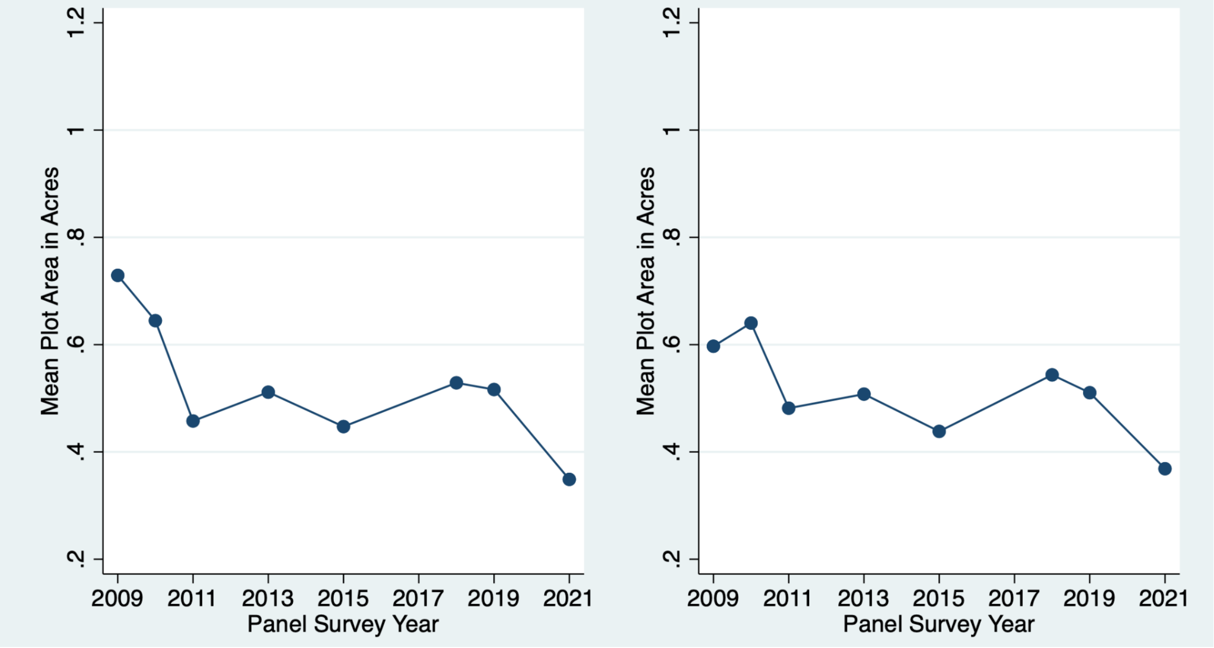
**Figure 5: Kigezi crop area trends: Total plot area for a crop divided by the total number of households, by year**



Source: Authors, Uganda National Panel Survey data, Uganda Bureau of Statistics.

Note: The trend is calculated by the total cultivated area for the crop for each year, divided by the number of households in the sub-region.

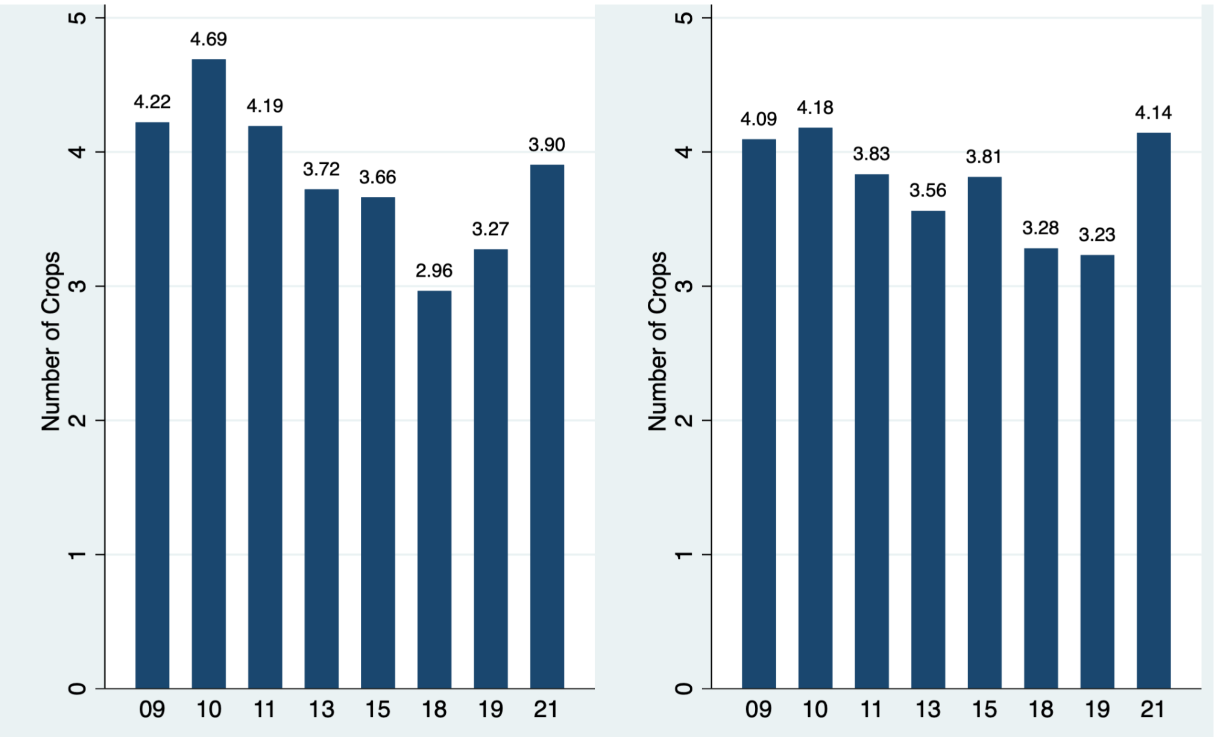
**Figure 6: Mean plot size over time, for season 1 (left panel) and season 2 (right panel)**



Source: Authors, Uganda National Panel Survey data, Uganda Bureau of Statistics.

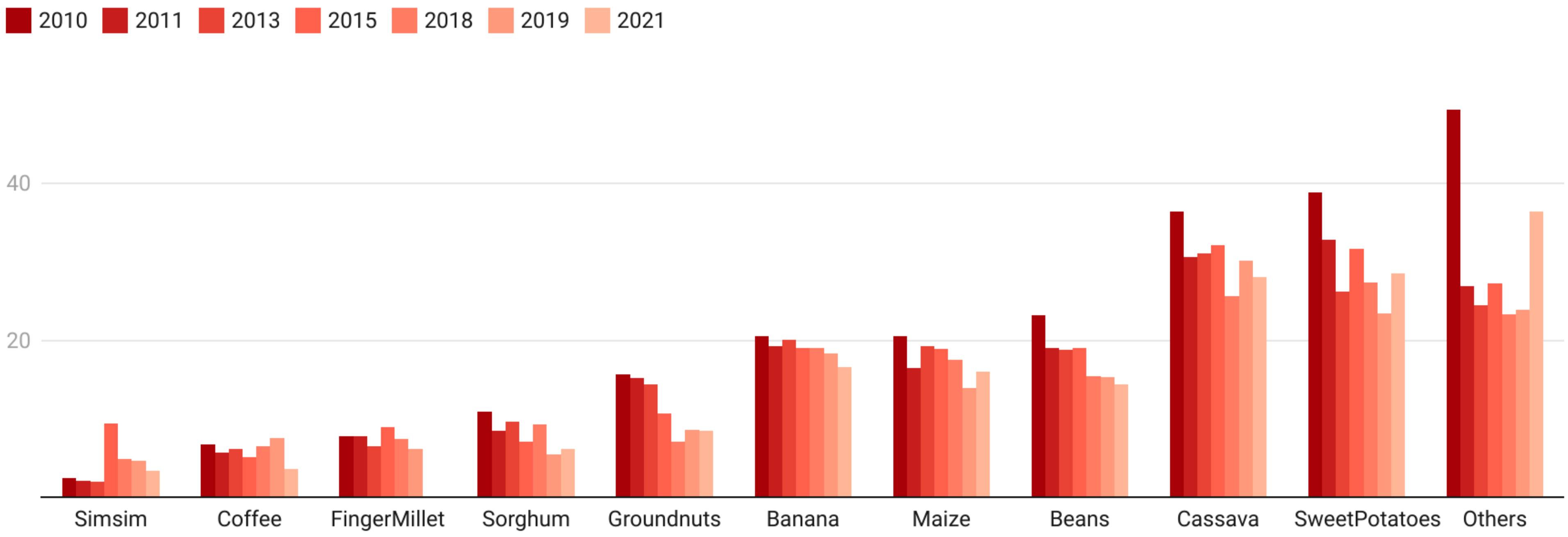
Note: Total area operated by the household is divided by total number of plots in a year.

**Figure 7: Average number of distinct crops cultivated at a household level, for season 1 (left panel) and season 2 (right panel)**



Source: Authors, Uganda National Panel Survey data, Uganda Bureau of Statistics.

**Figure 8: Share of farmers with a single crop on the same plot, by crop, over time**



Source: Authors, Uganda National Panel Survey (UNPS) data, Uganda Bureau of Statistics (UBOS).

# 3. Methods and Data

Given the multiple compounding challenges facing Ugandan agriculture outlined in Section 2, CGIAR researchers have been working alongside their partners at the National Agricultural Research Organization (NARO) to develop and test innovations designed to help alleviate specific constraints. This section explains how we have identified a set of high-priority innovations and worked to collect data about their diffusion and potential adoption by farmers.

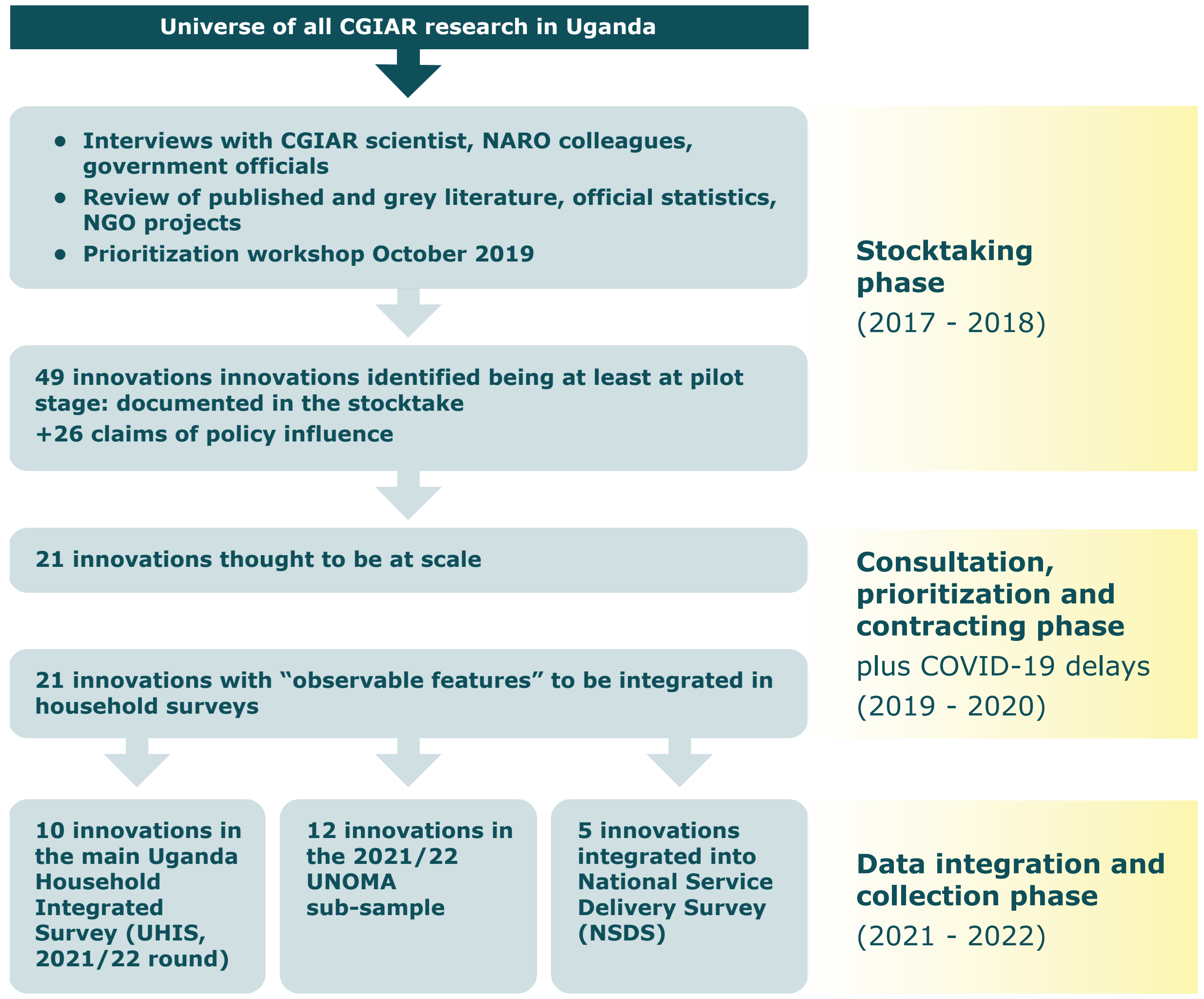
## 3.1 Identifying CGIAR-Related Innovations

The exercise of documenting the reach of CGIAR-related research starts with a basic set of questions: What has been the focus of CGIAR research efforts in Uganda? Where have these efforts been translated into specific innovations? Are these innovations likely to have reached farmers, consumers, and communities? We addressed these questions by systematically compiling key information on the past two decades of research activities (2000 – 2020). Our main objective was to take stock and document a list of potential innovations to consider for future data collection efforts.

First, we identified and drafted some potential priority topics and presented them for stakeholder consultation at a meeting in Munyonyo, Uganda, in February 2019. The stocktaking document summarizes the selection process of innovations for which measurement was integrated into national surveys and makes the information obtained through the process readily accessible. The schematic for prioritizing innovations is shown in Figure 9, and two example entries are provided in Table 1.

This stakeholder consultation, with CGIAR and NARO scientists, government officials from several ministries, and donor representatives, played an important role in the prioritization to determine which innovations to document scale through integration in national representative survey data. This approach was followed given the limited evidence available from other sources about the extent to which scaling efforts had been undertaken for particular innovations, with important exceptions, notably the scaling efforts for biofortified beans and maize. As such, the method followed for Ethiopia reported in Kosmowski et al (2020), where it was possible to get more systematic information on scaling through large projects and government systems, had to be adapted for the Ugandan context. This partly reflects the differences in institutional organization, extension services, and other scaling mechanisms between the two countries.

Figure 9: Schematic for prioritizing innovations to be selected for data collection



Note: There are 21 innovations with data collection, but some with more than one survey covering them, so the total is greater than 21.

## Table 1: Overview of 'One Must Do, Five Reductions' (1M5R) lenient and strict criteria

| Innovation | CGIAR-related efforts for development and/or dissemination | Description | Scale and location | Observable feature | Notes on dissemination strategies/ pathways |
|---|---|---|---|---|---|
| **Disease-resistant cassava varieties** | 1. African Cassava Agronomy Initiative (ACAI) (IITA, 2015-2020)<br>2. Breeding RTB (Roots, Tubers, and Banana) products for end-user preferences (RTBfoods) (IITA, 2017-2022)<br>3. Next Generation Cassava Breeding (Phase II) (IITA, 2018-2022)<br>4. Great Lake Cassava Initiative (GLCI) (CRS, IITA, 2008-2012) | Cassava mosaic disease (CMD) and cassava brown streak disease (CBSD)-resistant varieties. The varieties with different traits can be recommended targeting different value chains: fresh market, high-quality cassava flour, and starch. | Twenty-five elite varieties with tolerance or resistance to these two diseases are now evaluated in regional trials in Kenya, Uganda, Tanzania, and other countries. Thousands of farmers have been involved in the evaluation of the released varieties in all 32 countries in SSA where IITA is collaborating with NARS in germplasm development and evaluation. It is thought that varietal turnover may have happened in recent years in areas previously badly hit by viruses. | Genotype(s) can be identified from sampling farmers' fields | Operation Wealth Creation (OWC), Northern Uganda Social Action Fund (NUSAF), Agricultural Technology and Agribusiness Advisory Services (ATAAS) project strategic agricultural commodity |
| **Banana-coffee inter-cropping** | 1. APEP (Agricultural Productivity Enhancement Program) 2005-08<br>2. CCAFS (Climate Change, Agriculture and Food Security) CGIAR Research Program | Planting practice that pre-dates IITA's involvement. IITA researchers studied different aspects of the agronomy of intercropping banana and coffee, then facilitated planning by developing extension materials on it for NGOs and national partners. | Ntutasamo, Mbarara, Bushenyi in particular. Central and North are Robusta coffee-growing regions. East, South-West, and West Nile are Arabica coffee growing regions. | Planting both coffee and banana in the same plot | Being promoted by government extension officers |

## 3.2 Data Sources and Measurement Approaches

### *3.2.1 Uganda Harmonized Integrated Survey 2021/22*

The Uganda Harmonized Integrated Survey (UHIS) is an integration of the Uganda National Panel Household Survey (UNPS) and the Annual Agricultural Survey (AAS), under the auspices of the 50X2030 initiative. The goal of integrating these two surveys is to provide the data Uganda needs to understand the poverty dynamics, drivers of agricultural productivity and income, and their linkages with welfare and government programs. Before the integration, the UNPS and AAS surveys were conducted independently, yet both collected data on agricultural-related indicators. The integration aimed to avoid potential inconsistencies due to differing survey methodologies, establish a more cost-efficient approach to agricultural data production, and provide agricultural and socio-economic data in a coordinated manner (Ponzini et al., 2022).

The integration of the two surveys comprises three sets of samples, namely: an annual sample of agricultural and non-agricultural households from a) rural and b) urban areas (together making the annual panel sample – APS), complemented with c) an additional sample of agricultural households every two years (biennial cross-sectional sample (BCS)). The full UHIS sample size is 9,288 households in 774 enumeration areas (EAs). Of these, the APS represents 6,072 agricultural households in 506 rural EAs and 276 non-agricultural households from 23 urban EAs and is representative of agricultural statistics at the regional level (Ponzini et al, 2022). The BCS contributes an additional 2,940 cross-sectional agricultural households in 245 EAs to make more accurate agricultural statistics, making the combined APS/BCS sample representative at the sub-regional level in those years.

The UHIS fieldwork activities were initially planned to start in May 2020 and end in April 2021, to cover the 2020 agricultural season. However, due to the COVID-19 pandemic and then a scheduling conflict with the long-planned Uganda Livestock Census 2021, the UHIS activities had to be shifted. The survey finally commenced in October 2021 and was implemented over more than a full calendar year, concluding in December 2022. The fieldwork was conducted in three phases. The first phase started with a visit at the end of the second season planting period of 2021. This was followed by a second visit at the start of the 2022 first season post-planting period (and included retrospective questions for the 2021 second season). Finally, a third visit was carried out post-harvest for the first season of 2022.

The UHIS had four questionnaires, namely: (i) post-planting; (ii) post-harvest; (iii) annual; and (iv) community.

The post-planting questionnaire had eight modules: the household's parcel list; agricultural parcels roster; plot and crop rosters; Uganda National Study on Objective Measurement in Agriculture (UNOMA) leaf sampling; UNOMA crop diseases; UNOMA crop-cut; and seed acquisition modules. All UNOMA modules were administered to only the UNOMA samples (see Section 3.2.2), and all others were administered to the entire UHIS rural sample.

In the plot roster module, SPIA integrated questions related to sustainable land management practices for erosion control, irrigation systems and methods, land preparation methods, and questions about perceptions of soil quality.

In the crop roster module, SPIA integrated questions on the types of intercropping practiced, the quantity of seed used, the type of seeds (improved, local, certified, or quality declared seed), crop varietal mixing within the same plot, reasons for varietal mixing, and the names of varieties cultivated. SPIA also integrated orange-fleshed sweetpotato variety identification for all households using a visual aid.

The post-harvest questionnaire had seven modules: input use; input acquisition; labor input (from household); labor input (hired); temporary crop production; temporary crop disposition; and tree/permanent crop production and disposition. SPIA supported the development of the questions on input use, timing of application, and acquisition. The annual questionnaire had 21 modules capturing information on agricultural processing, livestock and aquaculture production, forest products, and households' use of agricultural extension services. In the community questionnaire, SPIA ensured the integration of agriculture-related questions, on topics including land rights, community-level access to inputs, crop and sustainable land management practices, relevant weather events, veterinary services, tree nurseries, milk collection centers, and farmer organizations.

While the current report does not draw on all the questions that were integrated with SPIA support, these questions allow for further analysis in future, more in-depth studies on innovations highlighted in this report.

### *3.2.2 Uganda National Study on Objective Measurement in Agriculture (UNOMA)*

SPIA partnered with the World Bank LSMS team, FAO, and UBOS to introduce objective methods for crop variety identification through tissue sampling and DNA analysis for six crops: maize, cassava, banana, sweetpotato, common bean, and groundnut. The choice of the six crops was based on CGIAR's involvement in breeding efforts and their importance for smallholder farmers in multiple regions of the country. A visual aid on pests and diseases for these same crops was also developed, to be used during data collection of the UNOMA module. These efforts were part of a bigger project to integrate objective measurements into the UHIS on an experimental basis, alongside plot area measurement with GPS, and maize production estimation using crop cuts. The goal of this work was to help mainstream such approaches into zonal-, regional-, and nationally representative surveys. A methods experiment – the Uganda National Study on Objective Measurement in Agriculture (UNOMA) – was agreed during the CGIAR-UBOS-MAAIF stakeholder consultation meeting held in Munyonyo in October 2019 and implemented as part of the Uganda Harmonized Integrated Survey (UHIS).

The UNOMA data collection was designed to be implemented within a subsample of 506 enumeration areas selected from the agricultural households under the APS. The choice of the APS was to leverage the technical assistance provided by the World Bank and SPIA and to build on successful experience with the 2015 and 2016 rounds of the Methodological Survey Experiment on Measuring Maize Productivity, Soil Fertility, and Variety (MAPS) (Gourlay et al., 2019; Lobell et al., 2020). This was implemented in Eastern Uganda by UBOS, with technical and financial support from the World Bank LSMS and SPIA.

Subsampling took advantage of the logistical organization of the three survey visits covering the two agricultural seasons. Specifically, each survey visit was divided into four trips lasting approximately one month, during which the enumeration team covered approximately 144 EAs[10]. The UNOMA modules for the six priority crops were only collected in a targeted subset of trips. Specific trips for sub-sampling, such as tissue sampling for subsequent DNA analysis, were necessitated by seasonality issues in some cases (samples need to be collected when the crop is growing) and to keep the overall burden on the enumeration teams manageable. The random selection of enumeration areas for each trip means that, by design, there was no geographic bias expected for these sub-samples.

Tissue was collected from leaf samples for five of the six crops. Sweetpotato and beans were sampled during Visit One on Trips One and Two (September and October 2021). It was done in all plots of each crop and up to a maximum of three farmer-declared varieties per plot. Cassava was sampled in Visit Two on Trips One and Two (March to May 2022), in all plots of each crop and up to a maximum of three farmer-declared varieties per plot. Banana was sampled across two different visits between March and December 2022[11]. Groundnut leaf samples were collected during Visit Two on Trip Four (Aug 2022) and Visit Three on Trip One (Sept 2022). Maize samples were taken using crop cuts. Two 8m x 8m subplots were laid (see Gourlay et al, 2019 for protocol) on one randomly selected plot during Trips Two and Three (May – July 2022) and later harvested by a separate team immediately before the farmer was ready to harvest (July – Aug 2022).

Data on crop varieties were collected at the plot x crop x variety level, using survey-based subjective/self-reported methods during the post-planting survey visit. The responses were provided by the manager of the randomly selected plot in each instance. Questions included the name they gave the variety (noted for subsequent manual coding into meaningful groups of very similar names), whether the farmer thought the variety was local or improved, and whether the sweetpotato flesh was considered orange with the support of a visual aid. In addition, a sample of plant tissue (leaf for beans, sweetpotato, banana, cassava, and groundnut; grain from the crop-cut for maize) was collected and used to identify the crop variety using DNA fingerprinting (see Section 3.2.3 and Appendix B for details on the DNA fingerprinting methodology used).

In the case of the subjective methods (farmers' self-elicitation of varieties grown), farmers were asked to report on the names of their crop varieties at two different moments during the data collection. The first time was when asked to list all plots and crops, including varietal information, during the regular data collection administered at home before the enumerators visited the selected plot. The second was after walking to the selected plot when collecting the other data for the UNOMA leaf module (see below). At this point, the varietal questions were administered in the plot where specific varieties sown in distinct areas of the plot could

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[10] A trip consisted of a logistical planning period when the enumerators would go out from Kampala with supplies for that month, then return to rest and re-stock, and is a random subset of the overall sample of EAs.

[11] Initially the number of varieties per plot was unlimited, as farmers can plant many different banana varieties in order to hedge against different biotic stresses. However, this approach became a problem during implementation, with enumerators reporting many varieties per plot in some cases and the time taken to implement the protocol for each one led to delays and caused some logistical difficulties. A similar limit of three varieties per plot was then instituted for the remainder of the sample.

be determined, based on a conversation between the enumerator and the respondent. After a series of questions on each variety, leaf samples were taken.

The UNOMA leaf module captured information on varietal names, varietal mixing, types of varieties, source planting material, price, whether local or improved, biofortified or not (beans, sweetpotato), hybrid or open pollination (maize), and varietal trait questions. Trait questions asked about farmers' perceptions of the variety in terms of yield, taste, nutrition, cooking properties, disease and pest resistance, maturation time, drought tolerance, marketability, aspects of crop management, and storage. The UNOMA crop pests and diseases module contains questions specific to the crop in question and uses photo aids as shown in Appendix C.

### *3.2.3 DNA Fingerprinting of Six Crops*

#### 3.2.3.1 Reference Library Compilation

A comprehensive reference library is key for successful crop varietal identification with DNA fingerprinting (Poets et al, 2020). No prior comprehensive reference libraries existed for the six crops in this study, and this necessitated compiling one for each crop. SPIA partnered with NARO, whose scientists took the lead in compiling the reference libraries for cassava, sweetpotato, maize, and groundnut. Researchers at the International Institute of Tropical Agriculture (IITA) and the Alliance of Bioversity and CIAT compiled the reference libraries for banana and common beans, respectively. For each crop, the following steps were followed: (i) compiling an updated list of all the released varieties for each crop, (ii) documenting what is known about popular landraces for each crop; (iii) assembling the plant tissue (seed or leaf) used for genotyping from each crop; and (iv) preparing the plant tissue (flour or leaf discs) for shipment to the genotyping laboratory in Australia (Diversity Arrays).

Priority was placed on securing reference samples of as many of the released varieties as possible. In a few cases, it was impossible to obtain reference samples for released varieties that had never been widely disseminated (or in a few instances, had been disseminated but had fallen out of use in recent years). The landrace accessions included for each crop aimed to capture regional variation, with numbers largely at the discretion of (and reflecting the genotyping research interests of) the NARO researchers supporting the reference library compilation.

**Maize**

Maize represents the most challenging reference library to construct owing to the presence of commercial seed companies and the complications of the plant's biology and breeding strategies used to improve it. Maize varieties in the Ugandan market fall into two broad categories: open-pollinated varieties (OPVs) and hybrids. OPVs are composed of genetically diverse individual plants (i.e., heterogeneous populations) that are intercrossed to maintain vigor. Hybrid varieties in Uganda are either varietal hybrids or three-way hybrids (3WHs). To create varietal hybrids, two OPVs are crossed with each other. For 3WHs, three inbred lines are crossed in two steps to result in the finished hybrid. Details of the process taken to produce reference finished hybrids under controlled conditions on-station at NaCRRI are provided in Appendix D.

The completed maize reference library comprises four OPVs (MM3, LONGE 4, LONGE 5, and LONGE 5D), three varietal hybrids (UH5051, UH5052, and UH5053), and 20 three-way hybrids that are owned and maintained by NARO. To check on the validity of the crosses described above, and the purity of the inbred lines, 318 samples of inbred lines and 150 samples of single crosses were also submitted for genotyping. Furthermore, 18 varieties produced by commercial seed companies, either in Uganda or imported, are included. The full list is provided in Appendix E. References for these imported or hybrids produced by seed companies were procured from their agents or outlets, leaving open the possibility of these being genetically indistinguishable from other varieties. Seed samples were ground to a uniform fine flour consistency and then plated and shipped to Diversity Arrays.

### Banana

The banana reference library comprises 137 accessions[12], collected from the National Agricultural Research Laboratories (one of the institutes of NARO) conservation sites in Mbarara and Kawanda, and IITA fields in Sendusu. The largest group of references is the East Africa Highland banana (EAHB) landraces, known as "matooke" landraces (60 accessions), reference samples of which were collected by IITA, who also carried out ploidy analysis[13] on the samples. From the long-standing breeding program of NARO and IITA, there are the following accessions: four Honduran hybrids (Kabana 1H – 4H); one released landrace (Kabana 5H); seven improved matooke varieties that have been bred and released in Uganda under the partnership with IITA (Kabana 6H and 7H; NAROBan 1 - 5); and five matooke improved varieties (NARITA 4, 17, 18, 22, and 24) that are in final on-farm trial / pre-release in Uganda. These were included as they might have been taken up outside of the formal release process. Appendix F has the complete list of accessions and information on the releases. Leaf discs were taken and shipped to Diversity Arrays (DArTseq) and Intertek (KASP).

### Cassava

The cassava reference library was constructed from a collection of 51 cassava accessions, comprising 18 officially released varieties[14], 24 landraces[15], seven elite clones, and two candidate clones, that are maintained by cassava program at NaCRRI. Details are provided in Appendix G. Leaf discs were taken from the reference germplasm and shipped to Diversity Arrays.

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[12] This reference set was initially compiled by IITA but in carrying out ploidy analysis on the reference set, a tracking error was suspected so the entire reference set was resampled and resubmitted.

[13] Ploidy analysis establishes the number of sets of chromosomes present in the nucleus of cells. Bananas can be diploid (i.e., x2), triploid (x3) or tetraploid (x4). Ensuring that the accession had the expected ploidy level was an important check on potential tracking errors.

[14] This reference set was compiled by NACRRI. Six additional released varieties could not be found in the maintained germplasm, namely: Embwa Natereka (released in 1970 and considered obsolete); NASE 7 and 10 (1999 releases that were not popular); NASE 15, 17 and 18 (2011 releases and the most problematic absences from our reference set. We do, however, have three other 2011 releases in the set - NASE 13, 14 and 16 – so we can observe whether there has been any adoption of those from that same year cohort).

[15] Two landrace accessions were thought to be synonyms “Kwatamumpale” and “UG110304” of the same underlying genotype but are treated as separate accessions in the reference library.

### Common Bean

Breeders' seed for 36 of the 43 released bean varieties was obtained from the CIAT genebank in Kawanda[16]. Reference samples for 436 landraces were obtained from two sources, namely CIAT in Kawanda and the Plant Genetic Resources Centre (i.e., the Ugandan national genebank). This resulted in a total of 472 accessions in the bean reference library set (see Appendix H). The bean seeds were planted in pots and germinated, and leaf discs were taken from the young plants and shipped to Diversity Arrays as per the sweetpotato procedure outlined below.

### Sweetpotato

For sweetpotato, NARO multiplied the reference material of 26 released varieties and maintained it in buckets in a screenhouse. Five of these released varieties were advanced cultivars (farmer varieties) that had been evaluated by NARO, with the remaining 21 having been bred through hybridization schemes by the breeding program. Nine of the released varieties are orange fleshed. NARO also collected, multiplied, and maintained 106 accessions of popular sweetpotato germplasm from farmers' fields for evaluation for their distinctiveness as reference germplasm. These accessions were phenotyped for key agronomic traits. The total number of accessions in the reference library is therefore 132 (see Appendix I).

Four leaf discs were punched from each accession in the reference material that was conserved in the screenhouse. These discs were placed in pre-labeled microtubes that were assembled in 96-well plates. The uncovered microtubes were oven-dried for 24 hours to prevent spoilage in transit to the genotyping laboratory. These samples were later plated and transferred to the desiccator at NARO to maintain their dry state before shipment to Diversity Arrays.

### Groundnut

The reference library was compiled by staff at the National Semi-Arid Resources and Research Institute (NaSARRI) and comprises 20 official varietal releases, four candidate releases, and 13 samples of known landraces held and maintained by NaSARRI[17]. Details are provided in Appendix J. In addition, NaSARRI staff fielded a collection mission in early 2023 to collect samples of popular landraces for genotyping and phenotypic characterization. While not reference samples *per se*, these additional farmer landrace samples provide phenotypic information to link to specific genetic profiles, which is useful given the limited nature of the groundnut field sampling in UNOMA (i.e., collecting leaf samples only). NaSARRI's field mission yielded 303 such landrace samples that were treated as additional field samples. Leaf discs were taken and shipped to Diversity Arrays.

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[16] This is a quite comprehensive reference list, with the only omissions being: three "snap" bean varieties released in 2014 (NAROSnBe1, NAROSnBe2, NAROSnBe3); NABE 27C (2012 release known to the bean program but for which seed is not available); NABE 11C (2003) and NABE 7 (1999) but it is unclear if these are distinct from NABE 11 and NABE 7C respectively, which are in the reference set; and Banja 2 (1968 release with samples no longer available).

[17] This is a comprehensive reference library of varietal releases, the only omissions from varieties listed as officially released being five old varieties from 1969/70 which have long been obsolete, namely: Tatu 386, Roxo, Bukene, Mt Makulu Red, and Mwituude.

### 3.2.3.2 Genotyping Methods

After submission of reference and field-collected samples to Diversity Arrays, DNA extraction was done, followed by genotyping. The DArTSeqLD platform[18] was used to generate data for banana, cassava, and sweetpotato. Genotype data for the rest of the crops were generated using DArTag[19]. Both platforms produced sequence data, which were processed using custom pipelines to result in allele count data that reflected the proportions of alleles at each locus for all single nucleotide polymorphisms (SNPs) (Sánchez-Sevilla et al., 2015). The high-resolution counts data were used for downstream analysis of maize (bulked and outcrossing samples) as well as bean (inbred but bulked samples). For the rest of the crops, the counts were reduced to score data, which are analogous to output generated by other genotyping platforms and were sufficient for analysis of single-leaf inbred and clonally propagated crops. The number of SNP markers generated for each crop is summarized in Table 2. Information on the bioinformatic analysis behind the calling of varietal matches between references and field samples can be found in Appendix B.

Table 2: Summary of genotype data generated for the six crops

| Crop | System | Sample type | Platform | Data used | Analysis | References | Samples | SNPs |
|---|---|---|---|---|---|---|---|---|
| **Beans** | 1. Inbred | Bulked leaf | [a]DArTag | Counts | DAP | 436 | 714 | 1865 |
| **Groundnut** | 2. Inbred | Single leaf | [b]DArTag | Score | Distance | 37 | 353 | 2500 |
| **Banana** | 3. Clonal | Single leaf | DArTseqLD | Score | Distance | 133 | 3006 | 14625 |
| **Cassava** | 4. Clonal | Single leaf | DArTseqLD | Score | Distance | 50 | 1953 | 8205 |
| **Sweetpotato** | 5. Clonal | Single leaf | DArTseqLD | Score | Distance | 132 | 1302 | 1611 |
| **Maize** | 6. Outcrossing | Bulked seed | aDArTag | Counts | Purity | 351 | 706 | 3305 |

Notes:

[a] DArTag SNPs based on mid-density panels available at https://excellenceinbreeding.org/toolbox/services/mid-density-genotyping-service.

[b] The mid-density panel is not yet available for public use, but it is accessible to CGIAR institutions.

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[18] DArTSeqLD, a variant of DArTSeq, is a complexity reduction genotyping technique that uses a combination of enzymes optimized to develop a representative library of the genome for sequencing (Kilian et al., 2012).

[19] DArTag differs from DArTSeqLD, in that, the final output is limited to pre-defined marker data curated from prior projects or publicly available SNP panels.

### 3.2.4 National Service Delivery Survey

In 1992, the Government of Uganda introduced its decentralization policy, transferring substantial planning and service delivery functions from the central government to the local government units. The National Service Delivery Survey (NSDS) was institutionalized to monitor and evaluate the delivery of public services and obtain feedback from service recipients regarding their availability, accessibility, affordability, and utilization of these services. Agriculture is one of the sectors covered alongside others such as education, health, water, and sanitation.

The first NSDS was conducted in 2000 by a consortium of firms led by Development Consultants International (DCI). The Administrative Reform Secretariat of the Ministry of Public Service coordinated the survey, and the Uganda Bureau of Statistics (UBOS) provided technical support. In 2004, the second NSDS was conducted as part of a continuous series that provides periodic updates on the performance of public services regarding availability, accessibility, utilization, and satisfaction of services. The 2004 survey was conducted by UBOS in collaboration with the Ministry of Public Service. The findings provided indicators to facilitate bottom-up planning through monitoring and evaluation of the performance of the various actors. Since then, a series of NSDS has been conducted, including in 2008, 2015, and most recently in 2021, the implementation of which was affected by the COVID-19 pandemic.

The overall objective of this fifth full-fledged NSDS was to provide a comprehensive assessment of the trends in service delivery, through comparisons with previous surveys on the topics previously covered, and to obtain baseline information on topics not covered. The specific survey objectives were to: (i) provide up-to-date information about the performance and impact of selected public services at the local government and national level; (ii) measure changes in service delivery in the selected sectors; (iii) identify constraints and gaps in the provision of selected government services by sectors; (iv) provide recommendations for improvement in service delivery; and (v) generate and disseminate information about services offered by selected government sectors.

The NSDS 2021 sample was designed to allow generation of separate estimates at the national level, for urban and rural areas, and for the 15 sub-regions of Uganda. A two-stage stratified sampling design was used. At the first stage, enumeration areas (EAs) were grouped by districts of similar socio-economic characteristics and by rural-urban location. The EAs were then drawn using Probability Proportional to Size (PPS). At the second stage, households were drawn using systematic random sampling. A total of 1,088 EAs were selected from the 2014 National Population and Housing Census (NPHC) list of EAs, which constituted the sampling frame. A sample of 9,338 households was interviewed, with a response rate of 87%. Unlike the 2004 NSDS, it was not possible to get district estimates. The survey was designed to generate representative data at the level of 15 sub-regions and therefore provide results at the sub-regional level and for rural/urban areas.

The survey deploys two types of questionnaires, namely household (service user) and institutional (service provider). The institutional questionnaires comprised specific versions for community/sub-county, district, and enterprise. The content was based on the previous NSDS rounds and recommendations from stakeholders during survey design. Respondents for the institutional questionnaires included Chief Administrative Officers, Heads of Departments (e.g., District Production Officers), Headteachers, Heads of Health Institutions, Community Development Assistants, Sub-County Chiefs, Extension Officers, Health Assistants, community leaders, and community members. The NSDS data is collected and directly captured electronically using Computer Assisted Personal Interview (CAPI) devices while in the field.

SPIA collaborated with UBOS and MAIFF to consult with agricultural stakeholders in Uganda to improve the NSDS through better agricultural modules. SPIA introduced questions on the delivery of agricultural extension services (production), agricultural technologies, marketing and nutrition, crop varieties, plant and animal regulation, climate change, crop and livestock diseases, and pest outbreaks. SPIA also inserted questions to the extension officer regarding their knowledge of the nutritional benefits of orange−fleshed sweetpotato, and recommendations they give related to banana wilt outbreaks and drought tolerance of maize varieties.

### *3.2.5 Companion Projects*

This report also draws on two companion projects in Uganda, which SPIA engaged with as complementary to the work on estimating the reach of CGIAR-related innovations. First, SPIA collaborated with the International Potato Center (CIP), the International Center for Tropical Agriculture (CIAT), and HarvestPlus to document the roll-out of biofortified beans and orange-fleshed sweetpotato at the sub-county level in Uganda. This was based on a compilation of existing Monitoring and Evaluation (M&E) databases, complemented with a targeted workshop to elicit information from local actors on the dissemination of biofortified planting material. SPIA then worked with CIP to conduct a long-term follow-up to a 2011 household survey on improved bean and sweetpotato adoption (LaRochelle et al, 2018). The original 2011 survey had been implemented as part of the Diffusion and Impact of Improved Varieties in Africa (DIIVA) project (Walker and Alwang, 2015). Merging the information on the national level roll-out with the data from the revisit to the DIIVA sample (in 2022), and to different rounds of the Ugandan Demographic and Health Survey (UDHS) allows evaluation of the extent to which dissemination efforts are predictive of the presence of biofortified varieties in farmers’ fields and their consumption. This then enables estimation of the causal impact of the roll-out of biofortified crops on child nutrition status (Macours, Mallia, and Okello, 2025). This work was carried out through a partnership between SPIA, CIP, Gaplink, and the Paris School of Economics.

Second, Professor Travis Lybbert (UC Davis, now SPIA Chair) and Dr Enid Katungi (CIAT) secured funding from the Feed the Future Innovation Lab for Markets, Risk and Resilience (MRR-BASIS), for a study to collect and genotype seed samples from different points in the seed system for maize and beans in Uganda. The objective of this study is to see if there are distinct break points in the seed system at which the varietal identity, purity, and other indicators of seed quality (e.g., germination rate) deteriorate. This work was carried out in partnership between SPIA, UC Davis, CIAT, the Department for Crop Inspection and Certification (DCIC) within MAAIF and NARO. The objective of linking this work with the on-farm sampling from maize and beans plots carried out in UNOMA is that it allows us to understand whether instances of genetically mixed plots found in Uganda can be partly attributed to impurities introduced high in the seed supply chain.

#### 3.2.5.1 Longitudinal Panel Study on Dissemination, Adoption, and Nutritional Impact of Biofortified Crops

In 2019-2020, SPIA worked with Harvest Plus, CIP, and CIAT to construct a sub-county-level database of the dissemination of biofortified planting material during the 2010-2020 period, by assembling information from the M&E systems of Harvest Plus, bilateral projects by CIP and CIAT, and M&E data from the NGO partners engaged in dissemination efforts.

To complement this information, SPIA conducted regional workshops across Uganda, focused on the timing and location of dissemination activities for biofortified bean, and sweetpotato. Workshops were organized in Kampala (Central Uganda), Mbarara (Western Uganda), Gulu (Northern Uganda), and Kumi (Eastern Uganda) by the Kampala-based SPIA team and researchers from Bioversity International, CIP, CIAT, and HarvestPlus. Participants were drawn from national and local government agencies, NGOs, NARO scientists from the Zonal Agricultural Research and Development Institutes (ZARDIs), agricultural officers from the districts, seed multipliers, seed companies, and farmer organizations. Details of the workshop activities are included in Appendix K.

The 2011 DIIVA sample was designed to be nationally representative of bean and sweetpotato household producers, comprising 1,908 farming households in 108 rural communities in 54 sub-counties throughout Uganda. Full details of the 2011 sample are provided in LaRochelle et al (2018). The original data collection took place in two rounds – during the second season of 2011 and post-harvest and marketing of that same season (between February and March of 2012). A 2022 follow-up panel survey was conducted to resurvey these same households. The original households included in 2011 were sampled, plus additional households to offset the potential loss of statistical power due to attrition. A total of 2,150 households were sampled in 2022, comprising 1,732 households from the original 2011 sample (representing a 9.2% attrition rate) along with 432 newly sampled households (randomly drawn among current bean and sweetpotato farmers in the 108 sample communities). The 2022 follow-up survey focused on sweetpotato varieties and their traits, production, inputs, and cultivation practices (Macours, Mallia, and Okello, 2025).

The same 2,150 households were then revisited one year later (between January and April 2023) to obtain health outcome data, as well as height measures for all children potentially exposed to sweetpotato distribution during childhood (defined as below 15 years of age at the time of the 2023 follow-up survey). Further, retrospective and current health outcomes were solicited by asking mothers about their children’s health at ages two and five. In both the 2022 and 2023 surveys, households and individual children who had moved out of the village were tracked to reduce attrition (Macours, Mallia, and Okello, 2025). Between the two survey rounds, and in a random subset of the 108 rural communities, households received individualized and group feedback about varietal identification based on the DNA fingerprinting conducted on the 2022 sample. See Mallia (2025).

#### 3.2.5.2 Seed System Study

One of the key themes of the discussion in the Munyonyo workshop was the widespread perception of significant problems in the seed system for the major crops. Bold et al (2015, 2017) highlighted this problem in their influential paper on fake agricultural inputs in Uganda, in which they found the prevalence of counterfeit maize seed to be so high as to make the economic returns to their adoption much lower than would be the case if quality assured. Their analysis is unable to isolate where the problem lies – whether this is primarily a problem of quality control high up in the supply chain, or whether inputs that start as high quality are degraded/diluted as they pass down through the input supply chain. Barriga and Fiala (2020) developed this case a step further, sampling from different points in the maize supply chain, finding that mishandling is a more likely explanation for poor seed quality than outright counterfeiting[20].

To further disentangle the origins of these quality problems and improve on measurement, the seed system study worked within the confines of the existing system for seed inspection by having enumerators accompany seed inspectors during their work, through a partnership with the Department for Crop Inspection and Certification (DCIC) within MAAIF. For both maize and beans, the goal was to determine varietal identity and genetic purity of seed samples taken at different levels of the seed system. For maize, the top seven varieties by 2021 seed production share (per planting returns data shared with us by DCIC) were chosen as the scope of the study, namely: Bazooka, FH6150, LONGE 10H, LONGE 5, LONGE 5D, LONGE 7H, and UH5051. Samples of seed were taken by DCIC inspectors at the production stage (both from seed companies' plots and contracted outgrower plots), aggregation stage (i.e., company seed lots), and distribution stage (agrodealers). The agrodealer samples were taken through both declared audits by inspectors and mystery shopper visits. A total of 891 maize seed samples were collected, then ground, plated, and shipped for genotyping at Diversity Arrays. For beans, a pilot study focused on three biofortified bean varieties (NARO Bean 1, 2, and 3) with samples collected at production, aggregation, and distribution stages. Quality declared seed[21] samples were taken alongside certified seed samples from seed companies for each of these three varieties.

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[20] See https://blogs.worldbank.org/en/impactevaluations/devil-details-measuring-seeds for a discussion on the measurement challenges in this paper.

[21] Quality Declared Seed (QDS) is seed produced by entrepreneurial farmer groups that form Local Seed Businesses (LSBs). The QDS system has minimum certification requirements targeting specific food crops which are self-pollinated or vegetatively propagated. The seed produced by the LSBs is inspected and certified for QDS (i.e., seed sampling, testing and QDS labels printing) by MAAIF but to a different set of standards as those for certified commercial seed for maize.

# 4. CGIAR-Related Innovations in Uganda (2000-2020)

This section identifies and describes the major contributions from research collaborations across the core CGIAR research domains of animal agriculture, crop improvement, natural resource management, and policy/institutional innovation to Uganda's stock of agricultural innovations.

## 4.1 Overview

For the past 30 years, CGIAR centers have been undertaking research in Uganda, working closely with the National Agricultural Research Organization (NARO) and its 16 constituent institutes, including the National Crops Resources Research Institute (NaCRRI) and the National Semi-Arid Resources Research Institute (NaSARRI). CGIAR first became active in Uganda with the establishment of the International Institute of Tropical Agriculture (IITA) office in 1992. The East African Banana Breeding program was subsequently initiated in 1994 as a collaboration between IITA and NARO (Ortiz, 2001). In addition to IITA, five other CGIAR research centers currently have an official presence in Uganda: the International Food Policy and Research Institute (IFPRI), the International Potato Center (CIP); the Alliance of Bioversity International and CIAT, the International Livestock Research Institute (ILRI), and the Centre for International Forestry Research and World Agroforesty (CIFOR-ICRAF)[22]. The International Maize and Wheat Improvement Center (CIMMYT) and the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) do not have a physical presence in Uganda but work closely with NaCRRI and NaSARRI, respectively.

The full stocktaking exercise highlights the diversity of CGIAR research in Uganda. Covering the period 2000-2020, we grouped research outputs into 49 innovations that we could document. These fall into three broad domains of animal agriculture (n = 15), crop improvement (n = 23), and natural resource management (n = 11). As with prior SPIA country studies (Ethiopia – Kosmowski et al, 2020; Alemu et al, 2024; Vietnam – Kosmowski et al, 2024), most innovations, and their adoption and impact are not well-documented. Sources of data about their dissemination are very limited, so we have erred on the side of caution and been somewhat generous in our inclusion of innovations through the early filters of the scheme outlined in Figure 9.

The inclusion of innovations identified by stocktaking in the Uganda Harmonized Integrated Survey (UHIS), the Uganda National Survey on Objective Measurement in Agriculture (UNOMA), or the National Service Delivery Survey (NSDS) was negotiated on a case-by-case basis. Some were already included in the UHIS questionnaire, others could be included through minor wording or coding changes, whereas others required dedicated measurement efforts. In this section, we include information on those 21 innovations that we conservatively passed through to a data collection phase in one or more of the surveys.

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[22] See earlier note on the current relationship of CIFOR-ICRAF within CGIAR.

## 4.2 Animal Agriculture

### *4.2.1 Improved Dairy and Cattle Genetics*

Uganda’s dairy herd is characterized by a poor genetic base due to inbreeding and the use of bulls of unknown genetic pedigree. In the last two decades, the Ugandan government and development partners have been investing in improving dairy genetics through projects such as the East Africa Dairy Development Project (EADD), started in 2008 intending to double dairy-derived income among 179,000 smallholders. EADD was designed to have 36 hubs over both phases, organized into five geographic clusters (Kiboga, Central Region; Masak, Central Region; Mukono, Central/Eastern; “Near East”, in Eastern Region; and “South Western”, in Western Region). A full list of hubs and clusters is given in Appendix L.

EADD was implemented through a consortium led by Heifer International (HI) and other partners, including TechnoServe (TNS), ILRI, African Breeders Total Cattle Management (ABS-TCM), and CIFOR/ICRAF. EADD targeted dairy farmers living on small 1–5-acre plots and aimed to increase ownership of crossbred cows, increase the amount of milk their cows produce, and strengthen the farmers’ relationships with formal markets so that they can sell more milk. Additional ILRI efforts, such as the Germplasm for Dairy Development in East Africa (2010-2013) project, aimed to establish a link between appropriate genotypes and the different dairy production systems and how these can be delivered to smallholders. In that regard, artificial insemination services were central to the EADD project efforts, supporting the National Animal Genetic Resources Centre (NAGRC) and Data Bank (DB) to import Friesian, Jersey, and Guernsey semen. This was made available free of charge by the FAO Bovine Semen Donation Scheme.

The National Agricultural Advisory Delivery System (NAADS) also promoted livestock improvement by promoting crossbreeding of improved animals and local breeds of cattle, goats, and poultry through the distribution of improved breeds of male and female animals. Projects include the Regional Pastoral Livelihoods Resilience Project (RPLRP) that supports community breeding programs, and the Market-Oriented and Environmentally Sustainable Beef Meat Industry (MOBIP) in Uganda through the distribution of male animals in the cattle corridor. In cattle, for example, *Sahiwals* (from Kenya) and Friesians have been crossbred with *Zebus*, *Borans* and *Ankole* cows. No information exists on what types of breeds of cattle, goats, and poultry have emerged. Although Kabi et al. (2016) argue that the use of exotic breeds reduces the genetic diversity of indigenous breeds, we have limited information on the extent of diffusion and adoption of these technologies.

In the UNPS and UHIS, farmer-reported data were collected on crosses and exotic animals. In the UHIS, data is also collected on the use of artificial insemination, which is the measure used to capture the reach of improved cattle genetics in this report. This topic could be a candidate for DNA fingerprinting of breeds in future rounds.

### 4.2.2 Improved Fodder Shrubs for Dairy Systems

Through the EADD project, ICRAF supported Heifer International by promoting the production and distribution of improved animal feed and fodder. The primary entry point was through farmer training, including for the production and processing of improved feeds and through the establishment of feed demonstration plots. ICRAF trained volunteer farmer trainers on a variety of feeding practices. These included improved feed conservation (crop residue and storage), silage making and using grass cutters, using maize bran to feed milking cows and feeds/fodder to housed cattle, as well as mineral licks and blocks. The fodder shrubs introduced through this training included Calliandra and Gliricidia, and grasses introduced included Napier, Elephant grass, *Bracharia spp*., and *Chloris gayana (Rhodes)*. The farmer trainers, in turn, trained fellow dairy farmers in their village. A large-scale randomized control trial established the cost-effectiveness of this training and showed that it led to improvements in milk productivity among smallholder dairy farmers (Behaghel, et al, 2020). Data on the use of fodder shrubs for dairy feeding were collected from the annual module of UHIS and the community questionnaire to document the reach of these improved feeding practices. Data on the provision of information about fodder shrubs by extension agents were collected in the NSDS.

### 4.2.3 Milk Collection Centers

Milk collection centers (MCCs) have a history in Uganda that long pre-dates CGIAR research. A history is provided in the evaluation report by Balikowa et al (2021). The prevailing national trend in milk production shows steady growth, with an estimated 450 million liters produced in 1990, increasing to an estimated 2.8 billion liters by 2021. Of this, less than 5% was marketed through formal channels in 1990, a share that had grown to an estimated 46% by 2020 (Balikowa et al, 2021). However, the quality of the operations at milk collection centers, particularly for chilling milk and testing for quality, has remained a concern. Furthermore, the same evaluation found that most MCCs (77.7%) pay their suppliers every 15 days, whereas 1.9% pay monthly, 17.5% pay weekly, and only 2.9% pay on the same day as receipt of delivery. This potentially represents an obstacle to participation in MCCs for liquidity-constrained smallholders.

In 2014, the EADD project received a grant of USD 25.5 million to scale up the operation after the first phase was evaluated as successful. The second phase supported four variants of the milk collection centers, including: (i) farmer-owned chilling plants; (ii) processor-owned chilling plants; (iii) traditional market hubs with no chilling plants but that bulk milk; and iv) traditional market hubs that do not bulk milk. ILRI led the EADD Consortium on knowledge-based learning activities and was responsible for providing research support to inform EADD interventions. ILRI’s involvement in EADD was largely through three major tasks: documentation of innovation and research related to dairy production; knowledge sharing among partners; and informing project design.

The UHIS survey data provides a measure of the presence of an MCC in the community questionnaire, as well as a measure of milk quality testing occurring in the centers. These measures allow us to document the reach of these innovations, without attempting to decipher the marginal contribution of ILRI via EADD to the functioning and ongoing presence of the MCCs.

### 4.2.4 East Coast Fever Infection and Treatment Method

East Coast Fever (ECF) is a very significant disease of cattle across numerous countries in Sub-Saharan Africa, including Uganda. The only currently available method of immunization against ECF is known as the Infection and Treatment Method (ITM). ITM is a homogenized and partially purified preparation of infected ticks, which is administered simultaneously with a long-acting antibiotic, the latter being administered to prevent the development of severe clinical disease (Patel et al, 2019). Vaccinated calves are then ear-tagged. The treatment is expensive, estimated at between USD 6 and USD 10 per animal (GALVMed, 2015). This is particularly due to the liquid nitrogen cold chain typically required for storing and transporting the vaccine, which can be a significant constraint in countries like Uganda (Atuhaire et al, 2020).

The ECF-ITM method was initially developed by the East African Veterinary Research Organization, Mugugu in Kenya in the 1970s[23]. During the 1990s, the International Laboratory for Research into Animal Diseases (ILRAD, now ILRI) produced the first commercial batch of ECF-ITM vaccine. A later batch was produced by ILRI in 2008, which later ran out owing to high demand following registration at the national level in Kenya, Tanzania, and Malawi. Uganda did not initially approve the vaccine as it was found not to meet the standard for Good Manufacturing Practices (GMP) following an inspection by the Ugandan authorities (Peters, 2020). In 2011, ILRI assisted the Global Alliance for Livestock Veterinary Medicines (GALVmed) – a public-private partnership and registered charity in the UK – in a process of technology transfer to the Centre for Ticks & Tick-Borne Diseases (CTTBD) in Lilongwe, Malawi (GALVmed, 2015). Production of ECF-ITM at a commercial scale began soon after and following reinspection by the Ugandan authorities in the period 2015 - 2017, the vaccine was eventually approved for use in the country.

UHIS includes measures of the use of ECF-ITM collected through self-report in the animal section of the household survey. Such self-reports are, however, likely to suffer from measurement error.

### 4.2.5 Improved Forage and Sweetpotato Silage for Feeding Pigs

ILRI has researched the preparation of low-cost pig feed, such as silage using sweetpotato leaves and planting improved forage varieties. The Expanding Utilization of Roots, Tubers, and Bananas and Reducing Their Postharvest Losses project (RTB-ENDURE, 2014-2016) operated in three districts (Masaka, Mpigi, Kamuli) to make pig feed out of sweetpotato vines and roots. The Smallholder Pig Value Chains Development project (ILRI, 2012-2016) selected best bet forages (with low fiber and high protein) for feeding pigs in Masaka, Kamuli, Lira, and Hoima districts. We do not have evidence to suggest that these approaches have been scaled beyond these districts, nor sustained in project areas without sustained outside attention, and we therefore did not prioritize data collection. As these were innovations that the 2019 Munyonyo workshop identified as a priority, however, this is a potential focus area for future data collection.

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[23] A detailed historical narrative on the institutional and research developments underlying ECF-ITM is provided by Perry (2016).

## 4.3 Crop Improvement

We next present details on the contribution of breeding improved varieties of six major crops in Uganda. We start with the government priority crops of maize and cassava (as outlined in the National Development Plan III), followed by banana, beans, sweetpotato, and groundnut. Each has been the subject of sustained collaborations between CGIAR Research Centers and NARO.

### *4.3.1 Improved Maize Varieties*

Maize in Uganda, as is the case for most sub-Saharan African countries, is a major staple crop and is of high strategic importance for the government. In the 2020 Annual Agricultural Survey (AAS), data showed that maize was cultivated by 52% of agricultural households in the first season and 57% in the second season, on an estimated planted area of 2 million hectares. Annual production for the 2020 agricultural year was estimated at 3.5 million tonnes, with a slightly higher share (1.9 million tonnes) coming from the first season compared to the second season (1.6 million tonnes). In the UHIS 2021/22 data, we find that 72% of all rural households cultivated maize. Only 9% of households reported obtaining seed from the seed system for that season. The remainder either recycled their own seed or obtained it through informal channels.

Maize research in Uganda began in the 1930s, with varietal testing of materials introduced from South Africa, Kenya, and Tanzania. CIMMYT’s collaboration in maize research in Uganda started between 1972 and 1974, as a provider of germplasm for the Kawanda Composite B variety. This variety was never formally released due to the break-up of the East African Community, which was responsible for facilitating the multiplication of materials. A fundamental shift in maize breeding in Uganda took place in the early 2000s, when CIMMYT contributed germplasm towards the development of multiple stress-tolerant varieties to mitigate impacts of climate change, especially drought and diseases (Asea et al, 2023). The collaborative effort resulted in the release of 84 varieties between 2007 and 2020, with 39% of them derived from CIMMYT germplasm. The breeding efforts have largely been supported by the Drought Tolerant Maize for Africa project (2006 - 2015) and the Stress Tolerant Maize for Africa project (2016 - 2020). Besides providing germplasm, CIMMYT also undertakes capacity-building activities/training for maize breeders, technicians, and students, and provides ongoing technical support. IITA’s role in maize breeding in Uganda is indirect, with West and Central Africa being the focus regions for their maize improvement.

The UNOMA DNA fingerprinting data on maize varietal adoption allow us to document the reach of improved maize varieties resulting from the efforts described above.

The full list of varietal releases is provided in Appendix E and summarized in Table 3.

### Table 3: Maize varieties released, by germplasm origin (1990 - 2023)

| | 1990-99 | 2000-09 | 2010-2023 |
|---|---|---|---|
| **NARO origin exclusively** | 1 | 1 | 2 |
| **CGIAR-related: CIMMYT or IITA line(s) known to have been used in breeding** | 2 | 13 | 47 |
| **Commercially bred varieties (with unknown CGIAR contribution)** | 0 | 15 | 23 |
| **TOTAL** | **3** | **29** | **72** |

### *4.3.2 Improved Cassava Varieties*

Along with maize and banana, cassava is one of the most important staples in Uganda and is particularly valued for its ability to withstand tough environmental conditions that would challenge other crops. The traditional cassava growing areas are the Eastern and Northern regions (UBOS, 2019), but cassava production is widespread, and it is an important crop from the perspective of both food security and income generation (Nakabonge et al., 2018; Tomlinson et al, 2018). In the first season of 2019, cassava was grown by 44% of agricultural households, and in the second season by 55% (UBOS, 2020). In 2020, an estimated 1.7 million tonnes of cassava were produced from a planted area of 740,000 ha, with production much lower in the first season (0.61 million tonnes) compared to the second season (1.1 million tonnes). In the UHIS 2021/22 data, we find that 62.5% of rural households cultivate cassava. Only 11% of these report obtaining their planting materials from the seed system. Being vegetatively propagated, households can take cuttings to plant out and grow their cassava stands.

Intercropping cassava with other crops is a common practice in Uganda. The most important intercrops are short-season crops such as maize, beans, sorghum, groundnut, millet, and cotton (Fermont et al., 2009). Cassava is an important source of carbohydrates in the diet in Uganda. It is consumed in different forms, depending on local customs and the level of cyanogenic glucosides present in the flesh. Cassava roots harvested from ‘sweet’ varieties (low in cyanogens) may be consumed raw, boiled, roasted, fried as chips, or as paste after drying and pounding. Roots from ‘bitter’ varieties (high in cyanogens) are processed into flour after undergoing a heap fermentation process and subsequent sun-drying (Cardoso et al., 2005).

Cassava production is threatened by several diseases, with Cassava Brown Streak Disease (CBSD) and Cassava Mosaic Disease (CMD) being the most important that occur in all cassava-producing areas of Uganda (Tomlinson et al, 2018). CBSD damages the roots, making them unfit for consumption, whereas the leaves of plants severely infested with CMD appear chlorotic (i.e., yellowed) and mottled, leading to stunted growth. The damage caused by CMD and CBSD on roots can result in yield losses of up to 100% in farmers’ fields, either singly or in combination (Mukibi et al., 2019). Management of both CSBD and CMD relies heavily on the deployment and use of resistant varieties.

Formal cassava breeding started in Uganda in the late 1980s following the emergence of the second wave of CMD in the country. Before this the Ugandan government was acquiring

CMD-resistant varieties from Tanzania's national cassava breeding program. Since 1990, 24 cassava varieties have been released in Uganda, and IITA has played a significant role in developing them. For example, during the CMD outbreak, elite cassava clones combining yield and resistance to CMD were sourced from IITA and used in the development of CMD-resistant varieties, including NASE 1, 2, and 3 released in 1994 (Manze et al., 2021). A notable breakthrough was achieved with the release of NAROCASS 1 in 2015 – the first variety to have resistance to CBSD. It is thought to be increasingly demanded by name by farmers cultivating in CBSD hotspots. Another 2015 release, NASE 19, is merely tolerant of CBSD but is noted for its CMD resistance and desirable culinary qualities making it a popular variety with farmers.

IITA has also contributed to building the capacity of the breeding program by providing training for technicians, supporting master's and PhD students, and supporting professional development courses on new methods and approaches for scientists. This collaboration led to the Regional Centre of Excellence (RCoE) for East and Central Africa, established in Uganda with World Bank funding. IITA supported NARO with the use of infrastructure such as tools to enable diagnosis during the peak of the cassava brown streak disease epidemic in 2004, and laboratory equipment upgrades. Furthermore, IITA provides ongoing technical backstopping for NARO scientists, such as advising on standard operating guidelines for breeding and sampling in the field.

The full list of cassava references used in the analysis can be found in Appendix G and summarized in Table 4.

**Table 4: Cassava varieties released, by germplasm origin (1990-2022)**

| | 1990-99 | 2000-09 | 2010-2022 | Total |
|---|---|---|---|---|
| **NARO selection** | 0 | 0 | 2 | **2** |
| **IITA line / NARO selection** | 13 | 2 | 7 | **22** |
| **TOTAL** | **13** | **2** | **9** | **24** |

Operation Wealth Creation (OWC) and the National Agricultural Advisory Services (NAADS) programs have both featured the dissemination of cassava planting material purported to be of varieties resistant to the diseases. For example, during the 2019/2020 financial year, the Ugandan government procured and disseminated 245,651 bags of cuttings in 46 districts in Eastern, Northern, and West Nile regions. This was an attempt to mitigate the potential negative effects of COVID-19 on food security. However, media reports[24] have flagged concerns about the quality of the material disseminated through OWC, owing to a lack of both the technical expertise needed and clear incentives for managing the quality of the material being procured and disseminated.

We use UNOMA DNA fingerprinting data to estimate the reach of IITA cassava breeding.

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[24] Examples of media reports on poor quality cassava stems being distributed through OWC include:
https://thecooperator.news/farmers-reject-owc-cassava-inputs-over-poor-quality/
https://www.youtube.com/watch?v=Pv7J5EclqbA

### *4.3.3 Improved "Matooke" Varieties*

Cooking bananas, commonly known as "Matooke", have long been considered the major staple crop of Uganda, particularly in Western, Central, and Eastern Uganda. In 2020, bananas for food were grown by 56% of agricultural households in the first season and 59% in the second season. The total area planted was about 722,000 ha, and annual production was estimated at 11.1 million tonnes with a yield of 15.4 tonnes/ha. In UHIS 2021/22, we found that 52.9% of rural households grew banana. Only 9% of these households report obtaining banana planting material from the formal seed system. The sharing of banana suckers among neighbors and friends is a common cultural practice.

The process of breeding improved banana cultivars faces significant obstacles owing to the extremely low fertility of the crop. The East African Highland Bananas (EAHB) were long considered sterile (Batte et al, 2019), but in the mid-1990s, IITA and NARO scientists succeeded in detecting that 37 EAHBs were indeed female fertile. This discovery laid the foundation for banana crossbreeding efforts at NARO in the decades since, supported by IITA. Such is the importance of banana to the diet of Ugandans and its neighboring East and Central African countries, the region is considered a secondary genetic center for the crop globally after the center of its genetic origin in Indonesia. Owing to this farmer-maintained diversity, Bioversity International has had an active research agenda on banana landrace collection and conservation over many years.

An early batch of five banana cultivars, KABANA 1 – 5, was released in 1999 and 2000. KABANA 1 – 4 are Honduran hybrid bananas, developed and made freely available by Fundación Hondureña de Investigación Agrícola (FHIA – the Honduran Agricultural Research Foundation). These four cultivars were evaluated at NARO for their suitability for the Ugandan context before being the first official releases to Ugandan farmers. KABANA 5 (also known as Yagambi or KM5) was the first matooke (i.e., EAHB) to be officially released from the banana program in the country. It is a Ugandan landrace cultivar with some resistance to black sigatoka, fusarium wilt, and weevils, and is tolerant to nematodes.

NARITA 7 (also known as KABANA 6 H or Kiwangazi or M9), released in 2010, was the first improved matooke to have emerged from the NARO/IITA banana breeding program – the name acknowledging the years of joint effort (Tushemereirwe et al., 2014). Other cultivars, released between 2013 and 2019 (KABANA 7H and NAROBan 1 – 5), have the same agronomic traits as KABANA 5, but with incrementally greater consumer acceptability ratings – cooking and eating quality being considered a major constraint to wider adoption of improved matooke. A further batch of NARITA cultivars (NARITA 4, 17, 18, 22, 24) is currently under final evaluation, having shown the best results from a group of 25 cultivars developed by the breeding program (Tushemereirwe et al., 2014).

Given the immense challenges in working with banana using conventional breeding efforts, scientists have turned to the tools of genetic modification (GM) to try and introduce desirable traits. Target traits for GM banana research at the National Agricultural Research Laboratories (NARL) include addressing otherwise elusive disease resistance traits (e.g. BXW resistance) and provitamin A content as an additional strategy for addressing micronutrient deficiency. Biosafety laws in Uganda have, to date, prevented the official release of GM crops in the country.

The full list of banana references used in this analysis is included in Appendix F and summarized in Table 5. We use UNOMA DNA fingerprinting data to estimate the reach of the banana breeding activities of IITA.

Table 5: Banana varietal releases, by germplasm origin (1990 - 2022)

| | 1990-99 | 2000-09 | 2010-2022 | Total |
|---|---|---|---|---|
| **NARO selection (either from Honduras or local landrace)** | 2 | 3 | 0 | **5** |
| **NARO-bred improved matooke (with support from IITA)** | 0 | 0 | 6 | **6** |
| **NARO-IITA improved matooke**[25] | 0 | 0 | 1 | **1** |
| **TOTAL** | **2** | **3** | **7** | **12** |

### 4.3.4 Micro- and Macro-Propagation for Banana Planting Materials

Introduced by IITA, tissue culture or micro-propagation is the means through which planting material of newly bred varieties is developed for dissemination to farmers. Tissue culture is the only mechanism by which planting material can be reliably produced to be free of diseases. The existing biggest commercial labs in Uganda (AGT) sell seedlings to the Ugandan market and neighboring countries such as Rwanda and Kenya. CGIAR helped establish a nursery network for nurturing plantlets for further distribution to farmers. Healthy macro-propagation is described in a 2007 training manual developed by IITA. The manual describes the basic techniques needed for the propagation of healthy planting material (Njukwe et al, 2007).

The typical way that farmers source planting material is to take a sucker (a shoot that develops from a lateral bud on the rhizome and emerges from the soil usually near the parent plant – ProMusa definition) from established mats, severing it from the mat and transplanting it to a new location. This allows banana planting material to be shared among friends and neighbors at a low cost. The problem is that this sharing of suckers can be responsible for accelerating the spread of diseases.

The result of both expert micro- and macro-propagation is plantlets grown out in nurseries for sale to farmers. Given this, we could potentially differentiate farmers being reached by these techniques owing to their use of plantlets vs suckers in establishing their plantations. We had designed a visual aid about this topic for incorporation into the post-planting module for the UNOMA subsample, but during implementation, this was dropped so we do not have data to support our understanding further. This is therefore a potential topic for future data collection.

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[25] Five additional NARITA cultivars are in final evaluation: NARITA 4, NARITA 17, NARITA 18, NARITA 22 and NARITA 24

### *4.3.5 Improved Bean Varieties*

Common bean (*Phaseolus vulgaris*) is an important source of dietary protein in Uganda. It is grown in all regions and often in both agricultural seasons. In 2020, Annual Agricultural Survey (AAS) data show an estimated 45% of households cultivated beans in the first season, and 53% in the second season, producing a total of 670,000 tonnes from a total planted area of 1.1 million hectares. This corresponds to an annual yield of 0.6 tonnes/ha in the first season and 1.1 tonnes/ha in the second season. Both figures are low compared to the potential yield of 2.5–5 tonnes/ha (Muthoni et al., 2017). This gap is attributed to several field-based production constraints such as poor agronomic practices, soil infertility, low availability of seed from improved cultivars, moisture stress, weed competition, and damage by pests and diseases (Sinclair and Vadez, 2012). In the UHIS 2021/22, we find that 60.8% of rural households cultivate beans, but only 7% of households report obtaining their seed from the seed system for that year, the remainder buying grain to use as seed, recycling from prior years, or obtaining planting materials through informal channels.

CIAT, through the Pan-African Bean Research Alliance (PABRA), has, since 1996, partnered with the national bean program at NARO. Under different iterations of the Tropical Legumes project (2007–2019), common bean was prominent in Uganda, with thousands of tonnes of improved seed produced and made available to farmers. Varshney et al (2019) estimate the area under improved varieties of bean in Uganda to be in the hundreds of thousands of hectares (237,353 ha in the later Tropical Legumes project's third phase).

Under the Tropical Legume projects, three breeding priorities were pursued for both bush and climbing beans: breeding lines were bred for drought tolerance, high mineral content, East African Productivity Program; breeding lines with heat and/or drought tolerance; and breeding lines for insect pest and disease resistance (Mukankusi et al, 2019). In addition, biofortification has been a major focus, with sustained efforts to breed for higher iron and zinc levels as part of the HarvestPlus initiative. CIAT collaborates with NARO through joint priority setting, supporting germplasm collection, characterization, and conservation, and a range of capacity-building activities. As a result of these collaborative efforts, a total of 38 improved bean varieties have been released (Appendix H), summarized in Table 6. Seven of the most recent bean varietal releases, NAROBean 1, 2, 3, 4C, 5C, 6, and 7, have all been bred to have high levels of iron and zinc and thus are considered as biofortified beans.

We use UNOMA DNA fingerprinting data to estimate the reach of CIAT/PABRA support for bean breeding.

**Table 6: Bean varieties released, by germplasm origin (1990 - 2022)**

| | 1990-99 | 2000-09 | 2010-2022 | Total |
|---|---|---|---|---|
| **NARO selection** | 3 | 2 | 4 | |
| **CIAT germplasm line used in breeding** | 9 | 2 | 16 | |
| **TOTAL** | **12** | **4** | **20** | |

### 4.3.6 Community-Based Bean Seed System/Quality Declared Seed

Informal seed providers (i.e., grain vendors visually sorting their offering by market class, color, and occasionally by named variety) dominate the bean seed system in Uganda, but private seed company involvement has grown over time. By the end of 2018, there were 12 seed companies involved in the production of certified bean seed, contributing 8-10% of the national seed requirement per year (CIAT unpublished report, Mastenbroek, 2015). Seed companies supply their seed via a network of agro-dealers and/or via direct sales. The informal seed system has no written rules and regulations, supplying landraces and improved varieties. This system relies on seed saved from previous production seasons, in combination with seed obtained through social networks, and purchases of bean grain from the local market.

Community-Based Seed Multiplication Enterprises (CBSME) or Local Seed Businesses (LSBs) are an upgraded version of informal seed systems and are being promoted by the National Agricultural Research System (NARS), CIAT, Integrated Seed Systems Development (ISSD), and donors to increase the availability, accessibility, and affordability of quality seed by smallholder farmers. For example, between 2012 and 2018, 43 farmer groups from 11 districts across four regions were involved in seed multiplication of improved varieties with support from NARO and CIAT. The seed produced by CBSMEs is ‘Quality Declared Seed’ (QDS) rather than certified seed. The QDS system has less stringent certification requirements relative to the multiple field inspections per season that are required for producing correctly certified maize seed. QDS applies to crops that are self-pollinated or vegetatively propagated (FAO, 2006).

The Ugandan Seed Law was revised in 2019 to recognize QDS, following advocacy from CIAT, IFPRI, and ISSD. When producing QDS, farmer groups obtain early generation seed of improved varieties from NARO and are trained in seed production and quality management. QDS producers may also access certified seed from seed companies to multiply to produce QDS. The share of QDS in total bean seed production is thought to be modest, but with significant uncertainty as to the true extent. CBSMEs producing QDS largely sell their seed to institutional buyers, such as NGOs wanting seed for disaster relief operations, rather than to individual farmers. Furthermore, bean seed is procured by the Ugandan government on a large scale, including as an input for Operation Wealth Creation (OWC). For example, Nakazi et al (2017) report that in the financial year 2016-17, OWC distributed 2,234 tonnes of bean seed, aiming to reach 224,448 households. During the country’s strict COVID-19 lockdown in 2020, the Ugandan government imported large quantities of bean grain, including from neighboring Tanzania, to distribute for household consumption. Given the disruption to the bean seed system during this period (Nchanji et al, 2021), it is likely that this imported bean grain, of unknown genetic profile, was also used as seed in subsequent seasons.

We collect data on quality-declared seed use in both the UHIS 2021/22 post-planting visit and the UNOMA modules.

### 4.3.7 Improved Sweetpotato Varieties

Sweetpotato is the fifth most important crop in Uganda in terms of frequency of cultivation. In 2020, AAS data show that 22% of agricultural households cultivated sweetpotatoes in the first season of 2019, and 36% in the second season. In aggregate, an estimated 1.2 million tonnes were produced from an estimated planted area of 466,000 hectares. Yields were significantly higher in the second season: an estimated 3.4 tonnes/ha was the average yield in the first season, compared to 7.0 tonnes/ha for the second season. In the 2021/22 UHIS data, we find 39.5% of households cultivate sweetpotato. Of those, only 7% state that they obtained their planting material from the seed system, while most of the production is for self-consumption (only 18% of cultivated varieties are sold).

Sweetpotato breeding in Uganda is coordinated under an East Africa regional platform, formed under the Sweetpotato for Profit and Health Initiative (SPHI) – a multi-donor, multi-stakeholder program that ran for a decade starting in 2011. Disease resistance, in particular to sweetpotato virus disease (SPVD), has been a key breeding target. SPVD is caused by a combination of viruses, including chlorotic stunt virus, feathery mottle virus, and mild mottle virus. It can be agronomically devastating, with near-total yield losses in susceptible cultivars (Mwanga et al, 2001). This means that every new candidate cultivar in the breeding program is first screened for SPVD resistance. More generally, breeding attention to pest and disease resistance is reflected in all sweetpotato varieties released in Uganda having at least moderate resistance to SPVD, Alternaria, and/or weevils.

Groups of cultivars can be differentiated by color of flesh – white, cream, yellow, orange, and purple. Sweetpotato roots are boiled, steamed, roasted, or fried before consumption (Odora et al., 2000). The roots are also processed into several other products, including puree, dried chips and chunks, flour, pastries, and confectionery (Abong et al., 2016).

Several nutritional benefits are associated with sweetpotato consumption. It is an important source of β-carotene, anthocyanins, phenolics, dietary fiber, vitamins, minerals, and other bioactive compounds (Truong et al., 2018, Vimala et al., 2011). In particular, orange-fleshed sweetpotato (OFSP) contains large amounts of β-carotene that have the potential to reduce vitamin A deficiency (Vimala et al., 2011). Consumption of OFSP has been shown to improve vitamin A status among children, lactating mothers, and pregnant women in Africa (Low et al., 2007) and in Uganda in particular (Hotz et al, 2012; de Brauw et al, 2018).

Dr Robert Mwanga, 2016 World Food Prize laureate (awarded along with CIP colleagues Drs Maria Andrade, Jan Low and Howarth Bouis), has been at the center of this research agenda using sweetpotato breeding as an instrument for reducing vitamin A deficiency in Uganda. He established the Roots and Tuber Crops Program within NARO in 1986, with encouragement from the CIP regional office in Nairobi, and worked to build up the program as a Centre of Excellence for the region. In the 1990s, OFSP clones from CIP were evaluated and found to be either agronomically unsuitable or inconsistent with Ugandan consumption preferences. Dr. Mwanga instead began crossing OFSP with non-orange sweetpotato germplasm to find the right combinations with a particular emphasis on virus resistance, and he joined the research staff of CIP in 2009. Of the 27 varietal releases between 1990 and 2022, nine are orange-fleshed: NASPOT 5 (1999 release), Ejumula and Kakamega (2004 releases), NASPOT 7, NASPOT 8, NASPOT 9 O and NASPOT 10 O (2007 releases), NASPOT 12 O and NASPOT 13 O (2014 releases).

A full list of the reference varieties used in our analysis is provided in Appendix I and summarized in Table 7.

Table 7: Sweetpotato varietal releases, by germplasm origin (1990 - 2022)

| | 1990-99 | 2000-09 | 2010-2022 |
|---|---|---|---|
| **NARO selection** | 12 | 2 | 2 |
| **CIP germplasm line used in breeding** | 0 | 5 | 6 |
| **TOTAL** | 12 | 7 | 8 |
| **TOTAL** | **3** | **29** | **72** |

In Uganda, sweetpotato planting materials are distributed through three systems: formal, project-based, and informal (Gibson, 2013). The formal and project-based systems predominantly supply planting materials of released OFSP and white/cream fleshed varieties. The informal system mostly supplies landraces of varying genetic and phenotypic profiles and is predominant in areas with a long dry season in which farmers' vines cannot survive. The formal and project-based systems are sustained by government and NGO (local and international) interventions, whereas the informal seed system is based on farmers multiplying planting materials for their own use and to sell or gift to other farmers. Several efforts (previous and ongoing) have attempted to improve the system for farmers, to allow for a better flow of improved material to farmers, particularly OFSP. Externally funded projects to disseminate planting material of OFSP varieties in the past two decades include:

- The Vitamin A for Africa (VITAA) project (2001–2006) set the stage for over a decade of sustained activity on OFSP promotion in Uganda. The project convened a wide group of stakeholders and piloted different activities that would later become influential in HarvestPlus. The project included participatory testing of varieties for their adaptation and acceptability, community-based multiplication of planting materials, nutrition education, post-harvest processing for market and home consumption, promotion through social marketing, monitoring of impact on nutrition and health, and capacity building.
- The Promotion of OFSP Varieties Through Schools in Urban and Peri-Urban Communities of Kampala (2004–2006) was implemented by a multistakeholder partnership led by the Department of Agricultural Extension, Makerere University. The project established OFSP gardens and rapid multiplication technique (RMT) plots in 11 primary schools for the demonstration and multiplication of vines (Loechl and Lubowa, 2010). Several methods were used to train and transfer knowledge and technologies to beneficiaries in schools, including presentation-question answer meetings, on-plot demonstrations, drama, farmer-to-farmer extension, farm station visits, and the distribution of a resource book for pupils in upper primary schools (P5–P7). These evolved out of the school garden project implemented in Kampala (Kapinga et al., 2009).
- HarvestPlus, through the Reaching End Users (REU) project (2006–2009), introduced beta-carotene-rich OFSP and related messages concerning agronomy, nutrition, and marketing. This was to try and induce broad OFSP adoption, and with it, measurable increases in vitamin A intake in children and women in Uganda. The project subcontracted NGOs such as World Vision to distribute OFSP vines to households on a large scale. IFPRI and CIP collaborated with HarvestPlus/CIP on the breeding and agronomic aspects, while IFPRI led an influential impact evaluation (Arimond et al, 2010; Hotz et al, 2012) which demonstrated the short-run efficacy of this integrated strategy.

- In the Dissemination of New Agricultural Technology in Africa DONATA project (2008–2013), CIP developed and applied an Innovation Platform for Technology Adoption (IPTA) approach, involving multiple stakeholder groups including NARO, universities, community-based organizations, farmer organizations, and extension agents to scale OFSP technologies along the value chain (Kimenye and McEwan, 2014).
- The Sweetpotato Action for Security and Health in Africa (SASHA) Phase II (2009–2019) project focused on breeding approaches and locally adapted varieties, building sustainable seed systems and improved storage methods, and promoting vitamin A-rich varieties (CIP, 2019).
- An Innovative, Integrated Approach to Enhance Smallholder Family Nutrition project by BRAC Uganda (2013–2018) was implemented in South-Western Uganda. The project was intended to address nutrition and food security issues through a set of interventions aimed at improving access to, and use of, OFSP in the communities.
- More recently, since 2020, the SweetGAINS project has focused on increasing access to sweetpotato varieties and enhancing seed delivery systems to gender-responsive, well-managed sweetpotato breeding programs across Africa (CIP, 2020).

We use UNOMA DNA fingerprinting data to estimate the reach of CIP-related sweetpotato varieties, including OFSP.

### 4.3.8 Improved Groundnut Varieties

Groundnut is the second most important legume in Uganda after beans, grown mainly by smallholders for both food and income (Okello et al., 2010). It is an important, affordable source of dietary protein, and households sell their excess production for income. In 2020, AAS data show that 17% of agricultural households cultivated groundnut in the first and second seasons. Together, the aggregate production was an estimated 176,000 tonnes from an estimated total planted area of 458,000 hectares. Yields average 0.4 tonnes/ha for the first season, and 0.6 tonnes/ha for the second season. In 2021/22 UHIS data, we find that 29% of rural households cultivate groundnut. Of these, only 3% state that they obtain their seed through the formal seed system.

Groundnut is consumed in different forms, depending on the region. It can be eaten raw, boiled, roasted, blanched, as peanut butter (a rapidly growing domestic market), crushed and mixed with traditional dishes as a sauce, or as *binyebwa* (a cooked paste). As a legume, groundnut can help improve soil fertility by fixing nitrogen, and the haulms can be fed to animals. Traditional growing areas are Eastern and Northern regions, but production has also spread to the Western and Central regions. Despite the increasing demand for groundnut, on-farm yield lags the potential demonstrated on-station by over 70% (Okello et al., 2014). Important constraints affecting groundnut production include groundnut rosette disease, early leaf spot (*Cercospora arachidicola Hori*), unreliable rainfall and drought in some areas, lack of high-yielding cultivars, storage diseases, and pests (Okello et al., 2010).

ICRISAT’s collaboration with the groundnut breeding program dates to 1987 as a source of germplasm for improvement. Germplasm of advanced breeding lines was sourced, first from ICRISAT India in 1987 and later in 1990 from the ICRISAT Regional Center at Chitedze, Malawi, for fast evaluation and release (Okello et al., 2010). Since 1990, the National Semi-Arid Resources Research Institute (NaSARRI), through collaboration with ICRISAT, has developed several varieties with high yield potential, high quality, resistance to major pests and diseases, short- to medium-maturity periods, and drought tolerance. Specifically, ICRISAT provides advanced breeding lines (germplasm) for fast evaluation and release, technical backstopping, and capacity building for staff on new and novel approaches in research. All 17 varieties released in the last three decades were developed from advanced ICRISAT germplasm. A prior adoption survey of a sample of 945 households in seven groundnut-producing districts (Shiferaw et al, 2010) found a high rate of adoption, with 59% of households reporting that they cultivate an improved variety. However, coming before the application of DNA fingerprinting to crop varietal identification, this adoption study uses self-reported data from farmers, which is likely prone to significant measurement error owing to the informality of the seed system for groundnut.

To date, a total of 25 varieties have been released, detailed in Appendix J and summarized in Table 8.

We use UNOMA data to estimate the reach of ICRISAT-related groundnut varieties.

**Table 8: Groundnut varieties released, by germplasm origin (1990 - 2022)**

| | 1990-99 | 2000-09 | 2010-2022 | Total |
|---|---|---|---|---|
| **NARO selection** | 0 | 0 | 0 | **0** |
| **ICRISAT line / NARO selection** | 3 | 2 | 12 | **17** |
| **TOTAL** | **3** | **2** | **12** | **17** |

### 4.3.9 Improved Rice, Sorghum, and Millet

Rice, sorghum, and millet are all secondary cereal crops in Uganda. AfricaRice has supported the release of New Rice for Africa (NERICA) varieties in Uganda as NARIC 3 (NARO) and SuperICA 3 (NASECO). Efforts to promote these NERICA varieties have been supported by the Japan Overseas Cooperation Volunteers and Sasakawa Global 2000, which started in Uganda in 1996. UBOS AAS data suggest that 4% of agricultural households cultivated the crop in the first season of 2020, and 5% in the second season (UBOS, 2020).

ICRISAT has supported NARO on sorghum breeding dating back to the 1970s. This collaboration culminated in the establishment of a regional center for ICRISAT in Serere, Uganda focused on sorghum and millet improvement. ICRISAT has consistently supported the sorghum program through the provision of germplasm (breeding materials) and capacity-building initiatives, including technical backstopping. This partnership has resulted in the development and release of several improved sorghum varieties, including NAROsog 1, NAROsog 2, NAROsog 3, NAROsog 4, and Seso 3, all of which were developed with germplasm sourced from ICRISAT. Recent projects such as Accelerated Varietal Improvement and Seed Delivery of Legumes and Cereals in Africa (AVISA, ICRISAT, 2018-2022) have aimed to help overcome bottlenecks in getting sorghum varieties out to farmers. UBOS AAS data suggest that 10% of agricultural households cultivated sorghum in the first and second seasons of 2020 (UBOS, 2020). For millet, the breeding program has followed a similar path to that of sorghum, typically covered under the same projects and institutions. Six percent of agricultural households cultivated millet in the first season of 2020, and 9% in the second season.

This relatively low incidence of cultivation among rural households makes these crops less suitable for a major focus in a nationally representative survey. That is not to say that they are not locally important in specific agroecological niches. We simply collected farmer-reported data in the UHIS survey about the adoption of improved varieties of these crops.

## 4.4 Natural Resource Management

CGIAR researchers have engaged in a range of research under the broad umbrella of natural resource management. We focus on five innovations related to agroforestry and banana agronomic management, that have been disseminated at a sufficiently large scale to be observed in a nationally representative survey. Many other research outputs in natural resource management either have not been part of a national program with the potential to scale them up beyond one or two districts, or the research is not intended to lead directly to innovations that are observable in a household survey. In the latter case, we attempt to document instances where the research has plausibly influenced policy or institutions – these are recorded in the policy influence stocktake.

### 4.4.1 Improved Tropical Fruit Trees

ICRAF has long evaluated different tree species for their suitability for different agroforestry purposes. Much of this insight is summarized in a single tool for guiding species selection[26] (such as supporting NGO projects and providing advice for government extension workers). ICRAF also provided support to the efforts of NAADS to disseminate fruit trees, such as providing technical support on how to plant and care for them. Note that horticulture – especially vegetable breeding – is not a CGIAR mandate area, but the specific combination of trees into farming systems falls under the auspices of agroforestry.

In the UHIS data, we observe the cultivation of the tree species and where the farmers get their stock.

### 4.4.2 Single Diseased Stem Removal (Banana)

Single Diseased Stem Removal (SDSR) is a banana disease management package comprised of three actions. The first is cutting the diseased banana stem at ground level, and destroying its apical meristem to prevent re-sprouting, but leaving the banana mat intact. Second, cutting tools are sterilized after cutting all diseased plants in a field by using fire, bleach, or soap and water to prevent new infections when using the tool on unaffected plants. Third is removing male buds as early as possible using a forked stick to prevent insect-mediated transmission.

This management practice is based on the finding that when the bacteria that cause Banana Xanthomonas Wilt (BXW) are introduced into a banana plant, they do not spread to all the

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[26] https://apps.worldagroforestry.org/suitable-tree/uganda

suckers physically attached in a mat. Applied correctly, this combination of practices can prevent the complete loss of the banana mat and the remaining plants within the mat can continue to provide regular harvests. In field trials, SDSR reduced BXW incidence from 80% to below 2% within 3–4 months. Once a farmer is suitably trained, the costs of application appear to be low and relatively easy to apply when compared with the typical practice of uprooting whole banana mats and fields. SDSR has been promoted through farmer field schools, mass media, dissemination of information and communication materials, training by extension agents, and farmer-to-farmer training.

Kikulwe et al (2019) collected data in early 2016 on adoption of BXW control from a sample of 1,200 households in four regions of Uganda – southwestern (where banana is most commercialized), central, mid-western, and eastern. Two major sub-counties were purposively sampled within each of these regions, plus one additional randomly sampled sub-county. Adoption rates were quite high, though it is difficult to conclude this with confidence based on the unusual nature of both the sample and the way the results are reported.

Pagnani et al (2021) report findings from a 2018 survey of 1,058 farmers from the same four selected regions, in which data were collected about the constituent practices of the SDSR management bundle. While the individual constituent practices are adopted at a high rate, the combination of the three practices required for effective SDSR is adopted by 21% of this sample. The same study found that only four farmers out of the sample of 1058 reported that they procured clean planting material (i.e.; tissue cultured plantlets from certified labs) as part of their efforts to prevent recurring infections with BXW.

We collect data on this management practice as part of the community survey of the National Service Delivery Survey (NSDS). We also ask extension officers in NSDS about which specific practices are recommended for BXW control, including complete removal of the infected mat, and the three-component practices of SDSR.

### *4.4.3 Banana-Coffee Intercropping*

Coffee and banana intercropping is a common, traditional practice in East Africa. There are several potential benefits of shading valuable coffee crops with banana stands, such as nutrient cycling, protection from weather extremes, improved coffee quality, and risk mitigation. As there is also potential for plants to compete for limited nutrients or water, the agronomic wisdom of this practice has been ambiguous. During the early 2000s – a time when agricultural policy in Uganda was guided by a Plan for the Modernization of Agriculture – farmers might have abandoned this practice in favor of monocropping, as a common framing narrative at the time was the "African Green Revolution", implying a simplification of cropping systems to allow for standardized management.

IITA researchers carried out an on-farm agronomic study on 152 farmers' plots in both Arabica (around Mount Elgon) and Robusta-focused (Masaka, Rakai, Bushenyi) coffee systems in 2006-2007. Within each district, neighboring plots were selected that had coffee and matooke varieties as either intercrops or adjacent monocrops. The authors found that intercropping appears to be more profitable than monocropping, suggesting that encouraging farmers to abandon it would be counterproductive (Van Asten et al, 2011). These insights underpinned subsequent efforts by IITA and partners (particularly CABI, Wageningen) to promote the practice through NGOs (see Wairegi et al, 2014 for an example of an NGO guidance product from this research).

To capture the potential reach of those efforts, we collect data on the incidence of coffee and banana cultivation on the same plot in the UNOMA sub-sample.

### 4.4.4 Farmer-Managed Natural Regeneration

Farmer-managed natural regeneration (FMNR) is described as "the systematic regeneration of trees from tree stumps, seeds and roots… most of the indigenous trees [have] an inherent ability to coppice or re-sprout after they have been cut down… Farmers are encouraged to prune and protect the sprouts, or naturally growing tree seedlings, which could be found on either cropland or grazing land." (Nakyeyune et al, 2018). FMNR was introduced in Uganda in the Arua district by World Vision Uganda in 2012 and by 2014 it is claimed that use of the concepts had spread to 15 districts. ICRAF (with World Vision) supported a national conference in 2014 and in 2018 published a practical guide for communities (Nakyeyune et al, 2018) explaining the principles behind FMNR and the potential benefits. Data on community-level adoption of FMNR was collected as part of the NSDS.

### 4.4.5 Trees on Farms for Biodiversity

Farms in Uganda often have trees scattered throughout them. Uganda is one of several focus countries for a project on trees on farms for biodiversity (ICRAF-CIFOR, 2018-2022, funded by Germany (BMZ). ICRAF developed a biodiversity manual to help support the Ugandan government in meeting its national and global biodiversity targets.

In the UHIS, we collected data on whether households and communities report managing their trees to sustain biodiversity.

## 4.5 Policy and Institutional Innovations

The stocktake of policy influence claims details 26 instances in which the impact pathway from CGIAR research is via institutional capacity and/or an influence on specific policies. In this section, we highlight some of the more substantive ones that we think can plausibly be linked to CGIAR efforts. We do not pursue further investigation of these policy claims beyond some initial interviews with stakeholders. These can set the stage for further qualitative investigation.

### 4.5.1 National Plan for the Modernization of Agriculture

The Government of Uganda's Plan for the Modernization of Agriculture (PMA) has shaped the design and delivery of agriculture policy and planning services since 2000.

The seven pillars of the plan were:

(i) Research and technology development
(ii) National Agricultural Advisory Service (i.e., NAADS)

(iii) Agriculture

(iv) Improving access to rural finance

(v) Agro-processing and marketing

(vi) Sustainable natural resource utilization and management

(vii) Physical infrastructure.

IFPRI was a key partner organization supporting the formulation of the PMA, as evidenced by the fact that the first head of the PMA secretariat was an employee of IFPRI. The PMA enabled the establishment of NAADS in the years ahead.

### 4.5.2 Extension System Reforms

Under the PMA, the National Agricultural Advisory Service (NAADS) was formed in 2001 with funding from the World Bank. The goal of the NAADS reform was to unlock the potential of Ugandan agriculture to commercialize via demand-driven extension services (Benin et al, 2007).

NAADS aimed to:

- Increase effectiveness, efficiency, and sustainability (including financing, private sector participation, farmer responsiveness, deepening decentralization, and gender sensitivity) of the extension delivery service
- Increase farmers' access to and sustain knowledge (education), information and communication to the farmers
- Increase access to and sustain effective and efficient productivity-enhancing technologies to farmers
- Create and strengthen linkages and co-ordination within the overall extension services
- Align extension to Government policy, particularly privatization, liberalization, decentralization, and democratization.

*(MAAIF and MPED, 2000; cited in Benin et al, 2007)*

Initially, the program was rolled out in specific sub-counties in six districts (2001), then ten further districts were added (2002-2003), followed by thirteen more (2003-2005). Researchers at IFPRI were commissioned by the World Bank to evaluate NAADS in early 2005, in which data were collected from both households and farmer groups (Benin et al, 2007). The design of the initial evaluation was simple – to compare outcomes of interest for the initial six districts and the second cohort of ten districts, in comparison with randomly chosen non-NAADS districts. This evaluation concluded that NAADS was linked to positive changes in advisory services received by farmers, improving the adoption of new crops and livestock enterprises, and the use of modern technologies and practices. Improvements observed in the study were from a very low base but were sufficiently encouraging that the results were used to maintain investment in the program (Ephraim Nkonya, personal communication; World Bank, 2008). A subsequent impact evaluation (Benin, 2011) used econometric methods to estimate the impacts of NAADS on the income of people living in districts benefiting from the program, indicating positive impacts.

After this initial period of successful implementation (2001–2008), domestic political considerations came to the fore (described in detail in Kjaer and Joughin, 2012). President Museveni suspended the NAADS program in late 2007, putting everything on hold for several months while donors supportive of the program attempted negotiations to get the program reinstated. What emerged was a new NAADS, with the original private-sector-oriented design significantly amended to give a prominent role to government extension officers and a much more central role for the government in disseminating agricultural technologies. A series of excellent qualitative research papers (Kjaer and Joughin, 2012 and 2017; Rwamigisa et al, 2017) consider the political pressures that led to this reversal of the NAADS reforms. What followed in the 2010s was Operation Wealth Creation (OWC), with a further politicization of the process of agricultural input provision disseminated through army troops (Kjaer and Joughin, 2019). In February 2022, the government announced the launch of a Parish Development Model (PDM), a "multi-sectoral strategy for transforming subsistence households into the money economy" (Government of Uganda, 2022). In November 2022, the government decided that OWC would no longer be directly disseminating agricultural inputs but rather shift to being responsible for transferring development funds to the Parish-level SACCOs in support of the PDM.

### *4.5.3 Seed Policy*

The formal seed system for all crops other than maize is poorly developed in Uganda, with most farmers saving seed from their own plots or getting seed through their social networks. The formal seed system lacks private sector actors with the right incentives to invest in high-quality seed production, particularly given long-held concerns about lax regulation of the seed sector. Quality-declared seed (QDS), a system that can be characterized as semi-formal, was developed as a concept by FAO in 1993 and later revisited and refined in 2006 (FAO, 2006). QDS establishes production standards for seed production by registered community seed producers at local levels (zonal/district in the case of Uganda) for seed inspection using an inspection regime that is less onerous than that of certified seed. In Uganda, the main push for QDS to be institutionalized has been made by the Integrated Seed Systems Development (ISSD) program of Wageningen University.

In October 2018, MAAIF introduced the National Seed Policy. The text explicitly recognizes quality-declared seed as a way to "bridge the gap between the formal and informal systems". While ISSD was likely the main player in supporting the revision of the seed policy (Louwaars and de Boef, 2012), there were multiple research inputs to this process provided by Bioversity International and IFPRI in support of their suggested reforms.

### *4.5.4 Innovation Platforms*

An Innovation Platform (IP) is a forum established to foster interaction among a group of relevant stakeholders around a shared interest (Makini et al., 2013). The objectives of IPs vary depending on the level at which it is formed (e.g. village, regional, national) and the nature of the members involved – for example, to tackle a specific challenge or more general challenges in the community. In the framework of agricultural research for development (AR4D), IPs facilitate interaction and collaboration within and between networks of farmers, governmental and non-governmental service providers, policymakers, researchers, private sector players, and other stakeholders in the agricultural system (Schut et al., 2016). As a result, IPs have since gained popularity in increasing the impact of agricultural research and development (Ayele et al., 2012; Kilelu et al., 2013).

CGIAR Research Programs on Integrated Systems for the Humid Tropics (Humidtropics) and the Forum for Agricultural Research in Africa (FARA) Sub-Saharan Africa Challenge Program (SSA CP) are among several AR4D programs that adopted an innovation platform approach to try and achieve development impacts in Uganda. Together with other partners such as local government, the private sector, non-governmental organizations, and researchers, CGIAR initiated innovation platforms to help address some of the challenges farmers faced along the selected value chains or enterprises. Four IPs were established by the SSA CP, while the Humidtropics Program established two IPs.

CGIAR Research Programs have played a significant role in the operations of IPs in Uganda. Specifically, at the inception of Bubaare IP, CIAT facilitated platform members with logistical support, coordinated platform activities, and provided funds for capacity building for farmers. Notable achievements at the IP include the attainment of cooperative status at the national level, the successful promotion of improved varieties of sorghum, and a market linkage wherein sorghum is processed into a beverage. Some of these IPs appear to remain functional while others have become defunct or obsolete. Similarly, in Mukono-Wakiso IP, Humidtropics funded AR4D activities including research experiments and surveys (Schut et al., 2019).

IPs are formed with clear strategies to address the selected problems in the community. However, their success is constrained by many factors – most profoundly, the availability of resources to keep the platform functional beyond the life span of an AR4D project. Strong local support, especially from the private sector, is key to sustaining the platforms. Additionally, institutionalizing the platforms through attaining a formal registration status at the district or national level can help them receive additional support for maintaining platform operations.

We collect community-level data in the UHIS on the existence of farmer groups and, further, whether the farmer group provides links to innovation platforms.

# 5. Results: Adoption of CGIAR-Related Innovations

## 5.1 Animal Agriculture

### *5.1.1 Improved Dairy and Cattle Genetics*

In the household level Uganda Harmonized Integrated Survey (UHIS) data, we find high rates of ownership of large ruminants (i.e., cattle or dairy cows) at 27.7% of all rural households (Table 9). Of those large ruminant-owning households, one in ten (9.9%) report that they use a controlled breeding strategy, and 16.3% report rearing exotic or cross-bred cows. Supporting this adoption of improved dairy and cattle genetics is a nascent system of artificial insemination service provision. Looking across rural communities in Uganda, artificial insemination is reported to be available for cattle and dairy farmers in 14.2% of communities (Table 10), but with significant variation in this rate across regions. In Central Uganda, rates are highest at one-third of communities (34.2% of EAs in UHIS), whereas Northern Uganda has very low rates of artificial insemination service provision (2.5% of EAs in UHIS).

**Table 9: Household-level use of controlled breeding strategies**

| | Household level (UHIS) | | UHIS enumeration areas (EAs) with household-level adoption > 0 | |
|---|---|---|---|---|
| | N | Mean (%) | N | Mean (%) |
| **All rural HHs** | | | | |
| Household has large ruminants | 3,914 | 27.7 | | |
| **Of rural HHs with large ruminants** | | | | |
| Household practices a breeding strategy for large ruminants (of rural HHs with large ruminants) | 1,086 | 9.9 | 307 | 22.8 |
| Household rears exotic or cross-bred cows (of rural HHs with large ruminants) | 1,083 | 16.3 | 307 | 31.6 |

**Table 10: Community-level provision of artificial insemination service (UHIS community module)**

| | UHIS community module, Rural Enumeration Areas | |
|---|---|---|
| | **N** | **Mean (%)** |
| **Community offers artificial insemination services for cattle** | | |
| Central | 38 | 34.2 |
| Eastern | 94 | 22.3 |
| Northern | 114 | 2.5 |
| Western | 107 | 11.2 |
| **Total** | **353** | **14.2** |

### 5.1.2 Improved Fodder Shrubs for Dairy Systems

We find only one instance in which a community reports having a nursery that sells Calliandra seedlings, as shown in Table 11.

**Table 11: Community-level adoption of improved fodder shrubs for dairy systems (defined as having a nursery that sells Calliandra spp.)**

| | Enumeration area level | |
|---|---|---|
| | **N** | **Mean (%)** |
| **Nursery sells Calliandra seedlings** | | |
| Central | 38 | 0.0 |
| Eastern | 94 | 1.1 |
| Northern | 114 | 0.0 |
| Western | 107 | 0.0 |
| **N** | **353** | **0.3** |

### 5.1.3 Milk Collection Centers

While livestock farming is widespread in Uganda, milk collection centers were found in only 5.4% of the communities (Table 12). Milk collection centers are most frequent in Western Uganda (13.1%) but are largely absent in Eastern Uganda (1.1%). In every case, wherever there is a milk collection center, respondents confirmed that it tests milk quality.

**Table 12: Community-level data on milk collection centers (Rural EAs, UHIS)**

| | **N** | **Mean (%)** |
|---|---|---|
| **Community has a milk collection center** | | |
| Central | 38 | 5.3 |
| Eastern | 94 | 1.1 |
| Northern | 114 | 1.8 |
| Western | 107 | 13.1 |
| **Total** | **353** | **5.4** |
| **Milk collection center tests for milk quality** | | |
| Central | 38 | 5.3 |
| Eastern | 94 | 1.1 |
| Northern | 114 | 1.8 |
| Western | 107 | 13.1 |
| **Total** | **353** | **5.4** |

### 5.1.4 East Coast Fever Infection and Treatment Method

We collected data on East Coast Fever Infection and Treatment Method (ECT-ITM) administration but found that farmers were not able to distinguish among different vaccines reliably, so we do not report those data here. From qualitative fieldwork carried out in 2022, we found that common vaccines are for Foot and Mouth Disease (FMD), Contagious Bovine Pleuropneumonia (CBPP), Contagious Caprine Pleuropneumonia (CCPP), and Peste des Petits Ruminants (PPR).

ECF-ITM is considered expensive, so the main control for ECF (and other tick-borne diseases) remains the preventative use of acaricides, despite concerns about resistance.

## 5.2 Crop Improvement

### *5.2.1 Deviations from Research Design*

Recall that the research design (described in Section 3.2.2) for the UNOMA sub-sample was based on sampling specific logistical ‘trips’ and then taking samples of each household cultivating the crop within that trip. Had this design been implemented perfectly, each sub-sample would be nationally representative. However, for each of the UNOMA crops, we observe imperfect compliance with this research design. The sub-samples are smaller than expected, whereby not every enumeration area that should have been sampled was sampled, and not every household cultivating the crop was sampled. This means that our samples are “selected”.

We analyze the nature of the selection into sampling in detail in Appendix T. In all cases, the selected samples are significantly different from the ideal random samples, due to a combination of different reasons. In the appendices, we observe those observable household characteristics that are correlated with being present in our sample, thus, the representativeness of the samples was jeopardized. Given that this is the nature of the available data, we caution against over-interpretation of the point estimates presented in this section. All shares reported based on the UNOMA modules come from these selected samples and therefore do not allow us to provide a nationally representative estimate of the total reach of the innovations. That said, the orders of magnitude of different types of varieties found in the sample are still informative on the approximate diffusion (or lack thereof) of different types of varieties.

### *5.2.2 Improved Maize Varieties*

Detailed sample-level results of the maize DNA fingerprinting analysis are provided in Appendix M. Here, we look at DNA fingerprinting data at a household level, with the aggregate picture outlined in (Table 13). Material bred by NARO, typically with CGIAR input, is found widely, with NARO open-pollinated varieties (OPVs) dominant. Private sector hybrids are found on 19.4% of maize-producing households, with 26.7% of households cultivating plots with no discernible genetic profile. At least one CGIAR-related variety is found in 57.8% of households (all the NARO hybrids are CGIAR related, as is Longe 5/Longe 5D, a NARO OPV), with the remainder being households with at least one private sector hybrids or households for which none of the samples had a discernible genetic profile. The latter could reflect landraces, material of a mixed and informal nature that doesn’t represent a prevailing genetic identity, or foreign genetic material that was not included in the reference library.

The CGIAR-related varieties were bred for drought and pest-resistance, so the same estimate of 57.8% of households also represents those who managed to access resistant varieties. This is a high share, and of a similar order of magnitude or even higher than results found for drought-resistant maize in 2022 in Ethiopia (Alemu et al, 2024). As samples were only collected in a third of the households from the representative sample, the magnitude should be interpreted with a large confidence interval around it. Even so, it reveals that at least for maize, CGIAR breeding efforts have allowed households to access resilience-enhancing varieties. This is relevant, as households report disease and pest susceptibility as well as drought-susceptibility as the main reasons for disliking the varieties they plant. See Appendix S.

### Table 13: Household-level adoption of maize varieties, by type

| | Households | | Enumeration areas (with adoption > 0) | |
|---|---|---|---|---|
| | N | Mean (%) | N | Mean (%) |
| **Private sector hybrids** | 315 | 19.4 | | |
| **NARO hybrids** | 315 | 19.4 | | |
| **NARO OPVs** | 315 | 57.5 | | |
| **Unassigned genetic material** | 315 | 26.7 | | |
| **Households with barcode sample successfully merged** | 1020 | 30.7 | | |
| **Barcodes present, but cannot merge with household dataset** | 1020 | 1.8 | | |
| **Households without a barcoded sample** | 1020 | 67.4 | | |
| **At least 1 CGIAR-related variety** | 315 | 57.8 | 104 | 82.7 |

For the vast majority of households for whom we found a CGIAR-related variety on their field, it was Longe 5/5D (Table 14). Longe 5D, released in 2012, is a drought-tolerant, disease-resistant version of the original popular OPV Longe 5 (released in 2000 and with parents from NARO and IITA). Both LONGE 5 and LONGE 5D are considered Quality Protein Maize varieties for having high content of essential amino acids lysine and tryptophane. Another relatively frequent variety is the cluster of drought-tolerant varietal hybrids UH5051/UH5052/UH5053 that are genetically very similar and therefore indistinguishable through genotyping. Overall, the results show that of the 33 CGIAR-related varieties in the reference library, 11 were found in farmers’ fields.

Presence of CGIAR-related maize varieties in farmers' fields varies across the country, with household-level adoption varying from 45.8% (Central) to 66.1% (Northern), as shown in Table 15. We combine genetic with subjective data to construct Table 16, finding that farmers do not generally perceive a drought-tolerant benefit from adoption of CGIAR-related material. Table 17 shows the average year of release as a share of samples to be 2009, which implies that the average age of improved varieties on farmers' fields was 13 years (i.e., maize found on farmers' fields was on average released 13 years earlier). This is lower than the equivalent finding for maize in Ethiopia, but still means there is a substantial lag between the release of varieties and their widespread diffusion. This also means that even if breeding focuses on the most recent diseases or climate threats, farmers' ability to benefit from such improved traits often comes only many years later.

### Table 14: Household-level adoption of CGIAR-related maize varieties. Adoption is defined by having at least one sample taken from their maize plots that is positively identified as being CGIAR-related

| | Varietal type | Households | |
|---|---|---|---|
| | | N | Mean (%) |
| **LONGE 5 / 5D** | OPV | 315 | 41.0 |
| **UH5051 / UH5052 / UH5053** | Varietal hybrid (OPV x OPV) | 315 | 10.2 |
| **LONGE 10H** | Hybrid | 315 | 3.8 |
| **Bazooka** | Hybrid | 315 | 2.9 |
| **ADV2309** | Hybrid | 315 | 0.6 |
| **ADV2310** | Hybrid | 315 | 0.6 |
| **FH6150** | Hybrid | 315 | 0.6 |
| **WE6103/Champion** | Hybrid | 315 | 0.6 |
| **LONGE 7H** | Hybrid | 315 | 0.3 |
| **No CGIAR-related varieties** | | 315 | 42.2 |

### Table 15: Household-level adoption of any CGIAR-related maize variety, by region

| | Household level | | EA level | |
|---|---|---|---|---|
| | N | Mean (%) | N | Mean (%) |
| **Central** | 48 | 45.8 | 19 | 68.4 |
| **Eastern** | 92 | 53.3 | 33 | 78.8 |
| **Northern** | 112 | 66.1 | 32 | 96.9 |
| **Western** | 63 | 58.7 | 20 | 80.0 |
| **Total** | **315** | **57.8** | **104** | **82.7** |

### Table 16: Sample-level subjective data (rows) for samples found using genotyping to be CGIAR-related, private sector hybrids or unassigned (columns)

| | CGIAR-related | | Private sector | | Unassigned | |
|---|---|---|---|---|---|---|
| | N | Mean (%) | N | Mean (%) | N | Mean (%) |
| **What do you like about this variety? Respondent mentions drought tolerance** | 349 | 9 | 62 | 13 | 156 | 12 |
| **Is this variety affected by any disease?** | 349 | 31 | 62 | 26 | 156 | 40 |
| **Source of seed: Another farmer (relative/neighbor)** | 349 | 39 | 62 | 31 | 156 | 40 |
| **Source of seed: Market** | 349 | 50 | 62 | 65 | 156 | 51 |

### Table 17: Year of release (determined following genetic identification) for all genetically assigned maize samples

| Year of release | Number of samples |
|---|---|
| 2000 | 119 |
| 2002 | 2 |
| 2004 | 7 |
| 2005 | 42 |
| 2009 | 22 |
| 2012 | 318 |
| 2013 | 19 |
| 2017 | 1 |
| 2019 | 39 |
| 2022 | 1 |
| **N** | **570** |
| **Overall mean** | **2009** |

Digging deeper into the varietal-level data, we see a pattern of intra-plot heterogeneity that reflects the complex reality of maize plots in Uganda. Recall that the design was for two crop-cut samples to be taken for each plot, unless the enumerator determined the plot to be too small or irregular so that a second crop-cut could not be laid. We have a sub-sample of 185 households where a single pair of samples was taken. If the plot is indeed a unit of somewhat uniform management planted with a single variety, then duplicate crop cuts from the same plot should reveal the same genetic identity each time.

As we can see in Table 18 this is not the picture that emerges all the time. In a small majority of cases (55.7%), duplicate crop-cuts from the same plot do indeed reveal the exact same genetic identity. However, in the remainder (44.3% of cases), a pair of crop cuts from the same plot reveal different genetic identities. This has implications for inference about measurement error. If plots are heterogeneous, a sample from one quadrant may not do a good job of capturing the true genetic nature of the entire plot. The lower panel of Table 18 shows that unassigned identities play a role to some extent, whereby 14.1% of pairs have one assigned and one unassigned varietal identity. This might indicate variable seed quality within those plots. In 17.3% of pairs, both samples are unassigned, suggesting that farmers are cultivating landraces, or material of a mixed and informal nature that doesn't represent a prevailing genetic identity.

### Table 18: Intra-plot heterogeneity in maize, revealed from duplicate pairs of crop-cuts in the same plots

| | Households | |
|---|---|---|
| Paired combination observed | N | Mean (%) |
| Same varieties in the pair | 185 | 55.7 |
| Different genetic identities in the pair | 185 | 44.3 |
| Both assigned a genetic identity | 185 | 68.6 |
| 1 identified, 1 unassigned | 185 | 14.1 |
| Both unassigned | 185 | 17.3 |

Further light can be shed on this phenomenon of mixed plots when we consider farmers' self-reported data about whether they are recycling their maize seed, and for how long. At a variety sample level, we asked the farmer at the time we took the crop-cut whether they obtained all their seed for the plot from outside their own farm. For those who stated that any amount of seed for the plot was recycled, we asked how long they had been recycling the seed. Those results are presented in Table 19 by varietal category as established using DNA fingerprinting. Maize farmers in Uganda recycle their seed a lot, with many responding that they recycle what we determine is a hybrid variety, though rates of recycling for OPVs are higher.

Table 19: Recycling of maize seed (subjective data, rows) for maize variety samples (DNA fingerprinting data, columns)

| | All | | NARO hybrids | | NARO OPVs | |
|---|---|---|---|---|---|---|
| | **Freq** | **%** | **Freq** | **%** | **Freq** | **%** |
| **All seed for the variety obtained from off farm** | 290 | 42.2 | 51 | 47.2 | 136 | 38.0 |
| **At least some recycling** | 397 | 57.8 | 57 | 52.8 | 222 | 62.0 |
| **For those recycling seed, number of seasons reported** | **Freq** | **%** | **Freq** | **%** | **Freq** | **%** |
| **0** | 7 | 1.7 | 2 | 3.5 | 4 | 1.8 |
| **1** | 26 | 6.4 | 6 | 10.5 | 9 | 4.1 |
| **2** | 133 | 32.6 | 19 | 33.3 | 69 | 31.1 |
| **3** | 91 | 22.3 | 11 | 19.3 | 58 | 26.1 |
| **4** | 89 | 21.8 | 12 | 21.1 | 45 | 20.3 |
| **5** | 15 | 3.7 | 2 | 3.5 | 10 | 4.5 |
| **6** | 9 | 2.2 | 1 | 1.8 | 5 | 2.3 |
| **8** | 7 | 1.7 | 0 | 0.0 | 5 | 2.3 |
| **10** | 16 | 3.9 | 1 | 1.8 | 7 | 3.2 |
| **14** | 1 | 0.2 | 1 | 1.8 | 0 | 0.0 |
| **15** | 6 | 1.5 | 0 | 0.0 | 6 | 2.7 |
| **16** | 1 | 0.2 | 0 | 0.0 | 1 | 0.5 |
| **100** | 7 | 1.7 | 2 | 3.5 | 3 | 1.4 |
| **Total** | **408** | | **57** | | **222** | |

### *5.2.3 Improved Cassava Varieties*

All CGIAR-related varieties are bred to be resistant to diseases, namely cassava mosaic disease (CMD) and/or cassava brown streak disease (CBSD). As Table 20 shows, 35.1% of households have at least one CGIAR-related variety (and rarely more than one), indicating the share of households potentially benefiting from these resilience traits. As shown in Table 21, the majority of these cases are the pair of 2015 releases NAROCASS 1 (13.9% of cassava-growing households) and NASE 19 (12.8% of cassava-growing households), representing relatively fast take-up with only six years between release and the year samples were taken (2021/22). Given that the vast majority of cassava-growing households report being affected by diseases (shown in Table 22), this is a relevant finding. At 69%, the share of households reporting diseases is significantly smaller for those cultivating CGIAR-related varieties than for those with landraces

(84%). This is consistent with the CGIAR-related varieties increasing resilience to the common cassava diseases, even if the problem is clearly not eliminated.

While 60% of farmers with CGIAR-related varieties report getting new planting material from outside of the farm, the remaining 40% report re-using improved cassava varieties for six seasons, which possibly explains reduced resistance. Moreover, even for the 60% of farmers who do not re-use their own material, 85% of them say they obtain planting material from neighbors. See Appendix N for further details and differences between variety types.

### Table 20: Adoption of CGIAR-related cassava varieties at the household level (DNA fingerprinting data, UNOMA sub-sample)

| Household has: | N | Sum | Mean (%) |
|---|---|---|---|
| All unassigned varieties | 646 | 233 | 36.1 |
| At least 1 identified landrace variety | 646 | 212 | 32.8 |
| No CGIAR-related varieties | 646 | 419 | 64.9 |
| **At least 1 CGIAR-related variety** | **646** | **227** | **35.1** |
| 1 CGIAR-related variety | 646 | 204 | 31.6 |
| 2 CGIAR-related varieties | 646 | 20 | 3.1 |
| 3 CGIAR-related varieties | 646 | 3 | 0.5 |

### Table 21: Share of households adopting specific CGIAR-related cassava varieties (DNA fingerprinting data, UNOMA sub-sample)

| Household has: | N | Observations | Mean (%) |
|---|---|---|---|
| NAROCASS 1 | 646 | 90 | 13.9 |
| NASE 19 | 646 | 83 | 12.8 |
| NASE 3 | 646 | 34 | 5.3 |
| NASE 12 | 646 | 15 | 2.3 |
| TMEB14 | 646 | 11 | 1.7 |
| IITA-TMS-IBA120067 | 646 | 11 | 1.7 |
| NASE 13 | 646 | 8 | 1.2 |
| NASE 1 | 646 | 8 | 0.2 |

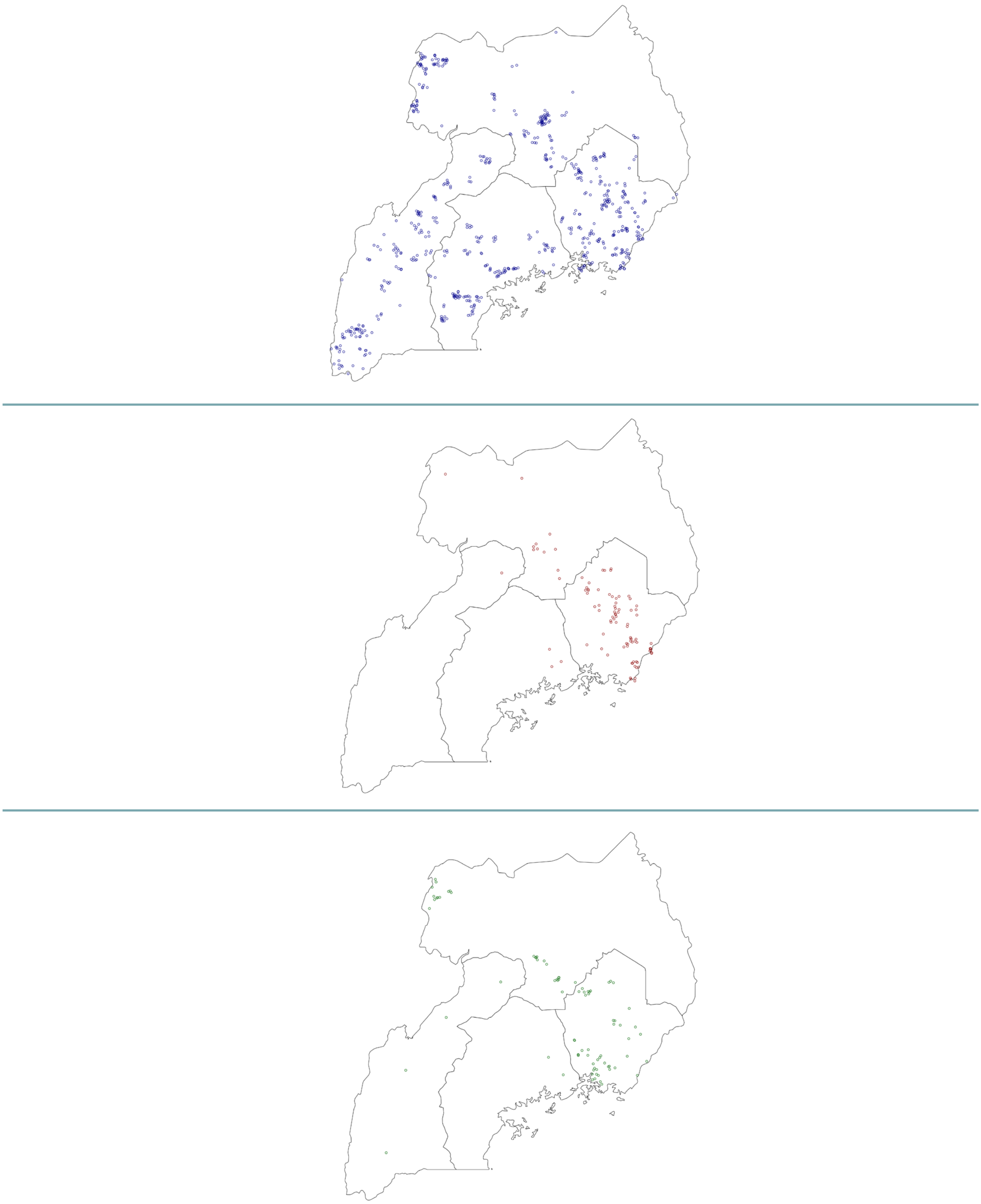
### Table 22: Sample-level subjective data (rows) for samples found using genotyping to be CGIAR-related, landraces, or unassigned (columns)

| | CGIAR-related | | Landrace | | Unassigned | |
|---|---|---|---|---|---|---|
| | N | Mean | N | Mean | N | Mean |
| New planting material for this variety obtained from outside their own farm | 343 | 58.5 | 351 | 36.2 | 703 | 45.1 |
| For planting material from own farm, how many years has it been recycled since last acquired from outside? | 149 | 5.7 | 228 | 9.4 | 405 | 6.8 |
| Currently affected by any diseases? | 335 | 69.3 | 349 | 84.2 | 694 | 72.5 |

Examining spatial patterns in adoption of these disease-resistant improved cassava varieties, we see a concentration in Eastern region, as detailed in Table 23 and revealed in the maps in

Figure 10. In terms of the age of adopted improved varieties, we find a large majority (66% of improved variety samples) having been released in 2015 (Table 24). Owing to the persistence of some older improved varieties from 1970 and 1994, the average year of release of improved varieties adopted is 2005, or 17 years of age (samples having been collected in 2022).

**Figure 10: Map of cassava-growing households from which samples were taken (top panel), and those found to be adopting NAROCASS-1 (center panel) and NASE-19 (bottom panel)**



### Table 23: Regional breakdown of cassava varietal adoption (DNA fingerprinting data, UNOMA sub-sample)

| | N | Sum | Mean (%) |
|---|---|---|---|
| **CENTRAL** | | | |
| HH has all unassigned varieties | 137 | 39 | 28.5 |
| HH has at least 1 NAROCASS-1 sample | 137 | 3 | 2.2 |
| HH has at least 1 NASE-19 sample | 137 | 3 | 2.2 |
| HH has at least 1 sample of any improved varieties | 137 | 6 | 4.4 |
| **EASTERN** | | | |
| HH has all unassigned varieties | 203 | 55 | 27.1 |
| HH has at least 1 NAROCASS-1 sample | 203 | 75 | 36.9 |
| HH has at least 1 NASE-19 sample | 203 | 49 | 24.1 |
| HH has at least 1 sample of any improved varieties | 203 | 139 | 68.5 |
| **NORTHERN** | | | |
| HH has all unassigned varieties | 153 | 67 | 43.8 |
| HH has at least 1 NAROCASS-1 sample | 153 | 11 | 7.2 |
| HH has at least 1 NASE-19 sample | 153 | 27 | 17.6 |
| HH has at least 1 sample of any improved varieties | 153 | 54 | 35.3 |
| **WESTERN** | | | |
| HH has all unassigned varieties | 153 | 72 | 47.1 |
| HH has at least 1 NAROCASS-1 sample | 153 | 1 | 0.7 |
| HH has at least 1 NASE-19 sample | 153 | 4 | 2.6 |
| HH has at least 1 sample of any improved varieties | 153 | 6 | 3.9 |
| **TOTAL** | | | |
| **HH has all unassigned varieties** | **646** | **233** | **36.1** |
| **HH has at least 1 NAROCASS-1 sample** | **646** | **90** | **13.9** |
| **HH has at least 1 NASE-19 sample** | **646** | **83** | **12.8** |
| **HH has at least 1 sample of any improved varieties** | **646** | **205** | **31.7** |

### Table 24: Distribution of year of release for all cassava samples that are positively identified as a released variety (sample-level)

| Year of release<br>**Overall mean = 2005** | N | Freq | % |
|---|---|---|---|
| 1970 | 359 | 49 | 14 |
| 1994 | 359 | 45 | 13 |
| 2000 | 359 | 20 | 6 |
| 2011 | 359 | 8 | 2 |
| 2015 | 359 | 237 | 66 |

Recall that enumerators were instructed to collect each farmer-declared cassava variety in duplicate. As shown in Table 25, we have a smaller sub-sample of households where this process of duplication was carried out effectively (395 out of a total of 646 households cassava samples were taken). In aggregate, farmer information about the extent of diversity in their cassava plots is quite good, as revealed when duplicate samples, from two distinct cassava plants of that variety selected by the farmer, actually match up. As we can see from the top two rows of Table 25, there is correspondence between these duplicated samples for

70.8% of households. The remainder are instances where the farmer knows that they are growing multiple varieties but their duplicates are genetically distinct from each other (5.3% of households), or where the farmer mistakenly either thinks they cultivate multiple varieties (11.9%) or a single variety (11.9%).

**Table 25: Farmer knowledge of the diversity of varieties cultivated in their plot**

| Farmer thinks they plant: | DNA shows: | Duplicates | N | Mean (%) |
|---|---|---|---|---|
| Single variety | Single variety | Match | 395 | 47.8 |
| Multiple varieties | Multiple varieties | Match | 395 | 23.0 |
| Multiple varieties | Multiple varieties | Don't match | 395 | 5.3 |
| Multiple varieties | Single variety | | 395 | 11.9 |
| Single variety | Multiple varieties | | 395 | 11.9 |

### 5.2.4 Improved Banana Varieties

Detailed, sample-level analysis of the banana data is provided in Appendix O. The most important result we established with the bioinformatics analysis is that there are many different reference genotypes for "matooke" landraces that we used in the reference library, but the majority of them cluster into a single genetically uniform clone. They may have phenotypic differences, but genetically they are identical. In Table 26 we look at the aggregate picture by type of banana. Most banana-growing households (71.5%) only plant matooke in their banana plots. Some households (21.1%) plant both matooke and other non-matooke types (Gros Michel, Bluggoe, Honduran hybrids, Cavendish, Kamaramasenge, Pisang Awak, Ney Poovan, Ibota) and only a small share (7.4%) specialize in these non-matooke types. Of the matooke samples taken in UNOMA, almost all are from the matooke landraces. We find only three examples of households adopting improved matooke in our data. By contrast, when asked in the UNOMA module whether they are cultivating an improved matooke variety, 12% of households (from a total of 976 households) respond that they do.

**Table 26: Household level adoption by banana types (DNA fingerprinting data, UNOMA sub-sample)**

| Banana type | N | Sum | Mean (%) |
|---|---|---|---|
| **Matooke only** | **719** | **514** | **71.5** |
| Improved (CGIAR-related) matooke | 719 | 3 | 0.4 |
| Landrace only | 719 | 511 | 71.1 |
| **Both matooke and non-matooke types** | **719** | **152** | **21.1** |
| **Only non-matooke types** | **719** | **53** | **7.4** |

Farmers report maintaining their matooke planting material for twice as long as the non-matooke types (top row in Table 27), for an average of 12 growing seasons (compared to six for non-matooke types). Regardless of type, farmers almost always report obtaining their planting material from a relative or neighbor. Table 27 also shows the significant shares of farmers reporting their plantations being currently affected by pests and diseases.

### Table 27: Subjective data (sample level) on source of banana planting material and perceptions of current pest and disease burden

| | Matooke | | Non-Matooke types | |
|---|---|---|---|---|
| | N | Mean % | N | Mean % |
| **For planting material obtained from own farm, for how many seasons has this variety been used since being acquired?** | 986 | 12.4 | 160 | 6.1 |
| **Destiny of the harvest: Sell** | 1763 | 32.5 | 323 | 40.3 |
| **Source of planting material** | | | | |
| NAADS | 1777 | 0.3 | 324 | 1.2 |
| Government / OWC / MP | 1777 | 0.2 | 324 | 2.8 |
| Farm group / multiplier | 1777 | 2.6 | 324 | 3.7 |
| Another farmer (Relative / Neighbor) | 1777 | 93.6 | 324 | 90.1 |
| **Currently affected by any pests? Y = 1** | 1003 | 23.9 | 226 | 31.9 |
| **Currently affected by any diseases? Y = 1** | 1003 | 43.5 | 226 | 37.6 |

### Table 28: De facto (DNA fingerprinting) genetic diversity at plot level

| Number of varieties in the plot | N | Mean (%) |
|---|---|---|
| 1 | 454 | 72.9 |
| 2 | 454 | 21.6 |
| 3 | 454 | 4.6 |
| 4 | 454 | 0.9 |

Table 28 shows the de facto level of genetic diversity we observe at the plot level, with 72.9% of plots having a single variety as determined through DNA fingerprinting of multiple farmer-declared varieties. In Table 29, we see a pattern whereby half of the plots are planted to a single cultivar, and yet the farmer believes there to be multiple cultivars present (bottom left cell of 2x2 matrix in Table 29). Of the 117 instances in which farmers knowingly plant multiple cultivars, 74 plots have matching duplicate samples, suggesting that farmers differentiate well among the multiple cultivars they have. The remaining 43 plots have duplicates that do not match, suggesting that there is even more genetic diversity present in those plots than the farmer acknowledges.

### Table 29: Matrix comparing farmers' opinions on intra-plot diversity vs DNA fingerprinting

| | | DNA fingerprinting results (N = 454 plots) | |
|---|---|---|---|
| | | Single cultivar | Multiple cultivars |
| Farmers’ opinion (N = 454 plots) | Single cultivar | 22.9% | 1.3% |
| | Multiple cultivars | 50.0% | 25.8% |

In Table 30, the shaded cells on the diagonal signify plots where the same number of cultivars are identified by the farmer, as is confirmed by genetic analysis. Thus, for 39.2% of plots, the farmer has good information about the number of cultivars they have on their plot. The errors off-diagonal are almost exclusively in the direction of less de facto diversity than the farmer thinks there is. The vast majority of East African Highland Bananas (EAHBs) are genetically identical, despite displaying phenotypic variation in fruit size, shape etc. Therefore, farmers may manage for phenotypic diversity but have no genetic diversity in their plots. This matters, owing to the numerous disease and pest pressures on banana in Uganda – a whole banana plot can be lost to the same biotic threat with no genetic variation in tolerance or resistance to those threats.

**Table 30: Farmer-reported diversity vs actual within-plot diversity**

| | Genetically distinct cultivars | | | | |
|---|---|---|---|---|---|
| **Farmer-reported cultivars** | 1 | 2 | 3 | 4 | **Total** |
| **1** | 104 | 6 | 0 | 0 | **110** |
| **2** | 175 | 68 | 12 | 1 | **256** |
| **3** | 50 | 24 | 6 | 3 | **83** |
| **4** | 2 | 0 | 3 | 0 | **5** |
| **Total** | **331** | **98** | **21** | **4** | **454** |

### 5.2.5 Micro- and Macro-Propagation for Banana Planting Materials

We were not able to collect data on these innovations.

### 5.2.6 Improved Bean Varieties

Detailed sample-level analysis of the bean DNA fingerprinting data is provided in Appendix P. Germplasm from CGIAR-related bean varieties was found in plots belonging to 26.5% of households in the UNOMA bean sub-sample (Table 31). A small minority of these cases were genetically uniform (1.4%), with the remainder being mixed. Most plots are positively identified as landraces or are unidentified owing to a lack of a distinct genetic identity, given farmers' informal sources of seed and purposive mixing. Of the households cultivating a CGIAR-related variety, Table 32 shows that there is a large spread of 17 different bean varieties, each adopted at low rates (with the exception of NABE 20). Released varieties are much more widely adopted in the central region (58.2%) than in the other three regions (see Table 33).

**Table 31: Household-level adoption of CGIAR-related and all released varieties in uniform or mixed states**

| | N | Sum | Mean % |
|---|---|---|---|
| Any CGIAR-related material | 366 | 97 | 26.5 |
| Uniform released, CGIAR-related variety | 366 | 5 | 1.4 |
| Mixed released, CGIAR-related variety | 366 | 93 | 25.4 |
| Uniform released, not CGIAR-related | 366 | 13 | 3.6 |
| Mixed released, not CGIAR-related | 366 | 20 | 5.5 |

### Table 32: CGIAR-related bean varieties found to be cultivated by households (DNA fingerprinting results, household-level)

| Household has at least one sample of: | N | Sum | Mean % |
|---|---|---|---|
| K132 | 97 | 1 | 1.0 |
| NABE 1 | 97 | 5 | 5.2 |
| NABE 10C | 97 | 3 | 3.1 |
| NABE 12C | 97 | 4 | 4.1 |
| NABE 16 | 97 | 7 | 7.2 |
| NABE 17 | 97 | 6 | 6.2 |
| NABE 2 | 97 | 3 | 3.1 |
| NABE 20 | 97 | 40 | 41.2 |
| NABE 21 | 97 | 3 | 3.1 |
| NABE 23 | 97 | 13 | 13.4 |
| NABE 6 | 97 | 1 | 1.0 |
| NAROBEAN1 | 97 | 1 | 1.0 |
| NAROBEAN2 | 97 | 10 | 10.3 |
| NAROBEAN 4C | 97 | 5 | 5.2 |
| NAROBEAN 5C | 97 | 5 | 5.2 |
| NAROBEAN 6 | 97 | 1 | 1.0 |
| NAROBEAN 7 | 97 | 1 | 1.0 |

### Table 33: Regional breakdown of adoption of released varieties, identified landraces, and unassigned genetic material (DNA fingerprinting results). Released and landrace categories comprise both uniform and mixed samples

| HH has at least 1 sample that is: | N | Sum | Mean (%) |
|---|---|---|---|
| **CENTRAL** | | | |
| Released | 98 | 57 | 58.2 |
| Landrace | 98 | 50 | 51.0 |
| Unassigned | 98 | 47 | 48.0 |
| **EASTERN** | | | |
| Released | 60 | 11 | 18.3 |
| Landrace | 60 | 37 | 61.7 |
| Unassigned | 60 | 23 | 38.3 |
| **NORTHERN** | | | |
| Released | 29 | 7 | 24.1 |
| Landrace | 29 | 20 | 69.0 |
| Unassigned | 29 | 4 | 13.8 |
| **WESTERN** | | | |
| Released | 179 | 45 | 25.1 |
| Landrace | 179 | 98 | 54.7 |
| Unassigned | 179 | 87 | 48.6 |
| **TOTAL** | | | |
| **Released** | **366** | **120** | **32.8** |
| **Landrace** | **366** | **205** | **56.0** |
| **Unassigned** | **366** | **161** | **44.0** |

Focusing on the NAROBEAN biofortified bean series, we find that only 6.3% of bean-growing households in our sample have bulked samples with DNA (almost all in mixed samples), indicating the presence of NAROBEAN in the plot (Table 34). The relatively low share, together with the fact that almost all those are in mixed samples, suggests that the benefits of the biofortification breeding program in beans were not reaching many farm households by 2021/22.

Table 34: Household-level adoption of biofortified beans (in either uniform or mixed state)

| | N | Sum | Mean % |
|---|---|---|---|
| NAROBEAN 1, 2, 3, 4C, 5C, 6 or 7 | 366 | 23 | 6.3 |
| Uniform or Mixed Releases, but not NAROBEAN | 366 | 100 | 27.3 |

As shown in Table 35, there are no clear distinctions in what farmers report they like about their varieties when comparing across CGIAR-related, all released varieties, confirmed landraces, or unidentified samples, even for traits that have been the focus of breeding, such as disease resistance and micronutrient concentration. This lack of clear distinctions may be related to the degree of mixing of genetic material, as shown in the dominance of genetically mixed samples, reinforced by the lack of clarity about the categories of traditional and improved in farmer-report data (as discussed in Section 7).

Table 35: Farmer reporting current problems with bean pests and diseases, and features they like about the bean variety (rows) by genetic class determined by DNA fingerprinting (columns)

| | CGIAR-related | | All released | | Landrace | | Unidentified | |
|---|---|---|---|---|---|---|---|---|
| | N | Mean % | N | Mean % | N | Mean % | N | Mean % |
| Currently affected by pests | 117 | 44 | 154 | 43 | 283 | 46 | 205 | 40 |
| Currently affected by diseases | 117 | 43 | 154 | 43 | 283 | 44 | 205 | 43 |
| **Farmer thinks the variety is good for:** | | | | | | | | |
| Yield | 117 | 72 | 154 | 72 | 284 | 68 | 205 | 72 |
| Nutrition (general) | 117 | 19 | 154 | 16 | 284 | 15 | 205 | 19 |
| Nutrition (mentions iron and/ or zinc) | 117 | 4 | 154 | 3 | 284 | 1 | 205 | 1 |
| Disease or pest resistance | 117 | 8 | 154 | 8 | 284 | 6 | 205 | 7 |
| Drought tolerance | **117** | 7 | **154** | 10 | **284** | 11 | 205 | 7 |

Of those variety samples that were identified as being released, the average year of release was 2010 (Table 36). Given the samples were collected in 2021, this puts the average age of those varieties at 11 years since release.

**Table 36: Distribution of year of release for all bean samples that are positively identified as a released variety (sample-level)**

| Year of release<br>**Sample average = 2010** | **N** | **Sum** | **Mean %** |
|---|---|---|---|
| 1994 | 154 | 2 | 1 |
| 1995 | 154 | 9 | 6 |
| 1999 | 154 | 4 | 3 |
| 2003 | 154 | 4 | 3 |
| 2006 | 154 | 14 | 9 |
| 2010 | 154 | 30 | 19 |
| 2012 | 154 | 66 | 43 |
| 2016 | 154 | 23 | 15 |
| 2019 | 154 | 2 | 1 |

### *5.2.7 Quality Declared Seed*

Farmers overwhelmingly obtain their seed through informal means, either from another farmer (friends, relatives, neighbors) or by buying from the grain market. Purchases from farmer groups or local multipliers indicate the reach of the quality declared seed (QDS) system. The data shows these are very low, with only 5.1% of farmer variety samples (39 out of 760 total) reported to have originated from a farmer group or local multiplier. The breakdown of planting material sources for the UNOMA bean sub-sample, as reported by farmers, is shown in Table 37. Samples found to be CGIAR-related releases (and indeed all released varieties) are twice as likely to be reported from QDS sources, compared to confirmed landrace or unidentified samples, but overall, only a very small share of farmers report using certified seeds, and the differences between released and other varieties are not significant.

**Table 37: Farmer-reported source of planting material for bean samples (rows), by class of genetic identity (from DNA fingerprinting, columns)**

| | **CGIAR-related** | | **All released** | | **Landrace** | | **Unidentified** | |
|---|---|---|---|---|---|---|---|---|
| | **N** | **Mean %** | **N** | **Mean %** | **N** | **Mean %** | **N** | **Mean %** |
| NGO/relief | 117 | 0 | 154 | 1 | 284 | 0 | 205 | 0 |
| NAADS | 117 | 1 | 154 | 2 | 284 | 3 | 205 | 4 |
| Government /OWC/ MP | 117 | 0 | 154 | 1 | 284 | 1 | 205 | 1 |
| Farmer Group/ Multiplier | 117 | 7 | 154 | 9 | 284 | 4 | 205 | 3 |
| Research Center | 117 | 1 | 154 | 1 | 284 | 0 | 205 | 0 |
| Another farmer (relative/ neighbor) | 117 | 45 | 154 | 43 | 284 | 45 | 205 | 45 |
| Market | 117 | 44 | 154 | 44 | 284 | 47 | 205 | 46 |
| Don’t know | 117 | 2 | 154 | 1 | 284 | 1 | 205 | 1 |
| Reports using certified planting material | 113 | 5 | 144 | 6 | 267 | 3 | 196 | 3 |

### 5.2.8 *Improved Sweetpotato Varieties*

Detailed sample-level analysis of the sweetpotato DNA fingerprinting data is provided in Appendix Q. Table 38 shows that only 10% of sweetpotato-growing households with DNA samples cultivate a NARO-released variety and 7% a CGIAR-related released variety. Adoption of orange-fleshed sweetpotato varieties (OFSP) is even lower, with only 3.1% of sweetpotato-growing households having at least one OFSP variety (Table 38). For about half of the samples collected, none of the varieties in the reference library matched the DNA obtained in the field, resulting in about two-thirds of households with at least one unidentified variety. Among those varieties for which a genetic match was found, most of them were landraces, resulting in two-thirds of households being confirmed as growing one of the 106 land races included in the reference library.

Since all sweetpotato breeding in Uganda targets resistance to pests and diseases, the share of households with CGIAR-related varieties (7%) also reflects the share with access to CGIAR-related varieties with disease resistance. In light of the focus on pest and disease resistance, and of the relatively low adoption rates shown in Table 39, it is notable that farmers are almost as likely to report plants being affected by pests (44%) and diseases (41%) for released varieties as for landraces and unidentified varieties, even if they report different types of diseases or pests for the released varieties (see Appendix S). Lack of disease or pest resistance is the most cited negative trait of a variety (32%), but disease or pest resistance is only mentioned as a positive reason for planting a variety for 6% of the varieties. Strikingly, farmers are not more likely to report disease or pest resistance as desired (or lack thereof as undesired) for the released varieties. This strongly suggests farmers do not perceive the pest and disease resistance of the released varieties, which can be a trait that is difficult to discern as it is state-dependent. Moreover, farmers may have difficulties identifying pests or diseases, and/or may attribute losses from pests and diseases to other factors (Mallia, 2025).

**Table 38: Household-level estimates of sweetpotato variety adoption (national, UNOMA sub-sample, DNA fingerprinting)**

| | Households | |
|---|---|---|
| | N | Mean (%) |
| At least 1 NARO-released variety | 590 | 9.8 |
| At least 1 landrace variety | 590 | 67.3 |
| At least 1 assigned variety | 590 | 72.2 |
| At least 1 unassigned variety[27] | 590 | 66.6 |
| At least 1 CGIAR-related variety | 590 | 6.9 |
| At least 1 orange-fleshed variety | 590 | 3.1 |

---

[27] The large share of samples that are unassigned has two explanations that are not mutually exclusive. The first is that the sweetpotato breeding program knows that there are approximately 1,000 landraces from a field mission in the early 2000s that were collected and evaluated but not maintained for use in the breeding program. NARO did keep approximately 300 for use in breeding and these form the basis for our reference library. The second is that novel clones could be generated, potentially including alleles originating from the breeding program, when farmers leave sweetpotato in the field to outcross, either inadvertently or deliberately. There is uncertainty and debate within the scientific community regarding the probability of a sweetpotato plant outcrossing when left in the field to go to seed, thereby generating new landraces. While in theory this is possible, the obstacles to this are numerous as: "even clones able to flourish in tropical regions, have low pollen viability, short flowering, slow pollen tube growth rate and seed malformation, in addition to the presence of dormancy" (Brito et al, 2021). Even if it were to be happening, it would be hard to argue we are missing a big contribution from the breeding program by not observing these novel outcrossed clones, as the majority of the alleles used in the breeding program originate from Ugandan landraces and it is precisely the specific combination of desirable traits into released varieties that represents the value-added of the breeding program.

### Table 39: CGIAR-related sweetpotato varieties found to be cultivated by households (DNA fingerprinting results, household-level)

| Households with at least one sample of: | N | Sum | Mean |
|---|---|---|---|
| Kakamega | 41 | 1 | 2.4 |
| NAROSPOT 1 | 41 | 32 | 78.0 |
| NAROSPOT 12O | 41 | 1 | 2.4 |
| NASPOT 8 | 41 | 7 | 17.1 |

Table 40 shows that, for released varieties, farmers are less likely to mention taste and more likely to mention the time to maturation and (notably) nutrition as positive traits (compared to both land races and unidentified varieties). The latter finding does suggest some possible awareness about biofortification among the relatively small share of farmers with released varieties, which contrasts with the findings about pest resistance and is consistent with flesh color being a more observable trait. While these empirical observations are merely descriptive, these patterns offer potential interesting hypotheses for deeper analysis on the reasons for adoption decisions.

### Table 40: Sample-level subjective data (rows) for sweetpotato samples found using genotyping to be released varieties, identified landraces, or unassigned (columns)

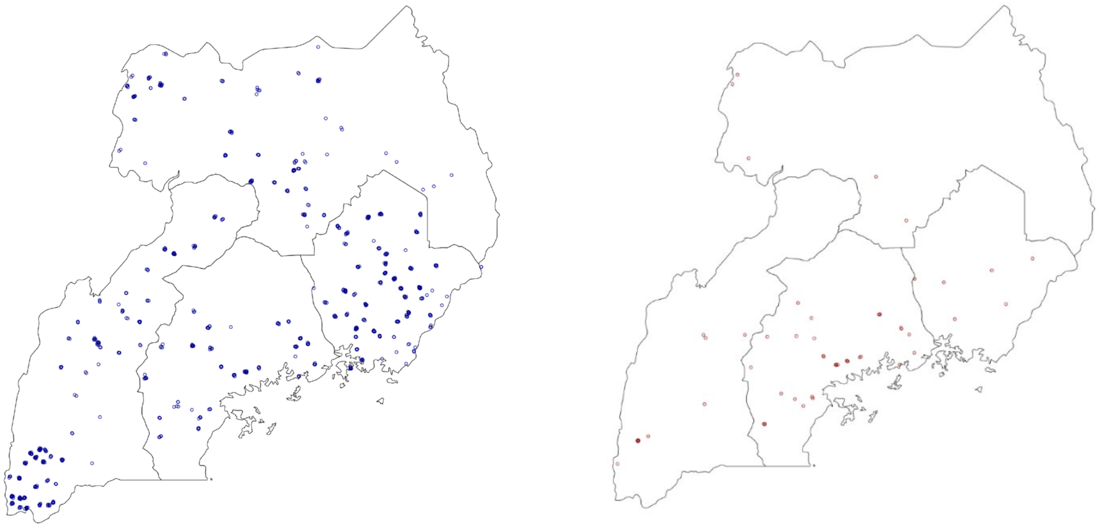
| | Released | | Landrace | | Unassigned | |
|---|---|---|---|---|---|---|
| | N | Mean | N | Mean | N | Mean |
| **For planting material from own farm, how many years has it been recycled since last acquired from outside?** | 35 | 9.6 | 290 | 11.1 | 307 | 11.7 |
| **Plot currently affected by any pests?** | 60 | 40.0 | 569 | 42.9 | 590 | 44.6 |
| **Plot is currently affected by:** | | | | | | |
| Leaf spot and stem blight | 28 | 25.0 | 223 | 59.2*** | 249 | 58.2*** |
| Sweet potato virus disease (SPVD) | 28 | 28.6 | 223 | 18.8 | 249 | 22.5 |
| **Like about the variety:** | | | | | | |
| Yield | 61 | 67.2 | 568 | 68.3 | 591 | 60.1 |
| Taste | 61 | 63.9 | 568 | 71.0 | 591 | 73.1 |
| Nutrition | 61 | 24.6 | 568 | 15.0 | 591 | 16.1 |
| Disease / pest resistance | 61 | 6.6 | 568 | 6.2 | 591 | 6.4 |
| Time to maturity | 61 | 31.2 | 568 | 23.2 | 591 | 23.0 |
| **Source of planting material:** | | | | | | |
| NAADS | 61 | 1.6 | 569 | 0.7 | 591 | 0.9 |
| Government / OWC / MP | 61 | 1.6 | 569 | 1.1 | 591 | 0.7 |
| Farmer group / local multiplier | 61 | 3.3 | 569 | 1.4 | 591 | 2.9 |
| Another farmer (relative / neighbor) | 61 | 86.9 | 569 | 91.7 | 591 | 90.9 |

Of the released varieties identified, more than half (54%) (Table 41) are a single 2017 release (the pale yellow-fleshed NAROSPOT 1). This suggests that this variety was able to reach households relatively quickly. The spatial distribution of adoption of all improved sweetpotato varieties seems to be concentrated in the central region, possibly due to proximity to the NARO station and related field activities (Figure 11).

### Table 41: Year of release among all sweetpotato samples positively identified as releases

| Year of release<br>**Sample average = 2009** | **N** | **Freq** | **Mean %** |
|---|---|---|---|
| 1995 | 61 | 11 | 18 |
| 1999 | 61 | 8 | 13 |
| 2004 | 61 | 1 | 2 |
| 2007 | 61 | 7 | 11 |
| 2013 | 61 | 1 | 2 |
| 2017 | 61 | 33 | 54 |

**Figure 11: Spatial distribution of sweetpotato growing households sampled (left panel) with at least one NARO-released sweetpotato variety (right panel)**



### 5.2.9 *Improved Groundnut Varieties*

All CGIAR-related varieties are bred to be resistant to diseases (rosette and/or leaf spots) or to be drought-tolerant. As shown in Table 42, 37.1% of households have adopted at least one CGIAR-related variety, which also indicates the share of households possibly benefiting from these resilience traits. Given that the majority of households report being affected by pests or diseases (see Appendix S), this is a relevant finding. Adoption of released varieties seems to be quite concentrated in the Eastern region, and close to Serere where NaSARRI is based (Table 43, Figure 12). This is also where more than half of the samples were taken, owing to the distribution of the incidence of cultivation of the crop. Details of the sample-level variety-specific results are given in Appendix R.

Table 42: Adoption of groundnut variety type (DNA fingerprinting data, household level)

| Household has: | N | Sum | Mean |
|---|---|---|---|
| At least 1 assigned variety | 132 | 101 | 76.5 |
| All unassigned varieties | 132 | 31 | 23.5 |
| At least 1 released variety | 132 | 66 | 50.0 |
| At least 1 CGIAR-related variety | 132 | 49 | 37.1 |

Table 43: Household-level adoption of groundnut varieties by region

| | N | Sum | Mean (%) |
|---|---|---|---|
| **CENTRAL** | | | |
| Released variety | 16 | 1 | 6.2 |
| Of which, CGIAR-related variety | 16 | 0 | 0 |
| **EASTERN** | | | |
| Released variety | 66 | 44 | 66.7 |
| Of which, CGIAR-related variety | 66 | 42 | 63.6 |
| **NORTHERN** | | | |
| Released variety | 32 | 11 | 34.4 |
| Of which, CGIAR-related variety | 32 | 7 | 21.9 |
| **WESTERN** | | | |
| Released variety | 18 | 10 | 55.6 |
| Of which, CGIAR-related variety | 18 | 0 | 0 |
| **TOTAL** | | | |
| **Released variety** | **132** | **66** | **50.0** |
| **Of which, CGIAR-related variety** | **132** | **49** | **37.1** |

Figure 12: Spatial distribution of groundnut-growing households initially sampled (left panel) and those found to be adopting a released groundnut variety (right panel)

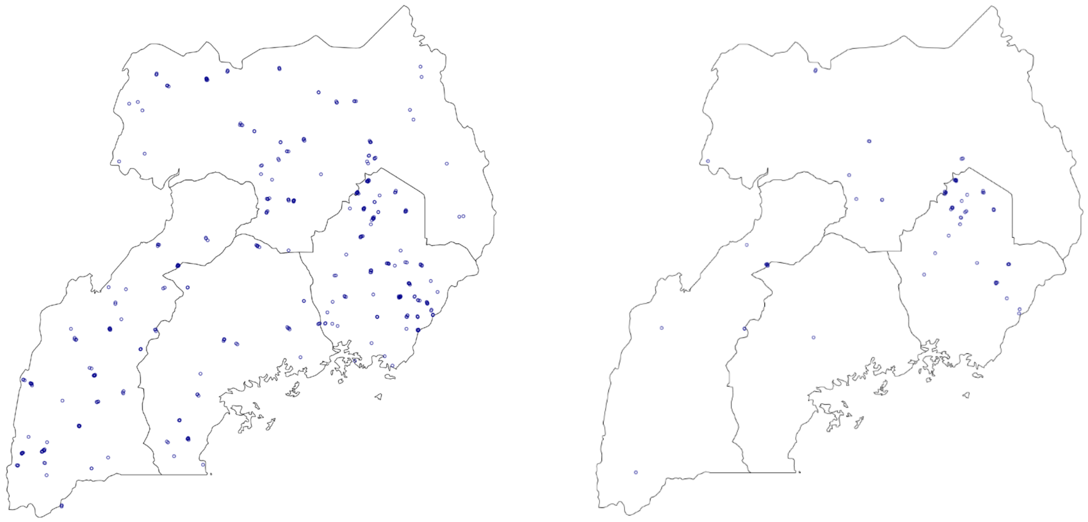


Table 44: Sample-level subjective data (rows) for groundnut samples found using genotyping to be CGIAR-related, assigned but not CGIAR-related, or unassigned (columns)

| | CGIAR-related | | Assigned, not CGIAR-related | | Unassigned | |
|---|---|---|---|---|---|---|
| | N | Mean % | N | Mean % | N | Mean % |
| **Destiny of the harvest for this variety? Sell** | 86 | 43 | 125 | 51 | 101 | 25 |
| **Plot currently affected by any pests?** | 86 | 40 | 125 | 31 | 101 | 51 |
| **Plot is currently affected by any diseases?** | 86 | 65 | 125 | 45 | 101 | 63 |
| **Like about the variety:** | | | | | | |
| Yield | 86 | 67 | 125 | 66 | 101 | 75 |
| Taste | 86 | 73 | 125 | 64 | 101 | 67 |
| Nutrition | 86 | 30 | 125 | 21 | 101 | 32 |
| Cooking properties | 86 | 41 | 125 | 15 | 101 | 16 |
| Disease / pest resistance | 86 | 2 | 125 | 10 | 101 | 4 |
| Time to maturity | 86 | 6 | 125 | 13 | 101 | 12 |
| **Source of planting material:** | | | | | | |
| NGO / Relief | 86 | 0 | 125 | 1 | 101 | 0 |
| NAADS | 86 | 0 | 125 | 0 | 101 | 0 |
| Government / OWC / MP | 86 | 0 | 125 | 0 | 101 | 0 |
| Farmer group / local multiplier | 86 | 1 | 125 | 0 | 101 | 1 |
| Research center | 86 | 0 | 125 | 0 | 101 | 0 |
| Another farmer (relative / neighbor) | 86 | 35 | 125 | 40 | 101 | 54 |
| Market | 86 | 64 | 125 | 56 | 101 | 45 |
| Don’t know | 86 | 0 | 125 | 3 | 101 | 0 |

### Table 45: Year of release among all groundnut samples positively identified as released varieties

| Year of release<br>**Sample average = 1996** | **N** | **Sum** | **Mean %** |
|---|---|---|---|
| 1966 | 119 | 33 | 28 |
| 1998 | 119 | 16 | 13 |
| 2002 | 119 | 4 | 3 |
| 2010 | 119 | 8 | 7 |
| 2011 | 119 | 58 | 49 |

Analysis of duplicate samples from the same plot reveals intra-plot diversity in groundnut. Most commonly, a farmer tells the enumerator that there is a single variety planted on the plot, which triggers the enumerator to collect two duplicate leaf samples from the same plot. Of these cases (N = 103), we find that approximately two-thirds are indeed the same variety (65%, see Table 46). The remaining 35% of samples are found to be of two different varieties. Where four samples were taken (N = 23), this is because the farmer noted two distinct varieties being planted in the same plot and showed the enumerator which plants related to each variety. Of these plots, both pairs of samples are identified as matching pairs in 43.5% of cases, with the remainder either revealing one mismatch out of two pairs (30.4%) or no matches at all among the four samples taken (26.1%), the latter implying highly heterogeneous plots (Table 46).

### Table 46: Analysis of duplicated varietal-level samples of groundnut

| **Household has:** | **N** | **Sum** | **Mean (%)** |
|---|---|---|---|
| A. Two samples, same variety | 103 | 67 | 65.0 |
| B. Two samples, different varieties | 103 | 36 | 35.0 |
| C. Four samples, both pairs with same variety | 23 | 10 | 43.5 |
| D. Four samples, one pair the same, one pair different | 23 | 7 | 30.4 |
| E. Four samples, no similarity across all four | 23 | 6 | 26.1 |
| F. Farmers with apparently accurate information about the number of varieties in their plot (rows A + C) | 126 | 77 | 61.1 |

## 5.3 Natural Resource Management

### *5.3.1 Improved Tropical Fruit Trees*

Planting tropical fruit trees is widespread across Uganda, with 13.5% of rural households carrying out a ‘scattered’ pattern of tropical fruit tree planting on their land, as distinct from a plantation in a single stand (Table 47). Among households with tropical fruit trees (mango, avocado, or oranges), 11% report having an improved variety. While many fruit trees in Uganda may have been planted a long time ago, about 13% of community nurseries sell fruit tree seedlings, suggesting there is some active planting occurring in selected places.

**Table 47: Adoption of tropical fruit trees at the household and community level**

| | Households | | | Enumeration areas/communities | | |
|---|---|---|---|---|---|---|
| | **N** | **Sum** | **Mean (%)** | **N** | **Sum** | **Mean (%)** |
| Household plants ‘scattered’ tropical fruit trees | 4082 | 551 | 13.5 | 388 | 219 | 56.4 |
| Household cultivates improved tropical fruit tree varieties | 741 | 82 | 11.1 | 258 | 59 | 22.9 |
| Community sells fruit tree seedlings in the tree nursery | | | | 353 | 46 | 13.0 |

### *5.3.2 Single Diseased Stem Removal (banana)*

The use of Single Diseased Stem Removal (SDSR) is a practice recommended only when there is high incidence of Banana Xanthomonas Wilt (BXW). Observing the use of this practice by itself does not really provide information about the reach of the innovation per se. In this case, it is arguably more relevant to know whether the correct information about the use of SDSR has the potential to reach the relevant (i.e., affected) farmers. As a way for approximating this knowledge transmission, we measured extension agents' knowledge about the combination of practices to employ in the NSDS survey. With only half of the extension agents knowing about the recommendation of removing the male flowers, transmission of knowledge appears to be imperfect (see NSDS analysis in Section 7).

### *5.3.3 Banana-Coffee Intercropping*

The practice of planting banana and coffee on a single plot seems to be relatively widespread, with 43% of farmers who have either coffee or banana, planting both on the same plot. The geographical spread of the practice reaches 60% of rural communities with those crops (Table 48).

**Table 48: Adoption of banana-coffee inter-cropping at the household and community level**

| | Households | | Enumeration areas/communities | |
|---|---|---|---|---|
| | **Observations** | **Mean (%)** | **Observations** | **Mean (%)** |
| HH plants banana and coffee together in the same plot | 2160 | 43.3 | 320 | 59.7 |

## 5.4 Institutional Innovations

Across rural enumeration areas, communities report having farmer groups in their community in an average of 10.8% of cases, with some variation across regions (Table 49). Among those, only a small minority report having specific links to innovation platforms. As participation in innovation platforms goes through farmer groups, this suggests that the reach of those innovation platforms is limited. Conditional on having a farmer group, communities in Northern and Western Uganda are much less likely to report having linkages to innovation platforms compared to Eastern and Central Uganda.

**Table 49: Community-level data on farmer groups and links to innovation platforms (rural enumeration areas)**

| | N | Sum | Mean (%) |
|---|---|---|---|
| **CENTRAL** | | | |
| Community has farmer groups | 38 | 5 | 13.2 |
| Community farmer groups provide links to innovation platforms | 38 | 2 | 5.3 |
| **EASTERN** | | | |
| Community has farmer groups | 94 | 5 | 5.3 |
| Community farmer groups provide links to innovation platforms | 94 | 4 | 4.3 |
| **NORTHERN** | | | |
| Community has farmer groups | 114 | 15 | 13.2 |
| Community farmer groups provide links to innovation platforms | 114 | 1 | 0.9 |
| **WESTERN** | | | |
| Community has farmer groups | 107 | 13 | 12.1 |
| Community farmer groups provide links to innovation platforms | 107 | 1 | 0.9 |
| **TOTAL** | | | |
| **Community has farmer groups** | **353** | **38** | **10.8** |
| **Community farmer groups provide links to innovation platforms** | **353** | **8** | **2.3** |

# 6. Who and Where Are the Adopters?

Many of CGIAR’s research efforts, explicitly or implicitly, target smallholder farmers, as well as those traditionally marginalized, whether they are poorer, more remote, younger, or female-headed households. Reaching the type of farmers for whom the innovations can potentially make the largest contribution in terms of contributing to rural poverty reduction, improved food and nutrition security, and better natural resource management is an important part of CGIAR's theory of change, and hence important to empirically analyze. In this section, we therefore shed light on the characteristics of adopters. The richness of the UHIS data allows us to document the characteristics of households reached by CGIAR-related innovations along several dimensions. We specifically analyze whether adoption is correlated with farm size (as smallholder farmers are often the specific target of CGIAR innovations) and remoteness. We also define a set of variables to measure gender, social inclusion, and youth dimensions and document their association with adoption. We focus this analysis on the subset of innovations for which there is sufficient variation in the data.

Table 50 shows that CGIAR-related crop varieties are reaching households with a broad range of socio-economic characteristics. As there are no significant correlations between many of the socio-economic variables and adoption rates, the innovations are reaching the different types of households with about equal probability. Hence, most of the CGIAR-related crop varieties are neither less nor more likely to reach poorer, female, young, more remote, or less educated farmers. This general finding is in line with findings for Ethiopia (Alemu et al 2024a, b) and goes against the common assumption that adoption levels are higher among those less disadvantaged. In Uganda, for cassava and groundnut varieties, the data show in fact that they are reaching poor households with a higher likelihood. This is encouraging as it suggests the disease-resilient traits in those varieties may particularly benefit the poor.

In contrast, the natural resource management (NRM) and livestock innovations we were able to measure at some scale are more likely to reach richer households with higher education levels, while they are less likely to reach younger and female farmers. As many of these innovations reach farmers through extension and veterinary services, this may point to possible weaknesses in the targeting of these scaling pathways, to which we return in Section 7.

Inequalities in the types of farmers that are being reached may also be capturing regional differences. Regional patterns in adoption have indeed been documented for the different innovations in the prior section. Summarizing some of the key insights, we noted that adoption of CGIAR-related maize varieties was relatively high in most regions, with the highest rates observed in the Northern region, where virtually all the surveyed communities have some farmers with CGIAR-related maize. For the other crops, CGIAR-related varieties were found in at most half of the sampled communities, and often much less. There are notable regional differences: while CGIAR-related varieties of beans and sweetpotato are the strongest in the Central region, we found more CGIAR-related germplasm for cassava and groundnut in Eastern Uganda, consistent with the focus of some of the regional research stations. Finally, in Western Uganda, the adoption of CGIAR-related varieties is low for all crops other than maize. Livestock and NRM innovations are more frequently observed in the Central region and are largely absent in the Northern region.

## Table 50: Variables associated with the adoption of agricultural innovations in Uganda (UHIS 21/22)

| Variable | Total size of parcels (acres) | Distance to nearest road (km) | Distance to nearest market (km) | Female member listed on parcel title | Female % of family labor is > 50% | PC expenditures below poverty line | Asset value (million UGX) | Maximum years of schooling in household | Age of household head |
|---|---|---|---|---|---|---|---|---|---|
| **Animal Agriculture (large ruminants)** | | | | | | | | | |
| HH practicing breeding strategy | n.s. | -1.21*** | n.s. | n.s. | -4.01** | -7.04*** | 0.24** | 1.10*** | 0.12** |
| HH with cross-bred cows | n.s. | -1.32*** | -0.88*** | n.s. | -5.56** | -14.08*** | 0.59*** | 1.70*** | n.s. |
| **Crop germplasm improvements** | | | | | | | | | |
| Maize varieties | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. |
| Bean varieties | n.s. | -0.02** | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. |
| Cassava varieties | n.s. | n.s. | n.s. | n.s. | n.s. | 0.22*** | n.s. | n.s. | n.s. |
| Groundnut varieties | n.s. | n.s. | n.s. | n.s. | n.s. | 0.30** | n.s. | n.s. | n.s. |
| Sweetpotato varieties | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. |
| **Natural resource management** | | | | | | | | | |
| Planting banana and coffee in same plot | n.s. | n.s. | n.s. | -5.76** | -7.60*** | -25.69*** | n.s. | n.s. | 0.30** |
| Plants scattered tropical fruit trees | n.s. | n.s. | n.s. | n.s. | -3.72*** | -8.08*** | 0.25*** | 0.54*** | 0.19*** |
| Cultivates improved tropical free tree variety | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. | n.s. | 0.73** | n.s. |

Note: Each cell is a coefficient estimate from a separate regression of the row variable on the column variable. For statistically significant relationships, the magnitude of the difference is indicated. Green shows a positive relationship, while red demonstrates a negative relationship. All estimates are based on the sample of rural households for which the innovations were measured (see Section 4). Data for distance to road and market are measured at the household level and imputed with the EA or subcounty median distance in case household-level distances were missing. The analysis excludes innovations adopted by fewer than 4 percent of households.

*** $p < 0.01$. ** $p < 0.05$. n.s = non-significant. UGX = Ugandan Shilling

# 7. Insights from Complementary Sources of Data

## 7.1 National Survey Delivery Survey

### *7.1.1 Extension Module*

The analysis thus far has shown relatively modest and mixed overall levels of adoption of CGIAR-related innovations. Pathways to scaling innovations can be complex, and in the absence of clear exogenous variation in scaling approaches[28] we do not aim to causally establish why these adoption levels are not higher. Even so, we draw on the unique source of information provided by the Ugandan National Service Delivery Survey (NSDS) to provide a diagnostic assessment of the possible role that extension may play in scaling, as well as the possible impediments. The NSDS was collected in 2021 (i.e., shortly before the UHIS), and as it covers all the districts of Uganda, it provides a relevant source of information. The geographical coverage allows us to provide a comprehensive aggregate estimate of service delivery as it relates to agriculture and livestock, and to show estimates for each of the agricultural zones and regions. The NSDS collects data at the district, community (enumeration area (EA)), and household level, covering 621 sub-counties, 1,088 EAs, and 10,246 households nationally.

At the national level, among households with some agricultural or livestock activity, 11% had received extension services on crop husbandry practices, while 6% reported extension support on animal husbandry. While these shares are low, information about agricultural practices can diffuse through many mechanisms, and farmers can learn from other farmers, so direct participation in extension may not necessarily be the most relevant indicator of access to information. At the same time, for information to diffuse, at least some farmers will need to get access to information before they can diffuse it. We hence draw on the NSDS community and district level information to understand to what extent the extension officers are likely to be fulfilling that role.

The community survey contains information from interviews with the subcounty extension worker/production officer who reports on each of the communities in the sample. Data at the district level are obtained from the district-level environment/natural resources officer, and the district production officer. The district-level data allow us to get a bird's eye view on the situation in terms of the presence of district-level agricultural and veterinary officers for each of the agroecological zones (named by the name of their Zonal Agricultural Research and Development Institute, ZARDI).

The NSDS shows that, on average, there are three veterinary officers and four agricultural officers in a district (filled posts), though there is important regional variation, with a relatively large proportion of districts. In Abi and Rwebitaba, there is not a single veterinary or agricultural officer. Taking the number of established district-level posts as given, the data show that 38% of agricultural officers and 50% of veterinary officer posts are vacant at the

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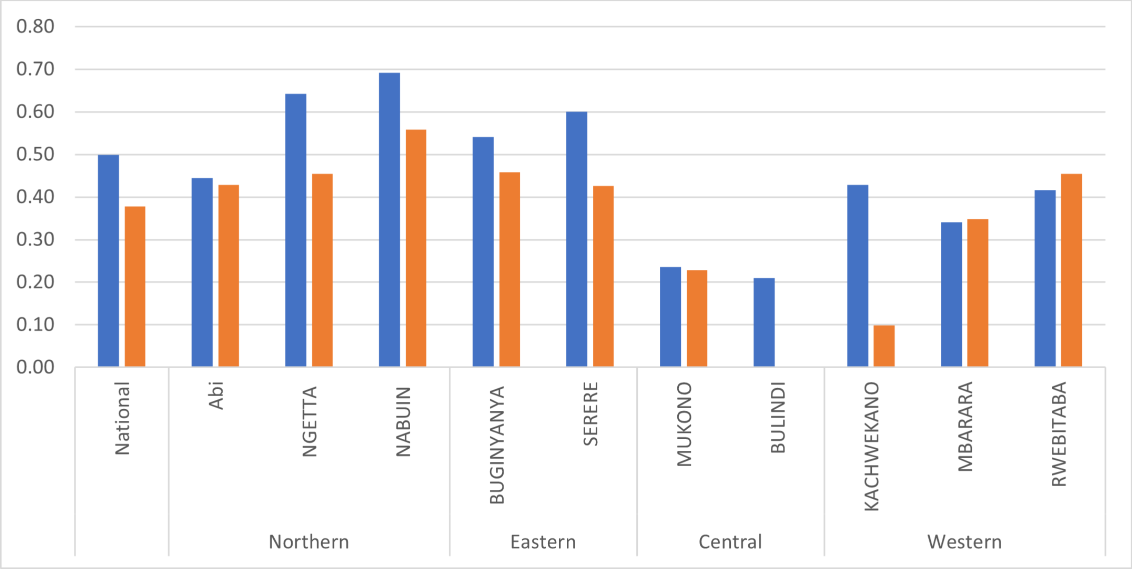
[28] See Meenakshi et al (2021) on how SPIA tries to line up sources of exogenous variation from project roll-out data and how this allows us to estimate impacts of innovations.

national level (Figure 13). The data further shows pronounced regional inequalities in the share of vacant posts, with the problem particularly acute in the North and the East. There are notably fewer vacancies in the Central region, but also in parts of Western Uganda. The latter suggests that vacancies are not only driven by remoteness (i.e., distance from Kampala).

The community survey of the UNPS provides complementary estimates, with community informants reporting that agricultural extension services are available in 63% of the villages (LC1), veterinary services in 78%, and community animal health workers in 39%[29].

**Figure 13: Average share of vacant posts among established district-level posts**



Note: Blue = vacant veterinary officer posts; orange = vacant agricultural officer posts.
Source: National Service Delivery Service (NSDS), 2021.

At the sub-county level, the NSDS collects data from agricultural extension officers, which suggests they provide information to farmers on a broad range of topics. Focusing on the innovations and policies of interest to this report, we can see that almost all agricultural extension officers report providing information about improved maize, while shares are also relatively high for improved beans and cassava (Figure 14). Regional patterns show high rates of access to information (through extension agents) on improved maize in all regions, but with more regional variation for beans and cassava (both being notably lower in Abi), while cassava information is also lower in parts of the West. The finding for cassava in Abi is striking, given the importance of the crop in the area. It possibly helps explain the relatively low share of NASE19 and NAROCass 1 in West Nile, and the large share of unassigned cassava varieties there.

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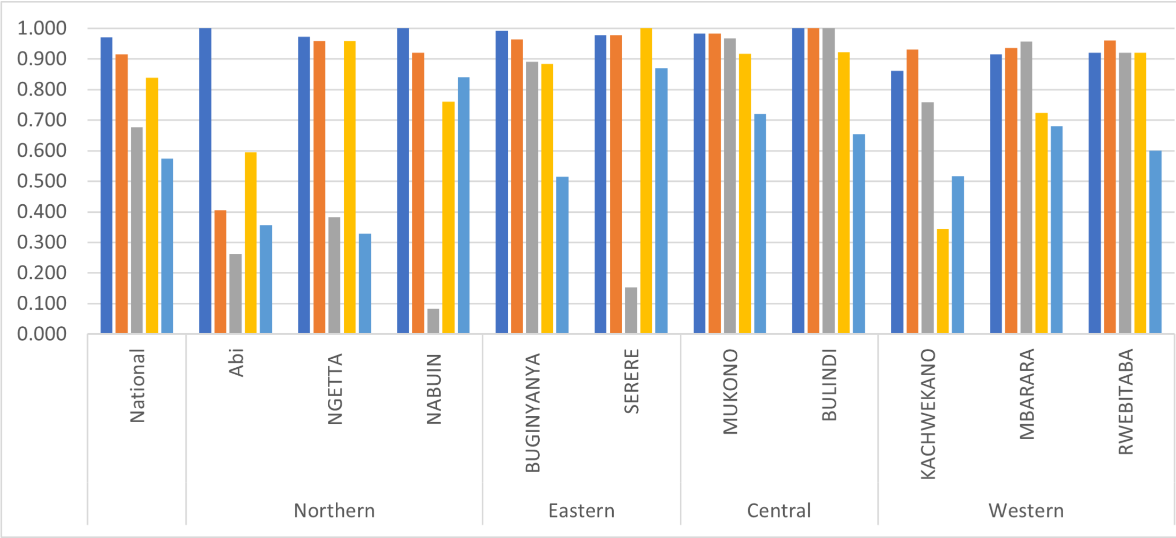
[29] The governments agricultural and veterinary officers are not the only source of information regarding agricultural practices and innovations, as there are also several NGO and private sector extension initiatives.

The data also show that more than 60% of the agricultural officers report providing information on improved bananas, with shares being high in all regions except Northern. It seems likely, therefore, that very low adoption rates of improved *matooke*, revealed through the DNA fingerprinting results, are not necessarily due to lack of attention by extension officers. Finally, of the five crops, information on OFSP is the least common, but even so, a majority of extension agents mention it. The NSDS does not include a similar question for groundnut.

**Figure 14: Share of agricultural extension officers reporting having provided information on improved varieties, by crop (sub-county-level)**

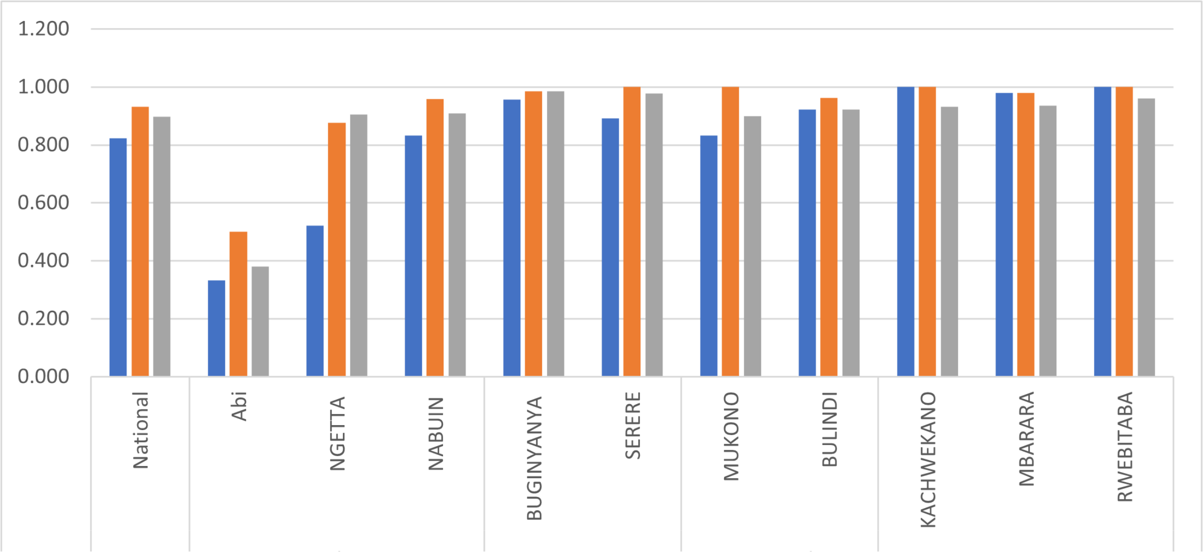


Note: Dark Blue = maize; orange = beans; grey = banana; yellow = cassava; light blue = orange-fleshed sweetpotato

Source: National Service Delivery Service (NSDS), 2021.

Looking beyond crop varieties, more than 80% of agricultural extension officers report providing information on various management practices (Figure 15). Shares are quite high in all regions except the Northern region, where information on sustainable land management practices appears particularly low. Information on fodder and trees is provided by more than 60% of officers, with shares again strikingly lower in the Northern region (Figure 16). This is consistent with lower adoption rates of some of the tree innovations in the Northern region.

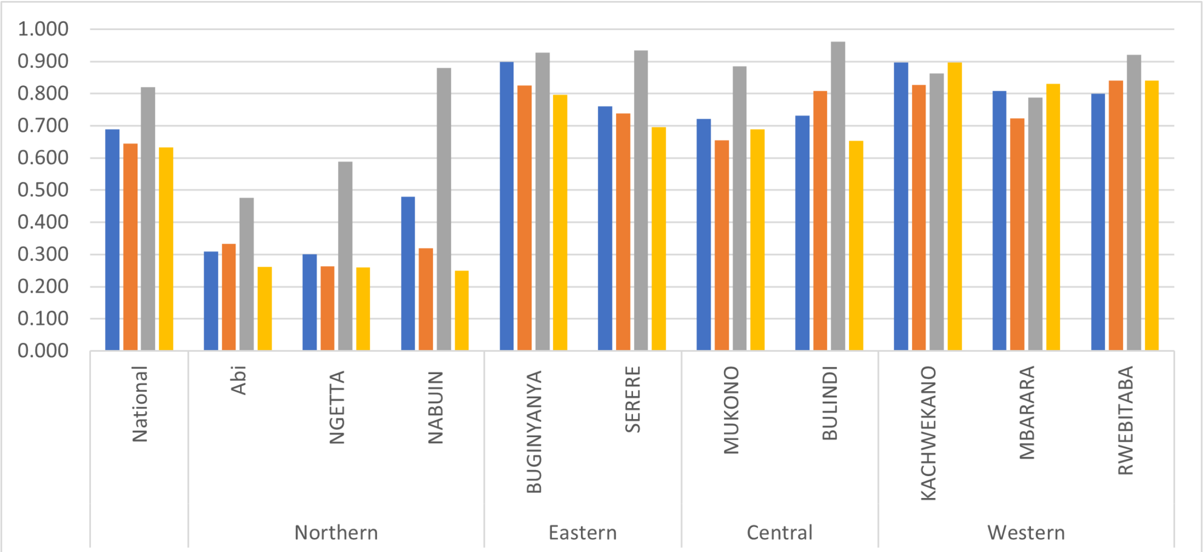
**Figure 15: Share of agricultural extension officers reporting providing information on management practices (sub-county level)**



Note: Blue = Sustainable land management; orange = crop pest and disease control; grey = livestock pest and disease control

Source: National Service Delivery Service (NSDS), 2021.

**Figure 16: Share of agricultural extension officers reporting providing information on fodder or trees (sub-county level)**



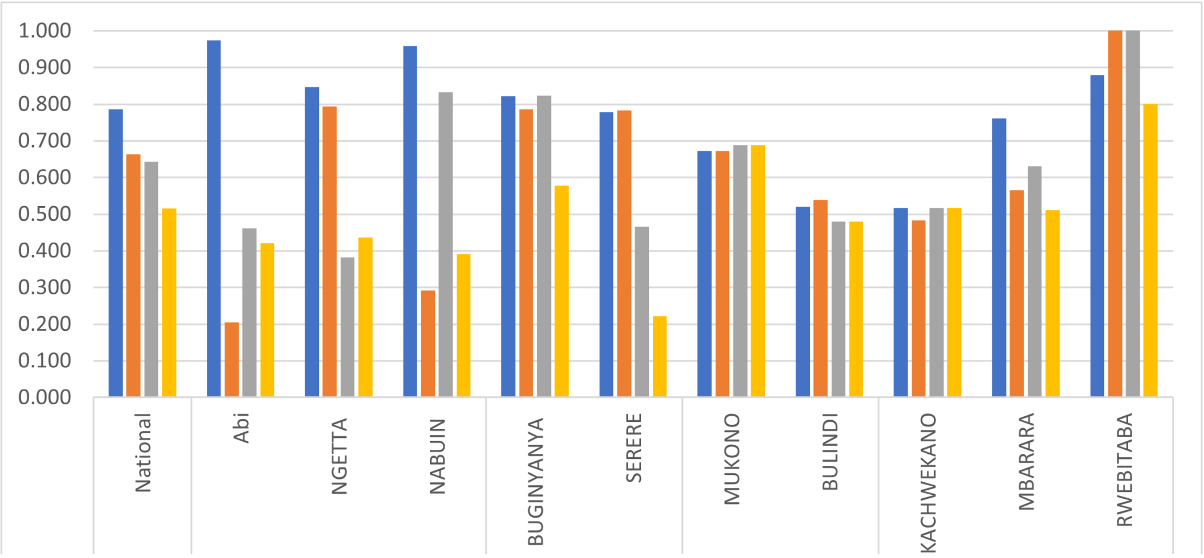
Note: Blue = fodder grasses; orange = fodder trees and shrubs; grey = fruit trees; yellow = fertilizer trees.

Source: National Service Delivery Service (NSDS), 2021.

The effectiveness of agricultural extension, apart from the coverage, also depends on the quality of the information provided. Extension officers having the right information about different innovations is therefore a useful step to check in the theory of change for achieving scale with innovations. With this objective, three knowledge questions related to important CGIAR innovations were integrated into the NSDS 2021 and asked of the extension officers. Specifically, the officers were asked to i) list which recommendations they give when there is a banana wilt outbreak; ii) list the nutritional benefits of OFSP when fed to young children, and iii) respond to which maize varieties have been bred for their drought tolerance.

Figure 17 shows that for management of BXW, extension officers more frequently mention removing the entire banana mat than cutting down a diseased stem. When there is low BXW incidence in a region, when a farmer observes BXW in their plot, the advice from Bioversity International research is to remove the entire mat. When there is high BXW incidence, a farmer is instead advised to follow SDSR, which combines the three other practices detailed in Figure 17 rather than lose the whole mat. This is in recognition that the disease will likely recur. For SDSR to be adopted correctly, all three practices must be adopted together. Recommending removing the male flowers appears to be the constraining practice within the package in terms of extension workers' knowledge.

**Figure 17: Recommendations about managing a Banana Xanthomonas Wilt (BXW) outbreak (sub-county level extension officers)**

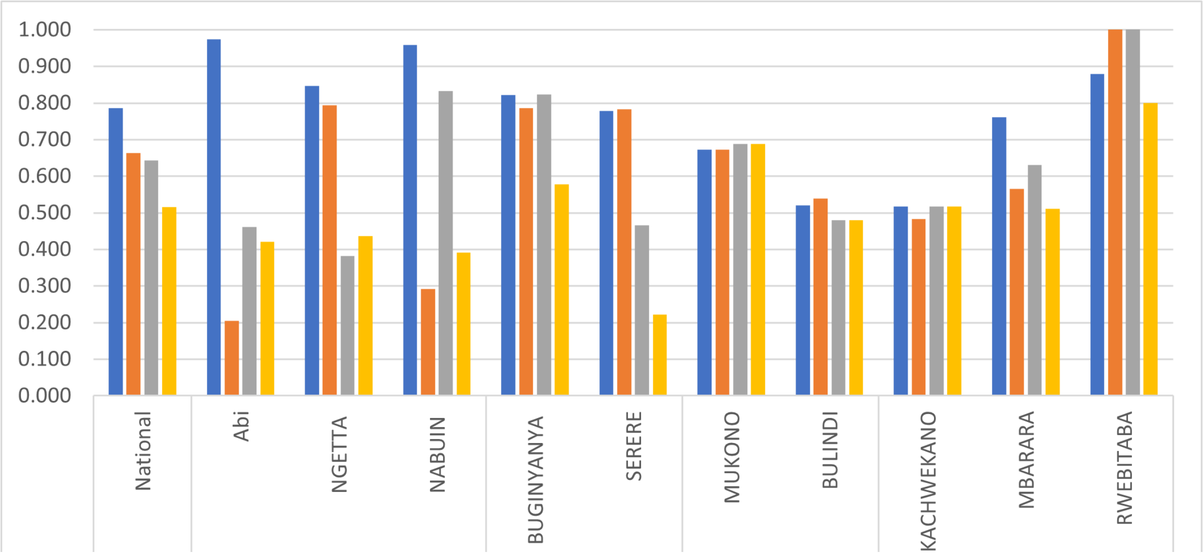


Note: Blue = remove all infected mats; orange = cut all diseased stems to soil level; grey = disinfect cutting tools; yellow = remove male buds after the last hands form.

Source: National Service Delivery Service (NSDS), 2021.

When asked about the nutritional and health benefits of consumption of OFSP, extension workers have much more knowledge about the impacts on Vitamin A deficiency than a potential positive impact on reducing diarrhea, or specifying that is particularly when fed to young children that a nutritional benefit from OFSP can be realized (Figure 18).

**Figure 18: Knowledge of the nutritional benefits of OFSP when fed to young children (sub-county extension officers)**

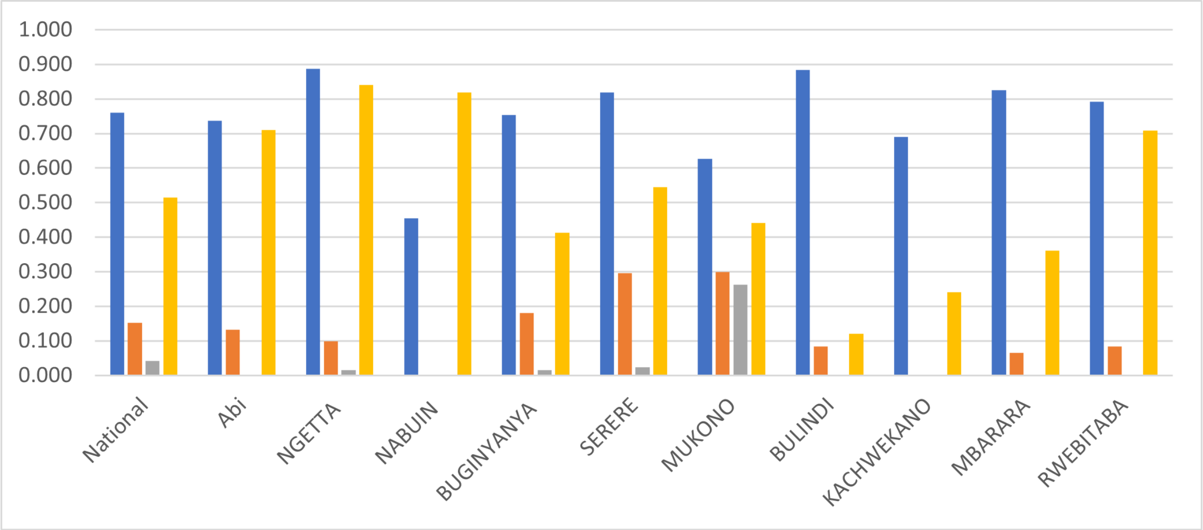


Note: Blue = OFSP reduces vitamin A deficiencies; orange = reduces diarrhea; grey = knows the former apply when fed to young children.

Source: National Service Delivery Service (NSDS), 2021.

Drought-tolerant maize varieties vary in terms of how well known they are by extension workers, with the LONGE series varieties much more likely to be recommended than other drought-tolerant maize varieties (Figure 19).

**Figure 19: Knowledge of drought-tolerant maize varieties (sub-county extension officers)**



Note: Blue = LONGE 9H/10H/11H; orange = UH5051/5052/5053; grey = VP Max; yellow = LONGE 5/5D

Source: National Service Delivery Service (NSDS), 2021.

### 7.1.2 Self-Reported Data vs DNA Fingerprinting

The following tables show the comparison between what the farmer thinks of as the type of variety when compared to the results of DNA fingerprinting. Data are at the level of individual variety samples, wherein the farmer is asked whether the variety is improved or traditional at the time the enumerator is collecting the tissue for DNA fingerprinting. Across the five crops for which we report these data , we find slightly different patterns, but all providing the same insight – that self-reported data from farmers about varietal type does not correspond to objective assessment from genotyping. This is consistent with a growing literature on varietal misclassification (Wossen et al, 2019; Euler et al, 2022; Stevenson et al, 2023).

In the case of maize (Table 51), farmers are as likely to report hybrid varieties as being traditional as they are improved. NARO-released open-pollinated varieties (OPVs) are more likely to be reported as traditional varieties than improved ones. For cassava, there is a stronger, albeit imperfect, relationship between genetic results and farmer self-reported data (Table 52). Beans (Table 53), sweetpotato (Table 54), and groundnut (Table 55) varieties are all much more likely to be reported as traditional, regardless of their genetic type.

**Table 51: Maize - comparison of farmer self-reported data (columns) for samples with DNA fingerprinting results (rows). Rows sum to 100%**

| | | Farmer self-reported data | | |
|---|---|---|---|---|
| | | Improved | Traditional | Don’t know |
| **DNA fingerprinting results** | Private sector hybrid | 48.4 | 48.4 | 3.2 |
| | NARO hybrid | 48.1 | 51.9 | 0.0 |
| | NARO OPV | 27.7 | 69.0 | 3.4 |
| | Unassigned | 42.3 | 51.9 | 5.8 |

**Table 52: Cassava - comparison of farmer self-reported data (columns) for samples with DNA fingerprinting results (rows). Rows sum to 100%**

| | | Farmer self-reported data | | |
|---|---|---|---|---|
| | | Improved | Traditional | Don’t know |
| **DNA fingerprinting results** | CGIAR-related varieties | 52.1 | 46.4 | 1.5 |
| | Known landraces | 19.7 | 77.5 | 2.8 |
| | Unassigned | 25.1 | 72.2 | 2.7 |

**Table 53: Beans - comparison of farmer self-reported data (columns) for samples with DNA fingerprinting results (rows). Rows sum to 100%**

| | | Farmer self-reported data | | |
|---|---|---|---|---|
| | | Improved | Traditional | Don’t know |
| **DNA fingerprinting results** | Released varieties | 26.0 | 72.7 | 1.3 |
| | Known landraces | 17.7 | 79.5 | 5.3 |
| | Unassigned | 25.7 | 71.9 | 2.4 |

**Table 54: Sweetpotato - comparison of farmer self-reported data (columns) for samples with DNA fingerprinting results (rows). Rows sum to 100%**

| | | Farmer self-reported data | | |
|---|---|---|---|---|
| | | Improved | Traditional | Don't know |
| **DNA fingerprinting results** | Released varieties | 34.4 | 60.7 | 4.9 |
| | Known landraces | 19.1 | 78.4 | 2.5 |
| | Unassigned | 14.9 | 82.9 | 2.2 |

**Table 55: Groundnut - comparison of farmer self-reported data (columns) for samples with DNA fingerprinting results (rows). Rows sum to 100%**

| | | Farmer self-reported data | | |
|---|---|---|---|---|
| | | Improved | Traditional | Don't know |
| **DNA fingerprinting results** | CGIAR variety | 31.4 | 65.1 | 3.5 |
| | Assigned non-CGIAR | 36.0 | 61.6 | 2.4 |
| | Unassigned | 22.8 | 77.2 | 0.0 |

### *7.1.3 Impact Evaluation of Long-Term Effects of Orange-Fleshed Sweetpotato Project on Child Health*

The lack of crucial micronutrients at early ages can have long-lasting consequences for health and cognition. The potential high returns to biofortification to address micronutrient deficiency motivated breeding efforts for vitamin A-enhanced sweetpotato (and separately for zinc- and iron-enhanced beans) in Uganda, and many other countries in Sub-Saharan Africa. Despite substantial investment in the last 10-20 years on this agenda, early recognition and experimental evidence of its potential, evidence on long-term large-scale outcomes is limited. To help address this gap, Macours, Mallia, and Okello (2025) combined data obtained from a targeted effort to reconstruct the 10-year national roll-out of biofortified vines through Harvest Plus and its partners at the sub-county level (see Appendix K), with primary data on child anthropometrics and morbidity, crop varietal identification through DNA fingerprinting and data on sweetpotato production and consumption to provide some of the first causal evidence of vitamin-A enhanced sweetpotato on children's longer term wellbeing. Complementary analysis with the UDHS allows them to further document the causal pathway.

To document the long-term impacts of childhood exposure to OFSP, Macours, Mallia, and Okello (2025) focus on height-for-age at later stages in childhood as a measure of long-term health (nutritional status). This is motivated by the fact that long-term height-for-age is largely determined by nutritional input between 0-5 years old. Results based on the national-level roll-out data of sweetpotato vine distribution show that sub-county level exposure to orange flesh sweetpotato during the earliest years of life leads to long-term gains in height-for-age scores (Table 56). With control for sub-county and age-fixed effects, impacts are identified by the year-to-year variation in the OFSP distribution within a sub-county, and by comparing children living in a sub-county where OFSP was distributed when they were 0-2 (or 0-5) years old, with children living in the same sub-counties in earlier or later years.

**Table 56: Impact of exposure to dissemination of OFSP in early years on height-for-age (HAZ) in 2023**

| | Exposure to OFSP when 0 – 2 years old | | Exposure to OFSP when 0 – 5 years old | | |
|---|---|---|---|---|---|
| | HAZ | HAZ | HAZ | HAZ | HAZ |
| Binary | 0.208**<br>(0.103) | 0.173*<br>(0.102) | 0.171*<br>(0.094) | 0.142<br>(0.095) | |
| Number of years | | | | | 0.197**<br>(0.078) |
| Numbers of years squared | | | | | -0.048***<br>(0.016) |
| Region and age fixed effects | Yes | Yes | Yes | Yes | Yes |
| Other baseline controls | No | Yes | No | Yes | Yes |
| Regions x two-year fixed effect | No | Yes | No | Yes | Yes |
| Number of observations | 1,733 | 1,733 | 2,014 | 2,014 | 2,014 |
| Adjusted $R^2$ | 0.039 | 0.039 | 0.058 | 0.060 | 0.060 |
| Mean | -0.538 | -0.538 | -0.606 | -0.606 | -0.606 |

Source: Macours, Mallia and Okello, 2025

Evidence along the causal chain helps interpret the main finding, as distribution of vines in a sub-county lead to larger presence of yellow and orange varieties in farmers' fields (validated with DNA fingerprinting), to higher consumption of vitamin-A rich foods (as measured through historical UDHS data), and to lower morbidity at the age of five years. Together, these results show that the health benefits of OFSP can be obtained at scale.

Sadly, despite the positive impacts from historical dissemination of OFSP vines and turning back to the UHIS data, we found that OFSP production was low (Table 38). This is further confirmed by self-reported information on OFSP consumption (Table 57). Together, these results suggest that by 2021/22 the potential returns were no longer being realized, pointing to the need to revisit the OFSP scaling model.

**Table 57: UHIS data from rural households on consumption of OFSP (UHIS 2021/22)**

| | Household level data – self-reports | |
|---|---|---|
| | N | Mean % |
| Household consumed OFSP in past 7 days | 4301 | 1% |
| Household with children aged 0 – 5 consumed OFSP in the past 7 days | 2678 | 1% |

### *7.1.4 Seed System Study Insights: Beans*

We used DNA fingerprinting information to analyze seed samples collected by inspectors from the Department of Crop Inspection and Certification (DCIC) along supply chains, focusing on germination rate, variety identification, genetic purity, and iron and zinc concentration levels in three biofortified bean varieties (NAROBEAN 1, 2, and 3). We collected a similar quantity of seed samples per variety at production, aggregation, and distribution stages, including from QDS sources.

Our results show that 29% of bean samples taken from grain markets – the most common channel through which farmers access seed – retained their purported varietal identity, as compared to 79% at Quality Declared Seed (QDS) outlets and 50% in agro-input stores. The low genetic purity suggested that variety mixing, or contamination, occurs at all supply chain stages. If the seed quality along the supply chain across three subsystems is genetically impure, and this impurity is passed on to the farmer, it would become increasingly difficult to genetically identify the variety the farmer believes they are growing after several cycles of recycling, without prior sorting. This underscores the importance of strengthening formal and QDS systems as better alternatives to the informal seed subsystem, which can not only support improving seed quality but may be important in supporting higher adoption of improved varieties with traits beneficial to farmers.

### *7.1.5 Seed System Study Insights: Maize*

In the maize seed system study, we also used DNA fingerprinting to analyze seed samples collected by the Department of Crop Inspection and Certification (DCIC) along the supply chains, focusing on germination rate, variety identification, genetic purity, moisture and inert matter content. The production stage was separated into seed companies' in-house fields and the fields of contracted outgrowers, aggregation and distribution. Basic seed and final commercial maize seed was collected in visits to seed company processing factories. A similar quantity of seed samples per variety was collected in each stage through DCIC inspections and, at the distribution by both DCIC inspections of agro-dealers and by sending mystery shoppers into the same locations at a later date.

Our results showed that compared to the seeds from in-house company fields, the seed purity is lower in all stages, especially during aggregation. Lower seed quality in mystery shopper samples also indicates a potential mechanism whereby agro-dealers may strategically provide seeds of different quality to inspectors in a formal audit setting versus those sold to farmers. If farmers perceive any of the issues outlined above, they may lack confidence in the quality of seeds available through formal channels and instead opt to recycle their own seeds or obtain seeds through informal exchanges with other farmers.

# 8. Discussion

We faced significant challenges in implementing the UNOMA sub-sample in the context of the first-ever UHIS round. These challenges were compounded by the residual effects of the COVID-19 pandemic during the data collection. In hindsight, the attempt to collect plant tissue samples for DNA fingerprinting for six crops in a single survey – unprecedented anywhere in the world, as far as we know – was possibly too ambitious. The result is a dataset that does indeed have DNA fingerprinting sub-samples, but not in the manner we designed. The sub-samples are not random sub-samples of the Ugandan population. While we have calibrated the sub-sample data to match observable features of the full sample, we cannot rule out residual selection into our sub-sample based on unobservable characteristics (i.e., features we do not have data about). For these reasons, we do not estimate upper and lower bounds for the reach of CGIAR in Uganda, in a similar way to the other countries we have implemented SPIA country studies (Ethiopia, Vietnam, Bangladesh).

However, we can learn a great deal about the nature of adoption of agricultural innovations even on this non-random sub-sample of households. Our data are very rich with regard to inter-cropped plots and varietal level adoption. Two distinct patterns emerge from this analysis, particularly when combined with complementary sources of data, as we do in the UHIS community surveys, seed systems study, the Diffusion and Impact of Improved Varieties in Africa (DIIVA) follow-up survey, and the National Service Delivery Survey (NSDS). The first is that the seed system for all crops is a significant constraint to farmers' ability to adopt CGIAR-related innovations. The second is that farmers adopt complex planting strategies, either intentionally or inadvertently, potentially in reaction to these seed systems issues, that result in a high degree of within-plot heterogeneity. While the share of households with at least one CGIAR-related variety on their plots is high in the case of maize or moderate in the case of groundnut, cassava and beans, wherever we collect samples in duplicates (maize, cassava, groundnut) or in bulked (beans, maize) we find evidence of substantial mixing of genetic material within plots.

Taken together, these two factors make it particularly difficult for CGIAR and NARO to achieve their objectives through plant breeding. The varieties may be excellent, but they will either not reach farmers in large numbers, or the varieties will reach them in a condition that makes it very challenging for farmers to perceive a benefit from cultivating them, as confirmed by the self-reported data on resilience traits of the improved varieties of these different crops.

### Table 58: Summary table of key results

| | % Households | % Communities* |
|---|---|---|
| **% CGIAR-related crop varieties among sampled households cultivating the crop** | | |
| Maize | 57.8 | 82.7 |
| Cassava | 35.1 | 53.9 |
| Banana | 0.4 | 1.2 |
| Beans | 26.5 | 48.9 |
| Sweetpotato | 6.9 | 17.7 |
| Groundnut | 37.1 | 28.8 |
| **% with innovation among rural households with large ruminants** | | |
| Practices controlled breeding strategy | 9.9 | 22.8 |
| Cross-bred cows | 16.3 | 31.6 |
| **% with NRM innovation among all rural households** | | |
| Banana-coffee intercropping** | 43.3 | 59.7 |
| Plants scattered tropical fruit trees | 13.5 | 56.4 |
| Cultivates improved fruit tree variety*** | 11.1 | 22.9 |

* Community where at least one household (HH) adopts

**Among households with banana or coffee

*** Among households with tropical fruit trees

# 9. Conclusion

This comprehensive report highlights both the opportunities and challenges of agricultural innovation adoption in Uganda. The findings show an innovation system that manages to reach a relatively large share of farmers, but with large variation between innovations and relatively large socio-economic and regional inequalities. While some of the results clearly point to the potential of innovations to contribute to improving resilience and addressing hidden hunger, they also clearly show that farmers may not be deriving all the intended benefits from the different innovations. This points to both challenges and opportunities around seed systems, extension, and other complementary investments that, when addressed, could contribute to augmenting and scaling the intended benefits from the AR4D investments. As environmental pressures continue to grow, such investments, together with renewed efforts in breeding, could potentially have large returns.

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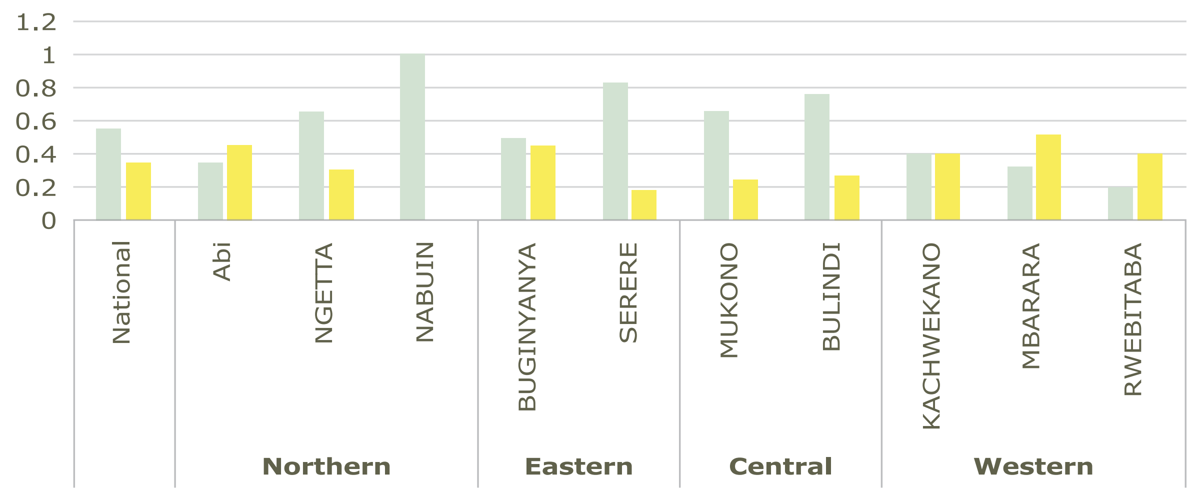
A market in Kitgum, near Gulu, Northern Uganda.
Credit: CIAT/Georgina Smith

# Appendices

## Appendix A. Subjective Perceptions of District Officers Regarding Environmental Quality in Their District Since 2000

**Figure 20: Subjective perceptions of district officers regarding environmental quality in their district since 2000**



Key: Light green = Worsened; Yellow = Improved.

Source: National Service Delivery Survey (NSDS) 2021

# Appendix B. Bioinformatic Analysis Used to Make Assignments Between Field Samples and Reference Samples

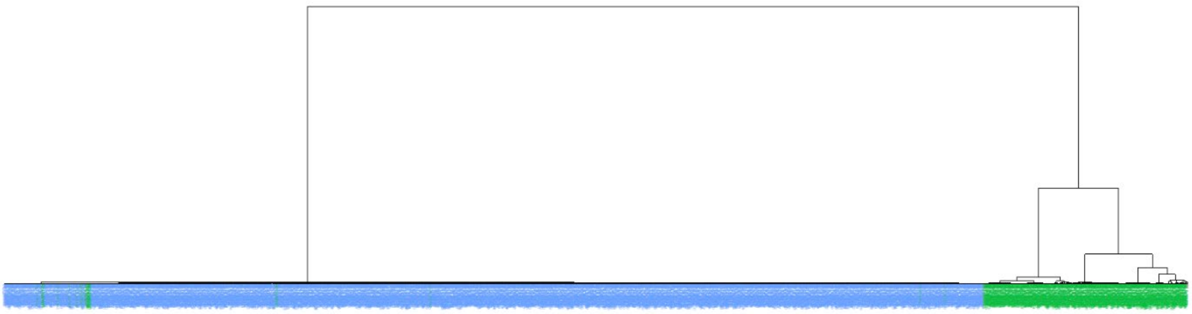
Using the genotyped data, field-collected samples were compared to the references to determine their varietal identities. Various assignment methods were used depending on the nature of the sample genotyped.

**Assignment by genetic distance: groundnut, banana, cassava, and sweetpotato**

For groundnut, banana, cassava, and sweetpotato, the assignment was done by calculating the genetic distance between the samples and the references. This method measures the degree of genetic divergence between individuals and works by comparing the similarity between samples and references at each locus. Genetic distance-based assignment was optimal for these crops because the samples were composed of single-leaf tissues. Additionally, groundnut is inbreeding while banana, cassava, and sweetpotato are clonally propagated, hence comparisons between samples and references could be made in a fairly straightforward way. Two distance methods were used, Identity by state (IBS) and Hamming distance. IBS entails determination of the likelihood that alleles at each locus are related. This is described in Choi et al., 2009 and implemented in the R package SNPRelate (Zheng et al., 2012). On the other hand, Hamming distance calculates the number of base differences between sequences of the sample and the reference as implemented in the R package dartR (Gruber et al., 2018; Mijangos et al., 2022).

IBS and Hamming distance matrices were created, showing the genetic distance between each sample and every reference. Samples were assigned to a reference by setting the threshold of similarity to a reference at the canonical genetic distance of ≤ 0.05 (Josia et al., 2021; Semagn et al., 2021) and confirmed or slightly adjusted based on the observation of the distribution of genetic distances for each crop. In some instances, a sample was assigned to multiple references. This was indicative of low distinctiveness between some references. To resolve this, the percentage similarity of loci between the samples and references was calculated. Assignment was established for references that had the highest percentage similarity of loci and lowest genetic distance within the defined threshold. The final tally of assigned samples was derived based on mutual assignment by both IBS and Hamming distance, as well as assignment by either one of the methods only. In the case of banana, a majority of the samples (>80%) had genetic distance to best reference below 0.01. Further analysis indicated that most of these samples were assigned to one variety (Matooke landrace) and had low heterozygosity values. The samples with higher genetic distances were observed to have higher heterozygosity values indicating higher heterogeneity and clustered separately when visualized on a dendrogram (Figure 21). The optimal genetic distance threshold of assignment for the latter group of samples was set at 0.07.

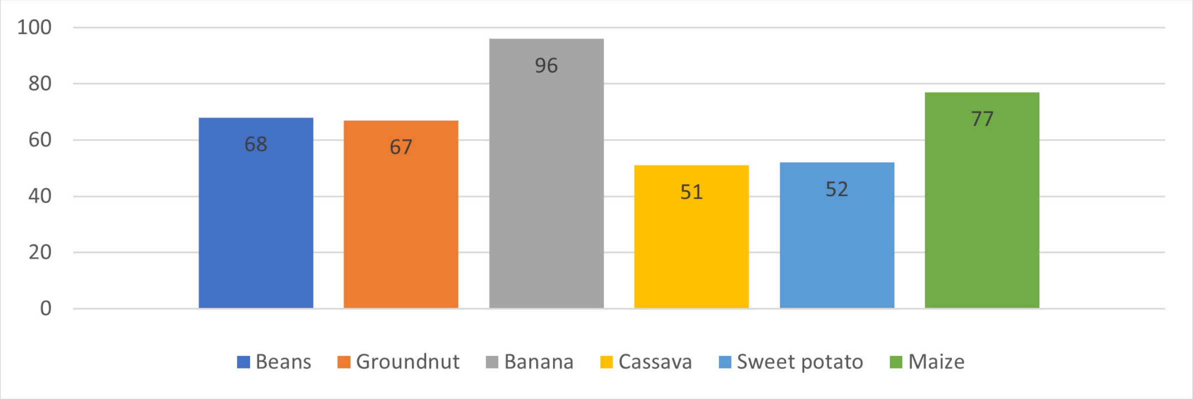
**Figure 21: Dendrogram showing clustering of banana field samples**



Note: The cluster on the left (blue) consists of samples with average heterozygosity of 0, that assign to one variety at low genetic distance (< 0.01). The right cluster (green) has samples with higher average heterozygosity (0.2) matching to a broader number of references.

The total number of samples assigned to a reference for groundnut was 238, translating to an assignment rate of 67%. For banana, cassava, and sweetpotato, the number of samples successfully assigned to a reference were 2,899, 989, and 675 respectively, translating to assignment rates of 96%, 51% and 52% respectively (Figure 22).

**Figure 22: Rates of assignment for each of the six crops**



While IBS and Hamming distance results were comparable, due to differences in algorithms of the two methods, a few cases of samples meeting the threshold for assignment for only one of the methods occurred. Generally, the best matches for either method were the same, but in instances where differences were observed, the reference from the method with the lower genetic distance was selected

Heterozygosity refers to the presence of two different marker alleles at a locus. When low, it indicates uniformity of the genome as can be observed in highly inbred crops. When high, it indicates heterogeneity of the genome as observed in outcrossing crops. Observation of high heterozygosity in inbred varieties can be a good indication of sample mixing.

### Assignment by Purity: Maize

Maize samples comprised of bulked seed, which in combination with the outcrossing nature of the crop resulted in a more complex sample set. Hence, the purity pipeline (DArT, personal communication) was used for assignment of the samples to references. The analysis entailed comparing the allele counts of field samples with allele counts of each reference. The proportion of alleles present in the field samples that were absent from the reference were regarded as impurities. The purity score was determined by taking the difference between one and the proportion of impurity. Rather than imposing a strict purity cutoff to determine assignment, the optimal threshold of assignment was estimated by considering the range of the purity scores that formed a continuous distribution, departure from which could be assumed to imply a significant jump of purity from the expected. The optimal purity score was set to 0.95 resulting in assignment of 547 samples, translating to an assignment rate of 77% (Figure 22)

### Assignment by DAP: Bean

While bean is a self-pollinated low diversity crop, the sampling strategy involved bulking of multiple leaf tissues from different plants, resulting in a more complex sample set. This was evident by the uncharacteristically high heterozygosity scores observed for the samples. Consequently, the DArT assignment probability (DAP) pipeline (DArT, personal communication) was employed for assignment analysis. Allele count data for both references and field samples were used to calculate allele frequencies for each individual at each locus. The allele frequencies were used to create a simulation of an expected population of genotypes that represented an individual. Based on principal component analysis, a 3-dimensional ellipsoid that captured all the simulated individuals was produced and its centroid was the representative individual for each sample. Following the transformation of the references and field samples to a PCA-defined 3-dimensional space as described above, a comparison of distance between a sample and each reference was done, resulting in DAP scores that showed the relationship of each sample to every reference.

The heterogeneity of the samples coupled with information from breeders and knowledge of the bean seed system implied that multiple varieties were being grown in most fields. This necessitated further analysis to best represent the assignments from these fields. In anticipation of this challenge the compiling of references material for bean was done exhaustively to comprehensively account for varieties present in Uganda. Thus, the reference set contained 44 released varieties and 436 landraces, with multiple similar lines present, particularly among the landraces.

To reduce the redundancy in the reference set, an IBS distance matrix was calculated from which closely related lines (IBS ≤ 0.05) were identified. For these, a representative reference was selected and the rest were removed from the reference set. The final set of non-redundant references had 221 lines. Assignment analysis proceeded as follows. For each sample, the distribution of DAP scores of each representative reference was observed. These ranged from 0, indicating no relationship to 1, indicating perfect identity. Empirical analysis showed a tendency for the scores tapering off at around 0.8 DAP. Thus, samples that did not have any references with DAP ≥ 0.8 were considered to be unassigned. For the rest of the samples, if the difference between the maximum and second maximum DAP score was larger than 0.05, the sample was classified as uniform, meaning that the field had one predominant variety. The rest of the samples were considered to be mixed, meaning that more than one variety was present in the fields. The samples were further classified based on whether they were released or landrace varieties, resulting in a total of five categories of samples as follows; uniform released (19), uniform landrace (154), mixed released (150), mixed landrace (158) and unassigned (228). The mixed released samples described fields that had multiple varieties, at least one of which was a release, while mixed landrace samples described fields with multiple varieties, all of which were landraces. This analysis resulted in an overall assignment rate of 68% (Figure 22).

# Appendix C. Visual Aids for Crop Pests and Diseases

Uganda Bureau of Statistics developed and incorporated a visual aid for assisting with identification of pests and diseases in the UHIS post-planting visit for 2021/22. An example page – for cassava pests – is shown below. The full resource is available as an online appendix on the SPIA website.

**Common Cassava Pests**

# Appendix D. Details of On-Station Work by NARO to Construct Maize Varietal References

Edited excerpt from a report to SPIA by Allan Waniale and Godfrey Asea (NARO)

### Introduction

Maize varieties on the Ugandan market falls two broad categories; open pollinated varieties (OPVs) and hybrids. The OPVs are composed of genetically diverse individual plants (heterogeneous) inter-crossed to maintain vigour. Maize hybrid varieties in Uganda are either varietal crosses or three way hybrids (3WHs). To create varietal hybrids, two OPVs are crossed with each other, whereas for 3WHs, three inbred lines are crossed in two steps (growing seasons) to come up with a finished hybrid. OPVs are composed of genetically diverse individuals so the total amount of genetic variability may be captured through a bulked sample of approximately 300 seeds; the higher the number, the better the representation. The same principle applies to the creation of varietal hybrids. Inbred lines are composed of genetically identical individual (homogeneous and homozygous). This implies that, in theory, a single seed can be used to represent the line, thus just a few seeds were used in the nurseries and for sample processing. To maintain genetic purity of the varieties, a recommended minimum isolation distance of 400m must be followed for breeder's seed samples.

### OPV reference samples

The OPV reference samples were obtained from NARO's breeders' seed for the highest level of genetic purity. These varieties have to be produced in isolation. For this project, seed volume was increased through chain sibbing, meaning that during pollination, pollen from one plant is tapped (harvested) and used to pollinate the next plant in a row. The tassel is then broken as that particular plant's pollen is represented. This is repeated until a representative number of plants are achieved.

### Hybrid reference samples

1. Varietal hybrids: Female and male rows are in a ratio of 3 female rows to 1 male row. At booting, female rows are de-tasselled before they start shedding pollen. For this project, 20 rows of 4 m were planted for both the female and male parent in the pollination nurseries. With each row having 17 plants, a total of 340 seeds were planted for each varietal parental. All plants were shoot capped (covering of ears before silking) and pollination was performed by tapping and carrying pollen from male parental plant and crossing with the female plants. Tassels whose pollen was used for a single pollination were broken as they had been represented (in a similar manner to chain sibbing).
2. Three-way hybrids: crossing is done in two steps or growing seasons. In the first step, two inbred lines (usually denoted as A and B) are crossed to obtain a single cross (also denoted as SX or AB). The representation of the two inbred lines in the SX is equal, which is 50% each. The SX the then planted as a female parent and crossed with the third inbred line, denoted as the C line. The percentage representation of the inbred lines is therefore 25% for A and B, while C contributes 50% in the final finished hybrid. It is this finished hybrid sample that serves as the reference material.

### Grinding and plating samples

A heavy-duty blender was used to grind maize samples into fine flour before plating. To avoid cross contamination of samples during grinding, the machines were first cleaned with a small paint brush before washing with 95% ethanol at 95% purity. This ensured that all DNA in the hard-to-reach parts of the machine was destroyed. Serviettes were used to wipe the machine dry before loading the next reference sample. Ethanol was also used to clean hands, surfaces, and all equipment used during grinding and plating of samples. A sample of the ground reference material was put in 50ml falcon tubes for taking a sub-sample into the eppendorf tubes for DNA extraction and analysis as well as for backup. The 50ml falcon tubes were kept in freezers at 0˚C. Grinding and plating was done following the guidelines provided by Diversity Arrays.

A total of 24 of the expected 37 NARO released hybrids have been recreated and are ready for grinding and plating. Since some of the hybrids are not actively sold on the market, some of the parental lines were not maintained in Uganda. Wherever possible, the missing parental lines were sourced from CIMMYT. To shorten the duration of the plants needing to be grown in the field, green ears could be harvested at 20 days after pollination, and then carefully dried before grinding.

For the seed company released hybrids, especially for the national companies, full hybrids and their parental lines were sourced from their officers. Hybrids of multi-national seed companies were procured from their agents whenever available, though it is not possible to avail of parental lines owing to their desire to protect their intellectual property.

In total, we have 50 reference varieties in the library: 4 OPVs (LONGE 4, LONGE 5, LONGE 5D, MM3) with the remainder being varietal or 3-way hybrids.

# Appendix E. Maize Varietal Reference Library

Light green bands indicate varieties with adoption > 0 in our sample.

### Table 59: Maize varietal reference library

| Variety name/code | Year of release | Source of parents | Days to maturity | OPV or Hybrid | Drought tolerant | CGIAR-related |
|---|---|---|---|---|---|---|
| Longe 4 (LP 16) | 2000 | NARO | 100 - 105 | OPV | 1 | |
| Longe 5 (Obatampa POP 63 QPM) | 2000 | NARO/IITA | 115 | OPV | 1 | 1 |
| PAN 15 | 2002 | PANNAR / CIMMYT | 120 | Hybrid | | 1 |
| Longe 6 H | 2002 | CIMMYT | 125 | Hybrid | | 1 |
| Longe 7 H | 2002 | CIMMYT | 125 | Hybrid | 1 | 1 |
| Longe 8 H | 2002 | CIMMYT | 125 | Hybrid | | 1 |
| H 614 | 2005 | KSCO | 200 - 210 | Hybrid | | |
| PHB 30 G 19 (PHB 3019) | 2007 | PIONEER | 125 | Hybrid | | |
| LONGE 9 H | 2009 | NARO/CIMMYT | 120 | Hybrid | | 1 |
| LONGE 10 H | 2009 | NARO/CIMMYT | 120 | Hybrid | 1 | 1 |
| LONGE 11 H | 2009 | NARO/CIMMYT | 120 | Hybrid | | 1 |
| Myezi Mitatu (MM3) | 2010 | NARO | 75 - 85 | OPV | 1 | |
| Longe 5 D | 2012 | NARO | 115 | OPV | 1 | 1 |
| UH 5051 (ECAVL1/ECAVL 18 | 2012 | CIMMYT | | Hybrid | 1 | 1 |
| UH 5052 (ECAVL 2/ECAVL 19) | 2012 | CIMMYT | | Hybrid | 1 | 1 |
| UH 5053 (ECAVL2 / ECAVIL18) | 2012 | CIMMYT | | Hybrid | 1 | 1 |
| FH 6150 | 2012 | UYOLE/CIMMYT | | Hybrid | | 1 |
| VP max (VP5120) / DT Max | 2012 | CIMMYT | | Hybrid | 1 | 1 |
| KH 500 – 43 A | 2012 | KARLO | | Hybrid | | |
| WE 2114 | 2013 | CIMMYT | | Hybrid | | 1 |
| WE 2115 | 2013 | CIMMYT | | Hybrid | | 1 |
| UH5354 / Bazooka / CKH 10769 | 2013 | CIMMYT | | Hybrid | 1 | 1 |
| UH5355 | 2013 | CIMMYT | | Hybrid | | 1 |
| WE 2101 | 2014 | CIMMYT | 120 | Hybrid | | 1 |
| WE 2103 | 2014 | CIMMYT | 120 | Hybrid | | 1 |
| WE 2104 | 2014 | CIMMYT | 120 | Hybrid | | 1 |
| UH5301 | 2014 | NARO / CIMMYT | | Hybrid | | 1 |

| Variety name/code | Year of release | Source of parents | Days to maturity | OPV or Hybrid | Drought tolerant | CGIAR-related |
|---|---|---|---|---|---|---|
| CKH 10773 / UH 5356 / Super Maize | 2015 | NARO/CIMMYT | | Hybrid | | 1 |
| NAROMAIZE 57 / CKH 0616 / UH 5557 | 2015 | CIMMYT | | Hybrid | | 1 |
| SC 719 | 2015 | SEED CO | | Hybrid | | |
| WE3103 | 2016 | CIMMYT | | Hybrid | | 1 |
| WE3106 | 2016 | CIMMYT | | Hybrid | | 1 |
| WE3109 | 2016 | CIMMYT | | Hybrid | | 1 |
| PAN7M-81 | 2016 | PANNAR | | Hybrid | | |
| VITAMU50 (Ex0629) | 2016 | NASECO/IITA | | Hybrid | | 1 |
| WE 5117 | 2019 | CIMMYT | | Hybrid | | 1 |
| WE 6103 / Champion | 2019 | CIMMYT | | Hybrid | 1 | 1 |
| ADV2309 | 2019 | CIMMYT | | Hybrid | | 1 |
| ADV2310 | 2019 | CIMMYT | | Hybrid | | 1 |
| SC403 (COMESA) | 2019 | SEED CO | | Hybrid | | |
| DK90-89 | 2012 (Kenya) | | 105 - 135 | Hybrid | | |
| WH301 | 2008 (Kenya) | | 90 - 120 | Hybrid | | |
| NARO Maize-62 | 2023 | | | Hybrid | | |
| NARO Maize-61 | 2023 | | | Hybrid | | |
| Wanak 624 | | | | Hybrid | | |
| H520 | 2019 (Kenya) | | 120-130 | Hybrid | | |
| H624 | 2004 (Kenya) | | 150 - 180 | Hybrid | | |
| SC303 | 2017 (Zimbabwe) | | Less than 100 | Hybrid | | |
| SC555 | 2022 (Kenya) | | 130 - 137 | Hybrid | 1 | |
| SC419 | 2017 (Kenya) | | 120 - 130 | Hybrid | 1 | |

# Appendix F. Banana Varietal Reference Library

Light green bands indicate varieties with adoption > 0 in our sample. The majority of field samples are matooke landraces, represented by the reference “Ekitawira”. Analysis of the reference library reveals these to be genetically identical, despite phenotypic variation, forming a single genetic cluster.

### Table 60: Banana varietal reference library

| Variety name/code | Year of release | Type | CGIAR-related |
|---|---|---|---|
| Embidde | N/A | Mbidde landrace | |
| Gonja Kakira | N/A | Plantain | |
| Muraru red bell (Thika) | N/A | Mchare/Muraru landrace | |
| Muraru green bell | N/A | Mchare/Muraru landrace | |
| Makyughu | N/A | Mchare/Muraru landrace | |
| Muraru Mshare | N/A | Mchare/Muraru landrace | |
| Muraru Mlalu | N/A | Mchare/Muraru landrace | |
| Huti red bud | N/A | Mchare/Muraru landrace | |
| Ndyali | N/A | Mchare/Muraru landrace | |
| Paka | N/A | TBD | |
| Makyugyu | N/A | Mchare/Muraru landrace | |
| Prata | N/A | Pome | |
| Kivuvu | N/A | Bluggoe | |
| Chinese Cavendish | N/A | Cavendish | |
| Dwarf cavendish | N/A | Cavendish | |
| Red Dacca | N/A | Red | |
| Atwarira | N/A | Matooke landrace | |
| Butobe | N/A | Matooke landrace | |
| Bwara | N/A | Matooke landrace | |
| Ekigamba | N/A | Matooke landrace | |
| Ekitawira | N/A | Matooke landrace | |
| Engote | N/A | Matooke landrace | |
| Engumba | N/A | Matooke landrace | |
| Enkongo | N/A | Matooke landrace | |
| Entazinduka | N/A | Matooke landrace | |
| Entudde | N/A | Matooke landrace | |
| Entundu | N/A | Matooke landrace | |
| Enyabakazi | N/A | Matooke landrace | |
| Enzirabushera | N/A | Matooke landrace | |
| Kaitabunyonyi | N/A | Matooke landrace | |
| Kisansa | N/A | Matooke landrace | |
| Lwadungu | N/A | Matooke landrace | |
| Lwamugongo | N/A | Matooke landrace | |
| Maganya | N/A | Matooke landrace | |
| Makara | N/A | Matooke landrace | |
| Mbirabire | N/A | Matooke landrace | |
| Mukazi aranda | N/A | Matooke landrace | |

| Variety name/code | Year of release | Type | CGIAR-related |
|---|---|---|---|
| Mukazi mugumba | N/A | Matooke landrace | |
| Mukubankonde | N/A | Matooke landrace | |
| Musakala | N/A | Matooke landrace | |
| Muvubo | N/A | Matooke landrace | |
| Nandigobe | N/A | Matooke landrace | |
| Nakanyara | N/A | Matooke landrace | |
| Nakibuule | N/A | Matooke landrace | |
| Nakinyika | N/A | Matooke landrace | |
| Nalhaki | N/A | Matooke landrace | |
| Nalukira | N/A | Matooke landrace | |
| Namaliga | N/A | Matooke landrace | |
| Ndibwabalangira | N/A | Matooke landrace | |
| Ngono | N/A | Matooke landrace | |
| Nsika | N/A | Matooke landrace | |
| Nyamabere | N/A | Matooke landrace | |
| Nyamwihogora | N/A | Matooke landrace | |
| Sira | N/A | Matooke landrace | |
| FHIA 17 | 2000 | Honduran hybrid | 0 |
| FHIA 25 | | Honduran hybrid | |
| FHIA 23 | 2000 | Honduran hybrid | 0 |
| FHIA 21 | | Honduran hybrid | |
| FHIA 1 | 1999 | Honduran hybrid | 0 |
| FHIA 2 | | Honduran hybrid | |
| FHIA 3 | 1999 | Honduran hybrid | 0 |
| Mbwazirume | N/A | Matooke landrace | |
| Kibuzi | N/A | Matooke landrace | |
| Sukali Ndizi | N/A | Kamaramasenge | |
| FHIA 18 | N/A | Honduran hybrid | |
| Huti Shumba nyeru | N/A | Mchare/Muraru landrace | |
| Huti RB | N/A | Mchare/Muraru landrace | |
| Mshale | N/A | Mchare/Muraru landrace | |
| Kahuti | N/A | Mchare/Muraru landrace | |
| Makyugu I | N/A | Mchare/Muraru landrace | |
| Morongo Princesa | N/A | TBD | |
| Mlelembo | N/A | Mchare/Muraru landrace | |
| Robusta | N/A | Cavendish | |
| Lacatan | N/A | Cavendish | |
| Ilalyi red | N/A | Mchare/Muraru landrace | |
| Ntindi II | N/A | TBD | |
| Nshonowa | N/A | Mchare/Muraru landrace | |
| Bluggoe | N/A | Bluggoe | |
| Silver Bluggoe | N/A | Bluggoe | |
| Pelipita | N/A | Pelipita | |
| Tani | N/A | Balbisiana | |
| Pisang Awak | N/A | Pisang Awak | |
| Kisubi | N/A | Ney Poovan | |

| Variety name/code | Year of release | Type | CGIAR-related |
|---|---|---|---|
| Cultivar Rose | N/A | Sucrier | |
| Pisang lilin | N/A | M. a. ssp. malacensis derivative | |
| Tuu gia | N/A | TBD | |
| Galeo | N/A | TBD | |
| Kokopo | N/A | M. a. ssp. banksii derivative | |
| Pisang Jari Buaya | N/A | Pisang Jari Buaya | |
| Kitarasa | N/A | TBD | |
| Ibwi | N/A | Mutika/Lujugira | |
| Haa haa | N/A | TBD | |
| Pisang ceylan | N/A | Mysore | |
| Saba | N/A | Saba | |
| NAROBAN 1 | 2017 | Released improved Matooke variety | 1 |
| NAROBAN 2 | 2017 | Released improved Matooke variety | 1 |
| NAROBAN 3 | 2017 | Released improved Matooke variety | 1 |
| NAROBAN 4 | 2017 | Released improved Matooke variety | 1 |
| NAROBAN 5 | 2019 | Released improved Matooke variety | 1 |
| KABANA 7H | 2013 | Released improved Matooke variety | 1 |
| Mpologoma | N/A | Matooke landrace | |
| Bogoya_Gros Michel | N/A | Gros Michel | |
| Kayinja | N/A | Pisang Awak | |
| Williams | N/A | Cavendish | |
| Muraru | N/A | Mchare/Muraru landrace | |
| Kamunyila | N/A | Mchare/Muraru landrace | |
| KABANA 6H_NARITA7 | 2010 | Released improved Matooke variety | 1 |
| NARITA 4 | Under on-farm (final) evaluation | Released improved Matooke variety | 1 |
| NARITA 17 | Under on-farm (final) evaluation | Released improved Matooke variety | 1 |
| NARITA 18 | Under on-farm (final) evaluation | Released improved Matooke variety | 1 |
| NARITA 22 | Under on-farm (final) evaluation | Released improved Matooke variety | 1 |
| NARITA 24 | Under on-farm (final) evaluation | Released improved Matooke variety | 1 |
| Nakawere | N/A | Matooke landrace | |
| Bitambi | N/A | Matooke landrace | |
| Namande | N/A | Matooke landrace | |
| Rwambarara | N/A | Matooke landrace | |
| Nakyetengu | N/A | Matooke landrace | |
| Nakabululu | N/A | Matooke landrace | |
| Nakitembe | N/A | Matooke landrace | |
| Gonja Nakatansesa | N/A | Plantain | |

| Variety name/code | Year of release | Type | CGIAR-related |
|---|---|---|---|
| Gonja Manjaya | N/A | Plantain | |
| Enyeru | N/A | Matooke landrace | |
| Entukura | N/A | Matooke landrace | |
| Nakayonga | N/A | Matooke landrace | |
| Nfuuka | N/A | Matooke landrace | |
| Tereza | N/A | Matooke landrace | |
| Kabucuragye | N/A | Matooke landrace | |
| Namwezi | N/A | Matooke landrace | |
| Enzirabahima | N/A | Matooke landrace | |
| Nakasabira | N/A | Matooke landrace | |
| Kazirakwe | N/A | Matooke landrace | |
| Valery | N/A | Cavendish | |
| Yangambi KM5 | 2000 | Ibota | 0 |
| Grande Naine | N/A | Cavendish | |
| Petite Naine | N/A | Cavendish | |
| Nante | N/A | Matooke landrace | |
| Etazinduka | N/A | Matooke landrace | |

# Appendix G. Cassava Varietal Reference Library

Light green bands indicate varieties with adoption > 0 in our sample.

### Table 61: Cassava varietal reference library

| Variety name/code | Year of release | CGIAR-related | Type |
|---|---|---|---|
| Bukalasa II | 1970 | 0 | Selected landrace |
| BAO | 1970 | 0 | Selected landrace, introduced from Tanzania (Manze et al, 2021) |
| NASE I (TMS 60142) | 1994 | 1 | Introduced from IITA as TMS 60142 (Manze et al, 2021) |
| NASE 2 (TMS 30337) | 1994 | 1 | Introduced from IITA as TMS 30337 (Manze et al, 2021) |
| NASE 3 (TMS 30572) | 1994 | 1 | 58308 x Branca de Santa Catarina; introduction from IITA (Manze et al, 2021) |
| NASE 4 (SS4) | 1999 | 1 | Introduction from IITA (Manze et al, 2021) |
| NASE 5 (SS5) | 1999 | 1 | Introduction from IITA (Manze et al, 2021) |
| NASE 6 (TMS 4(2)1425) | 1999 | 1 | Introduced from IITA as TMS 4 (2) 1425 (Manze et al, 2021) |
| NASE 8 (CE 98) | 1999 | 1 | Unclear but NARO confirm CGIAR-related |
| NASE 9 (TMS 30555-17) | 1999 | 1 | Introduced from IITA as 30555-17 (Manze et al, 2021) |
| NASE 11 (29/NA 2TC 1) | 2000 | 1 | Introduced from IITA as 92/NA-2 (Manze et al, 2021) |
| NASE 12 (MH95/0414) | 2000 | 1 | Unclear but NARO confirm CGIAR-related |
| NASE 13 | 2011 | 1 | Unclear but NARO confirm CGIAR-related |
| NASE 14 | 2011 | 1 | 192/0248 half sib; from IITA (Kawuki et al, 2017) |
| NASE 16 | 2011 | 1 | Bred from polycross mating scheme comprising five elite, CMD resistant lines from IITA (TME 5, TME 14, NASE 12, NASE 10, SE95/00036) and four local (Kakwale, Bao, Nyaraboke, Bamunanika) varieties (Kawuki et al, 2017) |
| NASE 19 (TZ /130) | 2015 | 1 | Bred from polycross mating scheme comprising five elite, CMD resistant lines from IITA (TME 5, TME 14, NASE 12, NASE 10, SE95/00036) and four local (Kakwale, Bao, Nyaraboke, Bamunanika) varieties (Kawuki et al, 2017) |
| NAROCASS 1 (MM 06/130 /NASE 20) | 2015 | 1 | Up to 5,000 open pollinated seeds were introduced from Tanzania. These seeds were derived from a polycross that had parental lines considered to be tolerant to CBSD. All this activity was undertaken in Tanzania by Dr. Edward Kanju. In April 2005, these seeds were established in a seed nursery for germination at Namulonge (Kawuki et al, 2015) |

| Variety name/code | Year of release | CGIAR-related | Type |
|---|---|---|---|
| NAROCass 2 | 2015 | 1 | Up to 5,000 open pollinated seeds were introduced from Tanzania. These seeds were derived from a polycross that had parental lines considered to be tolerant to CBSD. All this activity was undertaken in Tanzania by Dr. Edward Kanju. In April 2005, these seeds were established in a seed nursery for germination at Namulonge (Kawuki et al, 2015) |
| UG120024 | N/A | 0 | Elite clone - NARO |
| UG120183 | N/A | 0 | Elite clone - NARO |
| UG120156 / NAROCASS4 | N/A | 1 | Elite clone – NARO |
| UG120193 / NAROCASS 5 | N/A | 1 | Candidate line – NARO |
| UG110164 | N/A | 0 | NARO |
| MKUMBA / NAROCASS3 | N/A | 1 | Candidate clone – NARO |
| BALI | N/A | 0 | Landrace |
| TMEB14 | N/A | 1 | Elite clone - IITA |
| IITA-TMS-MM960608 | N/A | 1 | Elite clone - IITA |
| IITA-TMS-IBA120067 | N/A | 1 | Elite clone - IITA |
| UG110052 | N/A | 0 | Landrace |
| UG110309 | N/A | 0 | Landrace |
| UG110114 | N/A | 0 | Landrace |
| UG110304 | N/A | 0 | Landrace |
| KWATAMUMPALE / UG110304 | N/A | 0 | Landrace |
| EDYAL | N/A | 0 | Landrace |
| KABWA | N/A | 0 | Landrace |
| UG110310 | N/A | 0 | Landrace |
| KITENGA | N/A | 0 | Landrace |
| MAGANA | N/A | 0 | Landrace |
| UG110306 | N/A | 0 | Landrace |
| MUWOGO-MUMYUFU | N/A | 0 | Landrace |
| MASAKA_LOCAL-2 | N/A | 0 | Landrace |
| NYARABOKE | N/A | 0 | Landrace |
| MUREFU | N/A | 0 | Landrace |
| MACHUNDE | N/A | 0 | Landrace |
| LYAHOLORE | N/A | 0 | Landrace |
| OFUMBA-CHAI | N/A | 0 | Landrace |
| MERCURY | N/A | 0 | Landrace |
| NJULE-WHITE | N/A | 0 | Landrace |
| MASAKA_LOCAL-1 | N/A | 0 | Landrace |

# Appendix H. Common Bean Varietal Reference Library

Light green bands indicate varieties with adoption > 0 in our sample. The bean reference library has a total of 467 accessions in it. Listed below are the 36 released varieties in the library. The remaining accessions are landrace reference samples obtained from the Uganda National Gene Bank and the CIAT Kawanda collection.

### Table 62: Common bean varietal reference library

| Variety name/code | Year of release | CGIAR-related | Biofortified |
|---|---|---|---|
| K20 | 1970 | | 0 |
| K131 (MCM 5001) | 1994 | 1 | 0 |
| K132 (CAL 96) | 1994 | 1 | 0 |
| NABE 1 (OBA 1) | 1995 | 1 | 0 |
| NABE 2 (MCM1015) | 1995 | 1 | 0 |
| NABE 3 (MCM 2001) | 1995 | 1 | 0 |
| NABE 4 (POA 2) | 1999 | 1 | 0 |
| NABE 5 (SUGAR 73) | 1999 | 1 | 0 |
| NABE 6 (UBR92) 25ML | 1999 | 1 | 0 |
| NABE 7C (Vuninkingi) | 1999 | | 0 |
| NABE 8C (Ngwinurare) | 1999 | | 0 |
| NABE 9C (Gisenyi) | 1999 | | 0 |
| NABE 10 C Umubano | 1999 | 1 | 0 |
| NABE 11 (AFR 721) | 2003 | 1 | 0 |
| NABE 12 C (MAC 31) | 2003 | 1 | 0 |
| NABE 13 (RWR 1946) | 2006 | 1 | 0 |
| NABE 14 (RWR 2075) | 2006 | 1 | 0 |
| NABE 15 (NARBL-144) | 2010 | 1 | 0 |
| NABE 16 (NARBL 233-2) | 2010 | 1 | 0 |
| NABE 17 (NARBL 220) | 2012 | 1 | 0 |
| NABE 18 (NARBL 110 -1) | 2012 | 1 | 0 |
| NABE 19 (NARBL 50 – 1) | 2012 | 1 | 0 |
| NABE 20 (NARBL 50 – 3) | 2012 | 1 | 0 |
| NABE 21 (NARBL 53 – 3) | 2012 | 1 | 0 |
| NABE 22 (NARBL 40 – 3) | 2012 | 1 | 0 |
| NABE 23 (NARBL 252) | 2012 | 1 | 0 |
| NABE 26 C (F4:8 34 ML-14/4) | 2012 | 1 | 0 |
| NABE 28 C (F5:8 90 ML – 2/1/39 | 2012 | 1 | 0 |
| NABE 29 C (F6:8 90 ML – 5/13) | 2012 | 1 | 0 |
| NAROBEAN 1 (MOORE 88002) | 2016 | 1 | 1 |
| NAROBEAN 2 (RWR 2154) | 2016 | 1 | 1 |
| NAROBEAN 3 (RWR 2245) | 2016 | 1 | 1 |
| NAROBEAN 4C (MAC 44) | 2016 | 1 | 1 |
| NAROBEAN 5C (Nyiramuhondo) | 2016 | 1 | 1 |
| NAROBEAN6 | 2019 | 1 | 1 |
| NAROBEAN7 | 2019 | 1 | 1 |

# Appendix I. Sweetpotato Varietal Reference Library

Light green bands indicate varieties with adoption > 0 in our sample. Of 134 accessions in the reference library, 27 are released varieties, of which 16 are CGIAR-related.

### Table 63: Sweetpotato varietal reference library

| Variety | Flesh colour | CGIAR-related | Year of release | Type |
|---|---|---|---|---|
| New Kawogo | White |  | 1995 | Selected landrace |
| New kawogo |  |  | 1995 | Selected landrace |
| SOWOLA | Cream |  | 1995 | Selected landrace |
| Tanzania | Pale yellow |  | 1995 | Selected landrace |
| TORORO 3 | Cream |  | 1995 | Selected landrace |
| Wagabolige | White |  | 1995 | Selected landrace |
| NASPOT 1 | Pale yellow |  | 1999 | Bred and selected by NARO |
| NASPOT 3 | Cream |  | 1999 | Bred and selected by NARO |
| NASPOT 4 | Pale yellow |  | 1999 | Bred and selected by NARO |
| NASPOT 5 | Orange |  | 1999 | Bred and selected by NARO |
| NASPOT 6 | White |  | 1999 | Bred and selected by NARO |
| Ejumula | Deep Orange | 1 | 2004 | Selected landrace |
| KAKAMEGA | Orange | 1 | 2004 | CIP line, selected by NARO |
| Dimbuka Bukulula | Cream | 1 | 2007 | Bred and selected by NARO |
| NASPOT 10 | Dark orange | 1 | 2007 | Bred and selected by NARO |
| NASPOT 7 | Intermediate orange | 1 | 2007 | Bred and selected by NARO |
| NASPOT 8 | Pale orange | 1 | 2007 | Bred and selected by NARO |
| NASPOT 9 | Intermediate orange | 1 | 2007 | Bred and selected by NARO |
| NASPOT 11 | Cream | 1 | 2010 | Bred and selected by NARO |
| NASPOT 12O | Dark orange | 1 | 2013 | CIP parent, bred and selected by NARO |
| NASPOT 13 | Deep Orange | 1 | 2013 | Bred and selected by NARO |
| NASPOT 13O | Deep Orange | 1 | 2013 | Bred and selected by NARO |
| NAROSPOT 1 | Pale Yellow | 1 | 2017 | Bred and selected by NARO |
| NAROSPOT 2 | White | 1 | 2017 | Bred and selected by NARO |
| NAROSPOT 3 | Cream | 1 | 2017 | Bred and selected by NARO |
| NAROSPOT 4 | Cream | 1 | 2017 | Bred and selected by NARO |

| Variety | Flesh colour | CGIAR-related | Year of release | Type |
|---|---|---|---|---|
| NAROSPOT 5 | Cream | 1 | 2017 | Bred and selected by NARO |
| 2020-KUM-1 | Cream |  | N/A | Landrace |
| 2020-KUM-2 | Dark Cream |  | N/A | Landrace |
| 2020-KUM-3 | Cream |  | N/A | Landrace |
| 2020-KUM-4 | Cream |  | N/A | Landrace |
| ABARATA KERE/ KMI |  |  | N/A | Landrace |
| ADJUMANI-UNKN | Intermediate orange |  | N/A | Landrace |
| ADJ-WR-194 | Cream |  | N/A | Landrace |
| Beauregard | Deep Orange |  | N/A | Introduction (US) |
| Bundunguza Omukaire | Cream |  | N/A | Landrace |
| Covington | Orange |  | N/A | Introduction (US) |
| Dimbuka Omuyaka | Pale yellow |  | N/A | Landrace |
| EGOLA/ARA | Cream |  | N/A | Landrace |
| Family | Cream |  | N/A | Landrace |
| Huarmeyano | Dark Cream | 1 | N/A | CIP accession |
| IGA1005 | Dark cream |  | N/A | Landrace |
| IGA974 | Cream |  | N/A | Landrace |
| IGA978 | Dark cream |  | N/A | Landrace |
| IGA989 | Pale yellow |  | N/A | Landrace |
| IGA998 | Cream |  | N/A | Landrace |
| IGA999 | Cream |  | N/A | Landrace |
| ISUPU/ ATESEKE/KMI | Cream |  | N/A | Landrace |
| KASANDA (LOCAL) WKS | Dark Cream |  | N/A | Landrace |
| KAWOGO | white |  | N/A | Landrace |
| KBL UNK-1 | Cream |  | N/A | Landrace |
| KBL633 |  |  | N/A | Landrace |
| KBL649 | Cream |  | N/A | Landrace |
| Kibirkyabidi | Cream |  | N/A | Landrace |
| KIMOTOKA-MPG |  |  | N/A | Landrace |
| Kinana | Dark Cream |  | N/A | Landrace |
| KML872 |  |  | N/A | Landrace |
| KML879 | Cream |  | N/A | Landrace |
| KML886 | Cream |  | N/A | Landrace |
| KML888 | Dark yellow |  | N/A | Landrace |
| KML899 | Cream |  | N/A | Landrace |
| KML903 | Pale yellow |  | N/A | Landrace |
| KML905 | Dark yellow |  | N/A | Landrace |
| KML907 | Dark cream |  | N/A | Landrace |
| KML911 | Dark yellow |  | N/A | Landrace |
| KML912 |  |  | N/A | Landrace |
| KML916 | Cream |  | N/A | Landrace |

| Variety | Flesh colour | CGIAR-related | Year of release | Type |
|---|---|---|---|---|
| KML917 | Dark Cream | | N/A | Landrace |
| KML918 | Dark yellow | | N/A | Landrace |
| KML919 | Dark cream | | N/A | Landrace |
| KML920 | Purple Red | | N/A | Landrace |
| KML930 | Dark cream | | N/A | Landrace |
| KML931 | Dark Cream | | N/A | Landrace |
| KML932 | Cream | | N/A | Landrace |
| KML933 | Dark yellow | | N/A | Landrace |
| KML934 | Pale yellow | | N/A | Landrace |
| KML941 | white | | N/A | Landrace |
| KML942 | Dark yellow | | N/A | Landrace |
| KML944 | Cream | | N/A | Landrace |
| KML951 | Dark yellow | | N/A | Landrace |
| KML955 | Cream | | N/A | Landrace |
| KML957 | Dark cream | | N/A | Landrace |
| KYABAFURUKI-KBL | Cream | | N/A | Landrace |
| MAGABALI-KBL | Cream | | N/A | Landrace |
| MUGURUZI-KBL | Cream | | N/A | Landrace |
| MUNYEERA/MPG | Cream | | N/A | Landrace |
| Muwulu Aduduma | Cream | | N/A | Landrace |
| Namugwere | Cream | | N/A | Landrace |
| NDORE-KBL | Cream | | N/A | Landrace |
| NIMIRA ABAANA/MPG | Dark Cream | | N/A | Landrace |
| NKB105 | Orange | | N/A | Elite clone |
| NKB135 | Deep Orange | | N/A | Elite clone |
| NKB17 | Intermediate Orange | | N/A | Elite clone |
| NKB205 | Pale Yellow | | N/A | Elite clone |
| NKB3 | Deep Orange | | N/A | Elite clone |
| OSUAT/ OSUWAT/KMI | Dark Cream | | N/A | Landrace |
| PAL100 | Pale orange | | N/A | Landrace |
| PAL102 | Cream | | N/A | Landrace |
| PAL110 | | | N/A | Landrace |
| PAL112 | Cream | | N/A | Landrace |
| PAL118 | Cream | | N/A | Landrace |
| PAL132 | | | N/A | Landrace |
| PAL141 | Pale yellow | | N/A | Landrace |
| PAL143 | | | N/A | Landrace |
| PAL144 | Cream | | N/A | Landrace |
| PAL145 | Cream | | N/A | Landrace |
| PAL94 | Dark cream | | N/A | Landrace |
| PAL99 | Dark yellow | | N/A | Landrace |
| Ruddy | | | N/A | Introduction (US) |
| RWA-BETTY-KBL | | | N/A | Landrace |

| Variety | Flesh colour | CGIAR-related | Year of release | Type |
|---|---|---|---|---|
| RWA-BETTY-KBL | Cream | | N/A | Landrace |
| SAMIYIA | Dark Cream | | N/A | Landrace |
| Silk | Dark Cream | | N/A | Landrace |
| SIRONKO 1 | Pale Orange | | N/A | Landrace |
| SIRONKO-2 | Cream | | N/A | Landrace |
| SUKARI-KRE | Cream | | N/A | Landrace |
| TEREZA/KMI | Dark Cream | | N/A | Landrace |
| TESO | Dark Cream | | N/A | Landrace |
| Totanulula | Cream | | N/A | Landrace |
| UGN-40-72 | Dark Orange | | N/A | Breeding line |
| UGN-40-73 | Dark Orange | | N/A | Breeding line |
| Umbrella | Cream | | N/A | Landrace |
| UNK-3-KRE | Cream | | N/A | Landrace |
| UNKN-1-KRE | Cream | | N/A | Landrace |
| UNKN-1-MPG | Cream | | N/A | Landrace |
| UNKN-2-KBL | Pale Yellow | | N/A | Landrace |
| UNKN-2-KRE | | | N/A | Landrace |
| UNKN-2-MPG | Pale Yellow | | N/A | Landrace |
| UNKN-3 KBL | Dark Cream | | N/A | Landrace |
| UNKN-3 MPG | | | N/A | Landrace |
| UNKN-4 KRE | Dark Cream | | N/A | Landrace |
| UNKN-4 MPG | | | N/A | Landrace |
| UNKN-5-KABAROLE | Pale Yellow | | N/A | Landrace |
| UNKN-F5-KMI | Dark Cream | | N/A | Landrace |

# Appendix J. Groundnut Varietal Reference Library

Light green bands indicate varieties with adoption > 0 in our sample.

### Table 64: Groundnut varietal reference library

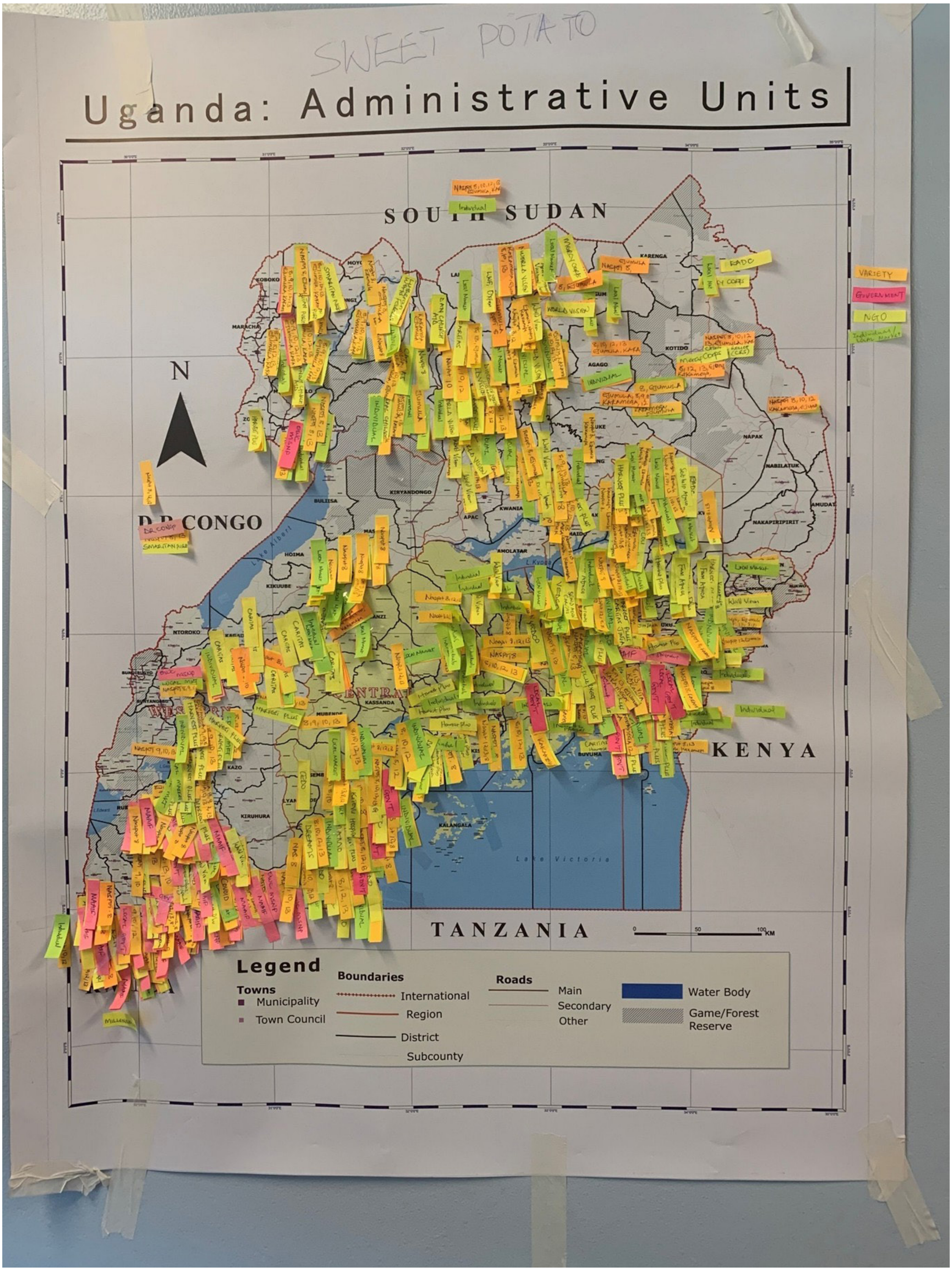
| Variety name/code | Year of release | CGIAR-related | Type |
|---|---|---|---|
| Red Beauty | 1966 | 0 | Landrace |
| Acholi white | 1966 | 0 | Landrace |
| Manipinter | 1969 | 1 | ICRISAT line ICGV - SM83708 (ICGMS42) |
| Igola 1 | 1995 | 1 | ICRISAT line RMP-12, SAMNUT-10 |
| Serenut 1R (ICGV - SM - 8370 / Serere Red) | 1998 | 1 | ICRISAT line CG 7 ICGV - SM83708 (USA 20 X TMV 10) |
| Serenut 2 (ICGV - SM90704 / Igola II) | 1998 | 1 | ICRISAT line ICGV - SM90704 (RG-1 X ManiPinter) |
| Serenut 3R (ICGV - SM93530) | 2002 | 1 | ICRISAT line ICGV - SM93530 (ICGV-SM85027 x RG-1) |
| Serenut 4T (ICG - 122991) | 2002 | 1 | ICRISAT Malawi introduction of Indian landrace |
| Serenut 5R | 2010 | 1 | ICRISAT line ICGV - SM93535 (ICGM522 x RG-1) |
| Serenut 6T | 2010 | 1 | ICRISAT line ICGV-SM99566 (ICGV 93437 x ICGV-SM93561) |
| Serenut 7T | 2011 | 1 | ICRISAT line SGV 99018 (CG7 X ICGV-SM90704) |
| Serenut 8R | 2011 | 1 | ICRISAT line SGV99019 (CG7 X ICGV-SM90704) |
| Serenut 9T | 2011 | 1 | ICRISAT line SGV99044 (CG7 X ICGV-SM90704) |
| Serenut 10R | 2011 | 1 | ICRISAT line SGV99024 (CG7 X ICGV-SM90704) |
| Serenut 11T | 2011 | 1 | ICRISAT line SGV99031 (CG7 X ICGV-SM90704) |
| Serenut 12R | 2011 | 1 | ICRISAT line SGV99048 (CG7 X ICGV-SM90704) |
| Serenut 13T | 2011 | 1 | ICRISAT line SGV99052 (CG7 X ICGV-SM90704) |
| Serenut 14R | 2011 | 1 | ICRISAT line SGV99064 (CG7 X ICGV-SM90704) |
| NARONut2T | 2021 | 1 | ICRISAT line DOK1R (ICGV-SM86715 X ICGV-SM90704) |
| NARONut1R | 2021 | 1 | ICRISAT line DOK2T (ICGV-SM86715 X ICGV-SM90704) |
| Erudurudu | N/A | 0 | Reference Landrace NaSARRI |
| Eepu | N/A | 0 | Reference Landrace NaSARRI |
| Lokoya Red | N/A | 0 | Reference Landrace NaSARRI |
| Olukluk Red | N/A | 0 | Reference Landrace NaSARRI |
| Ekalam | N/A | 0 | Reference Landrace NaSARRI |
| Ongwara | N/A | 0 | Reference Landrace NaSARRI |
| Emoit | N/A | 0 | Reference Landrace NaSARRI |
| Gwerinut Red | N/A | 0 | Reference Landrace NaSARRI |

| Variety name/code | Year of release | CGIAR-related | Type |
|---|---|---|---|
| Egoromoit Tan | N/A | 0 | Reference Landrace NaSARRI |
| Dokolo Brown | N/A | 0 | Reference Landrace NaSARRI |
| Abino Red | N/A | 0 | Reference Landrace NaSARRI |
| Kaboya | N/A | 0 | Reference Landrace NaSARRI |
| Eboss | N/A | 0 | Reference Landrace NaSARRI |

# Appendix K. Details of Workshop Activities Used to Construct Data on Locations and Dates of Dissemination of Biofortified Crops

The participants were asked to come with sales records (where relevant) to assist in filling out individual forms to elicit data on where, when, and why planting material of different varieties was distributed over the preceding 10 years. In the first workshop for the Central Region, these data were captured on laptops by the SPIA team. Subsequent workshops used CAPI (Survey Solutions app) on tablets or smartphones for data to be entered by student interns. The participants were also requested to hand over data records for digitization. Workshop participants were divided into groups to discuss their records but also their previously undocumented knowledge of past dissemination efforts, based on their districts of origin. The main objective of these discussions was to make a comprehensive mapping of which varieties have been disseminated in which sub-counties, and when those activities took place. A map from each region was produced, containing districts and sub-counties. Each group from each district was asked to indicate places where the varieties were disseminated and indicate partners or projects involved in the dissemination on the same map. Using the maps, groups identified the areas not reached with biofortified varieties and explained why they may not have been reached. After completing the regional maps, the teams were asked to indicate on the map places where the varieties disseminated beyond their regions, using specific types of stickers and indicating partners or projects involved in the dissemination. This information was also digitized.

## Common Cassava Pests



# Appendix L. East Africa Dairy Development Project Hubs

### Table 65: East Africa Dairy Development (EADD) project hubs

| Hub name | District | Region |
|---|---|---|
| **Phase 1** | | |
| Dwaniro | Kiboga | Central |
| Kiboga | Kiboga | Central |
| Aberwanaho | Kyankwanzi | Central |
| Tusubira | Mityana | Central |
| Kagau Mawagga | Mityana | Central |
| Kiusbi | Wakiso | Central |
| Bubusi | Wakiso | Central |
| Kkingo | Lwengo | Central |
| Mitala-Maria | Mpigi | Central |
| Nabitanga | Sembabule | Central |
| Sembabule | Sembabule | Central |
| Bugukya Ggulama | Masaka | Central |
| Kakyolu Farmers' | Kalungu | Central |
| Nampante | Mukono | Central |
| Buikwe | Buikwe | Central |
| Bugerere | Kayunga | Central |
| Butagaya | Jinja | Eastern |
| Baitambogwe | Mayuge | Eastern |
| Nawanyago | Kamuli | Eastern |
| Wankole | Kamuli | Eastern |
| **Phase 2** | | |
| Namwendwa | Kamuli | Eastern |
| Balawoli Kyebaja Tobona | Kamuli | Eastern |
| Buyende | Buyende | Eastern |
| Irundu Tugezeku | Buyende | Eastern |
| Nawaikoke* | Kaliro | Eastern |
| Luuka* | Luuka | Eastern |
| Bin | Ibanda | Western |
| Nyabuhikye | Ibanda | Western |
| Ishongororo | Ibanda | Western |
| Kitagwenda | Ibanda | Western |
| Abesigana | Isingiro | Western |
| Nyamitsindo | Isingiro | Western |
| Sanga | Kiruhuura | Western |
| Kyakabunga* | Kiruhuura | Western |
| Kanyaanya* | Kiruhuura | Western |

* Hubs that had been waiting for approval, unclear if eventually operational

# Appendix M. Sample-Level Analysis - Maize

### Table 66: Sample-level analysis - maize

| Variety | Number of samples | % share of samples |
|---|---|---|
| LONGE5D | 218 | 30.9 |
| Unassigned | 159 | 22.5 |
| LONGE4 | 108 | 13.6 |
| UH5051 \| UH5052 \| UH5053 | 56 | 7.9 |
| H520 | 39 | 5.5 |
| H614D | 38 | 5.4 |
| LONGE10H | 24 | 3.4 |
| Bazooka | 16 | 2.3 |
| KH500-43A | 14 | 2.0 |
| DK90-89 | 12 | 1.7 |
| H624 | 9 | 1.3 |
| WE6103 -Champion | 3 | 0.4 |
| ADV2310 | 2 | 0.3 |
| ADV2309 | 2 | 0.3 |
| LONGE7H \| PAN15 IR | 2 | 0.3 |
| FH 6150 | 2 | 0.3 |
| SC555 | 1 | 0.1 |
| SC419 | 1 | 0.1 |
| **Total** | **706** | **100** |

# Appendix N. Sample-Level Analysis - Cassava

### Table 67: Sample-level analysis - cassava

| Variety | Count | % share of samples |
|---|---|---|
| Unassigned | 964 | 49.4 |
| OFUMBA_CHAI | 185 | 9.5 |
| Nase 19 | 169 | 8.7 |
| Narocas 1 | 167 | 8.6 |
| Nase 3 | 72 | 3.7 |
| MUREFU | 70 | 3.6 |
| NJULE-WHITE | 45 | 2.3 |
| BALI | 44 | 2.3 |
| BAO | 38 | 1.9 |
| BUKALASA-11 | 35 | 1.8 |
| MERCURY | 26 | 1.3 |
| IITA-TMS-IBA120067 | 23 | 1.2 |
| NASE12 | 22 | 1.1 |
| TMEB14 | 20 | 1.0 |
| EDYAL | 15 | 0.8 |
| KWATAMUMPALE | 13 | 0.7 |
| Nase 13 | 12 | 0.6 |
| UG110114 | 9 | 0.5 |
| OFUMBA | 7 | 0.4 |
| MAGANA | 5 | 0.3 |
| NYARABOKE | 5 | 0.3 |
| MACHUNDE | 3 | 0.2 |
| Nase 1 | 2 | 0.1 |
| NASE8 | 1 | 0.1 |
| KITENGA | 1 | 0.1 |
| **Total** | **1953** | **100** |

# Appendix O. Sample-Level Analysis - Banana

### Table 68: Sample-level analysis - banana

| Final Reference | Count | % share of samples |
|---|---|---|
| Ekitawira | 1625 | 54.1 |
| Nakawere | 468 | 15.6 |
| Bwara | 272 | 9.0 |
| Unassigned | 107 | 3.6 |
| Sukali ndizi | 104 | 3.5 |
| Bogoya_Gros Michel | 96 | 3.2 |
| Atwarira | 43 | 1.4 |
| FHIA 17 | 42 | 1.4 |
| Kayinja | 42 | 1.4 |
| Bluggoe | 39 | 1.3 |
| Silver Bluggoe | 32 | 1.1 |
| Nyamwihogora | 32 | 1.1 |
| FHIA 23 | 18 | 0.6 |
| Lwamugongo | 17 | 0.6 |
| Petite Naine | 10 | 0.3 |
| Pisang Ceylan | 8 | 0.3 |
| Kisubi | 7 | 0.2 |
| Nante | 6 | 0.2 |
| KABANA 7H | 5 | 0.2 |
| Bugoya_Gros Michel | 4 | 0.1 |
| Yangambi KM5 | 4 | 0.1 |
| Chinese Cavendish | 4 | 0.1 |
| Williams | 3 | 0.1 |
| Ekigama | 3 | 0.1 |
| FHIA 1 | 3 | 0.1 |
| FHIA 25 | 3 | 0.1 |
| Bogoya_ Gros Michel | 2 | 0.1 |
| Dwarf cavendish | 2 | 0.1 |
| Makara | 1 | 0.0 |
| FHIA 18 | 1 | 0.0 |
| Maganya | 1 | 0.0 |
| Kaitabunyonyi | 1 | 0.0 |
| Gonja Nakatansensa | 1 | 0.0 |
| **Total** | **3006** | **100** |

# Appendix P. Sample-Level Analysis - Beans

### Table 69: Sample-level analysis - beans

| Type of sample | Count | % of all samples |
|---|---|---|
| Uniform, single variety | 173 | 24.2 |
| Mixed | 308 | 43.1 |
| Unassigned | 233 | 32.6 |
| **Total** | **714** | **100** |

| **UNIFORM SAMPLE** | | |
|---|---|---|
| **Variety** | **Count** | **% of uniform samples** |
| UNGB-5741 | 41 | 23.7 |
| UGK71 | 21 | 12.1 |
| UNGB-4431 | 16 | 9.2 |
| NABE13 | 14 | 8.1 |
| UNGB-4428 | 7 | 4.0 |
| UNGB-4429 | 7 | 4.0 |
| UNGB-5756 | 6 | 3.5 |
| UGK166 | 6 | 3.5 |
| UNGB-4394 | 6 | 3.5 |
| UGD.001 | 6 | 3.5 |
| UNGB-857 | 6 | 3.5 |
| UGK28 | 5 | 2.9 |
| UNGB-133 | 5 | 2.9 |
| UGK99 | 5 | 2.9 |
| UNGB-5737 | 2 | 1.2 |
| UNGB-4399 | 2 | 1.2 |
| Masindi Yellow Short | 2 | 1.2 |
| UGK145 | 2 | 1.2 |
| UNGB-5142 | 1 | 0.6 |
| UNGB-4972 | 1 | 0.6 |
| K132 | 1 | 0.6 |
| NAROBEAN7 | 1 | 0.6 |
| UNGB-5049 | 1 | 0.6 |
| UNGB-5740 | 1 | 0.6 |
| UNGB-3925 | 1 | 0.6 |
| NAROBEAN2 | 1 | 0.6 |
| NAROBEAN5C | 1 | 0.6 |
| UGD.007 | 1 | 0.6 |
| UNGB-5763 | 1 | 0.6 |
| UGK10 | 1 | 0.6 |
| NAROBEAN6 | 1 | 0.6 |
| UGK129 | 1 | 0.6 |
| **Grand Total** | **173** | **100** |

| **MIXED SAMPLE** | | |
|---|---|---|
| **Variety representing the mixture** | **Count** | **% of mixed samples** |
| NABE20 | 45 | 14.6 |
| UGD.001 | 26 | 8.4 |
| NABE15 | 20 | 6.5 |
| NABE23 | 19 | 6.2 |
| UGK71 | 17 | 5.5 |
| UGD.007 | 15 | 4.9 |
| NABE16 | 11 | 3.6 |
| UGK59 | 9 | 2.9 |
| NABE1 | 9 | 2.9 |
| NAROBEAN2 | 8 | 2.6 |
| NABE17 | 8 | 2.6 |
| UNGB-4427 | 7 | 2.3 |
| UNGB-5079 | 6 | 1.9 |
| UNGB-4394 | 6 | 1.9 |
| NAROBEAN4C | 6 | 1.9 |
| UGK166 | 6 | 1.9 |
| UNGB-5741 | 5 | 1.6 |
| UGK99 | 5 | 1.6 |
| UGK22 | 5 | 1.6 |
| UNGB-4431 | 4 | 1.3 |
| NAROBEAN5C | 4 | 1.3 |
| NABE12C | 4 | 1.3 |
| UGK24 | 4 | 1.3 |
| NABE21 | 4 | 1.3 |
| NABE10C | 3 | 1.0 |
| NABE2 | 3 | 1.0 |
| UGK130 | 3 | 1.0 |
| UNGB-1582 | 3 | 1.0 |
| UGK119 | 3 | 1.0 |
| UGK121 | 3 | 1.0 |
| UGK122 | 3 | 1.0 |
| UNGB-4170 | 2 | 0.6 |
| NAROBEAN1 | 2 | 0.6 |
| Masindi Yellow Short | 2 | 0.6 |
| NABE13 | 2 | 0.6 |
| UGK145 | 2 | 0.6 |
| UGK28 | 2 | 0.6 |
| UNGB-770 | 2 | 0.6 |
| UGK44 | 2 | 0.6 |
| UNGB-133 | 2 | 0.6 |
| UGK10 | 1 | 0.3 |
| UNGB-3861 | 1 | 0.3 |
| UNGB-4972 | 1 | 0.3 |
| UGK107 | 1 | 0.3 |
| UGD.005 | 1 | 0.3 |

| **MIXED SAMPLE** | | |
|---|---|---|
| **Variety representing the mixture** | **Count** | **% of mixed samples** |
| UGD.003 | 1 | 0.3 |
| UNGB-857 | 1 | 0.3 |
| UNGB-361 | 1 | 0.3 |
| UNGB-3740 | 1 | 0.3 |
| UGK139 | 1 | 0.3 |
| UNGB-149 | 1 | 0.3 |
| UNGB-741 | 1 | 0.3 |
| NABE6 | 1 | 0.3 |
| UNGB-2443 | 1 | 0.3 |
| K132 | 1 | 0.3 |
| UGK129 | 1 | 0.3 |
| **Grand Total** | **308** | **100** |

# Appendix Q. Sample-Level Analysis - Sweetpotato

### Table 70: Sample-level analysis - sweetpotato

| Variety | Count | % Share of samples |
|---|---|---|
| Unassigned | 627 | 48.2 |
| UNKN-4 KRE | 75 | 5.8 |
| SAMIYIA | 58 | 4.5 |
| Muwulu Aduduma | 38 | 2.9 |
| Bundunguza Omukaire | 37 | 2.8 |
| NAROSPOT 1 | 37 | 2.8 |
| SIRONKO-2 | 33 | 2.5 |
| KML905 | 24 | 1.8 |
| TESO | 21 | 1.6 |
| IGA989 | 20 | 1.5 |
| PAL145 | 20 | 1.5 |
| NIMIRA ABAANA/MPG | 19 | 1.5 |
| NDORE-KBL | 18 | 1.4 |
| Umbrella | 18 | 1.4 |
| KASANDA (LOCAL) WKS | 16 | 1.2 |
| UNKN-2-MPG | 13 | 1.0 |
| KML931 | 13 | 1.0 |
| KML899 | 12 | 0.9 |
| KML916 | 12 | 0.9 |
| Family | 12 | 0.9 |
| PAL102 | 11 | 0.8 |
| KML934 | 11 | 0.8 |
| NASPOT 8 | 9 | 0.7 |
| 2020-KUM-2 | 9 | 0.7 |
| MAGABALI-KBL | 9 | 0.7 |
| NASPOT 1 | 9 | 0.7 |
| IGA1005 | 8 | 0.6 |
| Tanzania | 8 | 0.6 |
| SIRONKO 1 | 7 | 0.5 |
| KYABAFURUKI-KBL | 7 | 0.5 |
| UNK-3-KRE | 6 | 0.5 |
| KML918 | 5 | 0.4 |
| 2020-KUM-1 | 5 | 0.4 |
| Dimbuka Omuyaka | 5 | 0.4 |
| PAL100 | 4 | 0.3 |
| UNKN-3 KBL | 4 | 0.3 |
| MUGURUZI-KBL | 4 | 0.3 |
| MUNYEERA/MPG | 4 | 0.3 |
| 2020-KUM-4 | 4 | 0.3 |
| KML888 | 4 | 0.3 |
| EGOLA/ARA | 4 | 0.3 |
| UNKN-F5-KMI | 3 | 0.2 |

| Variety | Count | % Share of samples |
|---|---|---|
| Kinana | 3 | 0.2 |
| KML955 | 3 | 0.2 |
| 2020-KUM-3 | 3 | 0.2 |
| UNKN-2-KBL | 3 | 0.2 |
| KML917 | 3 | 0.2 |
| TEREZA/KMI | 2 | 0.2 |
| KBL UNK-1 | 2 | 0.2 |
| KML932 | 2 | 0.2 |
| Silk | 2 | 0.2 |
| New Kawogo | 2 | 0.2 |
| Kibirkyabidi | 2 | 0.2 |
| SUKARI-KRE | 1 | 0.1 |
| KAKAMEGA | 1 | 0.1 |
| OSUAT/OSUWAT/KMI | 1 | 0.1 |
| KML920 | 1 | 0.1 |
| ADJUMANI-UNKN | 1 | 0.1 |
| PAL99 | 1 | 0.1 |
| PAL112 | 1 | 0.1 |
| NASPOT 12O | 1 | 0.1 |
| UNKN-5-KABAROLE | 1 | 0.1 |
| UNKN-1-KRE | 1 | 0.1 |
| UNKN-1-MPG | 1 | 0.1 |
| KBL 649 | 1 | 0.1 |
| **Total** | **1302** | **100** |

# Appendix R. Sample-Level Analysis - Groundnut

## Table 71: Sample-level analysis - groundnut

| Varieties | Count | % share of samples |
|---|---|---|
| Unassigned | 248 | 37.8 |
| Serenut 13T | 86 | 13.1 |
| Egoromoit Tan | 60 | 9.1 |
| Red Beauty | 59 | 9.0 |
| Ongwara | 36 | 5.5 |
| Erudurudu | 32 | 4.9 |
| Acholi white | 31 | 4.7 |
| Serenut 2 | 25 | 3.8 |
| Dokolo Brown | 23 | 3.5 |
| Serenut 4 | 15 | 2.3 |
| Serenut 6T | 13 | 2.0 |
| Kaboya | 8 | 1.2 |
| Serenut 14R | 6 | 0.9 |
| Igola 1 | 6 | 0.9 |
| Abino Red | 2 | 0.3 |
| Emoit | 2 | 0.3 |
| Serenut 10R | 2 | 0.3 |
| Serenut 11T | 1 | 0.2 |
| Serenut 12R | 1 | 0.2 |
| **TOTAL** | **656** | **100** |

# Appendix S. Summary of UNOMA Module Variables

## UNOMA Summary

## 1 Maize

Table 1: Summary of UNOMA Variety Covariates Among Different Varieties - Barcode Level

| | Pvt. Sector Hybrids | | NARO Hybrids | | NARO OPVS | | Unassigned Varieties | |
|---|---|---|---|---|---|---|---|---|
| | Mean | N | Mean | N | Mean | N | Mean | N |
| Destiny Of Harvest Of This Variety? Sell | 0.790 | 62 | 0.509 | 108 | 0.520 | 358 | 0.590 | 156 |
| Like About This Variety? Yield (High) | 0.871 | 62 | 0.778 | 108 | 0.656 | 358 | 0.763 | 156 |
| Like About This Variety? Taste (Good) | 0.597 | 62 | 0.556 | 108 | 0.662 | 358 | 0.558 | 156 |
| Like About This Variety? Disease Or Pest Resistance (Good) | 0.081 | 62 | 0.102 | 108 | 0.056 | 358 | 0.077 | 156 |
| Like About This Variety? Drought Tolerance (Good) | 0.129 | 62 | 0.074 | 108 | 0.070 | 358 | 0.122 | 156 |
| Dislikes About This Variety? Yield (Low) | 0.048 | 62 | 0.037 | 108 | 0.064 | 358 | 0.051 | 156 |
| Dislikes About This Variety? Disease/Pest Resistance (Susceptible) | 0.419 | 62 | 0.444 | 108 | 0.453 | 358 | 0.410 | 156 |
| Dislikes About This Variety? Drought Tolerance (Susceptible) | 0.452 | 62 | 0.407 | 108 | 0.338 | 358 | 0.340 | 156 |
| Affected by any pests: Yes/No? | 1.806 | 62 | 1.685 | 108 | 1.598 | 358 | 1.590 | 156 |
| Affected by any diseases: Yes/No? | 1.742 | 62 | 1.759 | 108 | 1.634 | 358 | 1.596 | 156 |
| Source Of The Planting Material: NGO/Relief | 0.016 | 62 | 0.009 | 108 | 0.011 | 358 | 0.013 | 158 |
| Source Of The Planting Material: NAADS | 0.000 | 62 | 0.028 | 108 | 0.000 | 358 | 0.025 | 158 |
| Source Of The Planting Material: Gov'ment/OWC/MP | 0.032 | 62 | 0.028 | 108 | 0.045 | 358 | 0.032 | 158 |
| Source Of The Planting Material: Farmer Group/Local Multiplier | 0.000 | 62 | 0.083 | 108 | 0.039 | 358 | 0.013 | 158 |
| Source Of The Planting Material: Research Centre | 0.000 | 62 | 0.000 | 108 | 0.000 | 358 | 0.000 | 158 |
| Source Of The Planting Material: Another Farmer (Relative/Neighbor) | 0.306 | 62 | 0.370 | 108 | 0.439 | 358 | 0.399 | 158 |
| Source Of The Planting Material: Market | 0.645 | 62 | 0.481 | 108 | 0.466 | 358 | 0.506 | 158 |
| Type of Variety: Improved | 0.484 | 62 | 0.481 | 108 | 0.277 | 358 | 0.423 | 156 |
| Type of Variety: Traditional | 0.484 | 62 | 0.519 | 108 | 0.690 | 358 | 0.519 | 156 |
| Type of Variety: Don't Know | 0.032 | 62 | 0.000 | 108 | 0.034 | 358 | 0.058 | 156 |

Table 2: Summary of UNOMA Variety Covariates Among Different Varieties - Barcode Level

| | CGIAR | | Pvt. Sector | | Unassigned | | (2)-(1) | | (3)-(1) | |
|---|---|---|---|---|---|---|---|---|---|---|
| | Mean | N | Mean | N | Mean | N | Diff. | P-val | Diff. | P-val |
| Destiny Of Harvest Of This Variety? Sell | 0.52 | 349 | 0.79 | 62 | 0.59 | 156 | 0.27*** | 0.00 | 0.07 | 0.15 |
| Like About This Variety? Yield (High) | 0.69 | 349 | 0.87 | 62 | 0.76 | 156 | 0.18*** | 0.00 | 0.07* | 0.09 |
| Like About This Variety? Taste (Good) | 0.61 | 349 | 0.60 | 62 | 0.56 | 156 | -0.02 | 0.80 | -0.05 | 0.27 |
| Like About This Variety? Disease Or Pest Resistance (Good) | 0.05 | 349 | 0.08 | 62 | 0.08 | 156 | 0.03 | 0.49 | 0.02 | 0.36 |
| Like About This Variety? Drought Tolerance (Good) | 0.09 | 349 | 0.13 | 62 | 0.12 | 156 | 0.05 | 0.29 | 0.04 | 0.24 |
| Dislikes About This Variety? Yield (Low) | 0.04 | 349 | 0.05 | 62 | 0.05 | 156 | 0.01 | 0.71 | 0.01 | 0.49 |
| Dislikes About This Variety? DiseaseResistance (Susceptible) | 0.48 | 349 | 0.42 | 62 | 0.41 | 156 | -0.06 | 0.39 | -0.07 | 0.17 |
| Dislikes About This Variety? Drought Tolerance (Susceptible) | 0.35 | 349 | 0.45 | 62 | 0.34 | 156 | 0.10 | 0.14 | -0.01 | 0.88 |
| Affected by any pests: Yes/No? | 0.38 | 349 | 0.19 | 62 | 0.41 | 156 | -0.18*** | 0.00 | 0.03 | 0.46 |
| Affected by any diseases: Yes/No? | 0.31 | 349 | 0.26 | 62 | 0.40 | 156 | -0.06 | 0.36 | 0.09* | 0.05 |
| Source Of The Planting Material: NGO/Relief | 0.01 | 349 | 0.02 | 62 | 0.01 | 158 | 0.00 | 0.92 | -0.00 | 0.88 |
| Source Of The Planting Material: NAADS | 0.01 | 349 | 0.00 | 62 | 0.03 | 158 | -0.01* | 0.08 | 0.02 | 0.22 |
| Source Of The Planting Material: Gov'ment/OWC/MP | 0.04 | 349 | 0.03 | 62 | 0.03 | 158 | -0.01 | 0.83 | -0.01 | 0.75 |
| Source Of The Planting Material: Farmer Group/Local Multiplier | 0.05 | 349 | 0.00 | 62 | 0.01 | 158 | -0.05*** | 0.00 | -0.04** | 0.01 |
| Source Of The Planting Material: Research Centre | 0.00 | 349 | 0.00 | 62 | 0.00 | 158 | 0.00 | . | 0.00 | . |
| Source Of The Planting Material: Another Farmer (Relative/Neighbor) | 0.39 | 349 | 0.31 | 62 | 0.40 | 158 | -0.09 | 0.17 | 0.01 | 0.90 |
| Source Of The Planting Material: Market | 0.50 | 349 | 0.65 | 62 | 0.51 | 158 | 0.15** | 0.03 | 0.01 | 0.87 |
| Type of Variety: Improved | 0.36 | 349 | 0.48 | 62 | 0.42 | 156 | 0.12* | 0.08 | 0.06 | 0.21 |
| Type of Variety: Traditional | 0.61 | 349 | 0.48 | 62 | 0.52 | 156 | -0.13* | 0.06 | -0.09* | 0.05 |
| Type of Variety: Don't Know | 0.02 | 349 | 0.03 | 62 | 0.06 | 156 | 0.01 | 0.70 | 0.03* | 0.09 |

Table 3: Distribution of Year of Release - Barcode Level

| | Freq | Mean | SD |
|---|---|---|---|
| Year of release | | 2006.75 | 5.135 |
| Year of release == 2000 | 119 | 0.21 | 0.407 |
| Year of release == 2002 | 2 | 0.00 | 0.059 |
| Year of release == 2004 | 7 | 0.01 | 0.110 |
| Year of release == 2005 | 42 | 0.07 | 0.261 |
| Year of release == 2006 | 239 | 0.42 | 0.494 |
| Year of release == 2009 | 22 | 0.04 | 0.193 |
| Year of release == 2012 | 79 | 0.14 | 0.346 |
| Year of release == 2013 | 19 | 0.03 | 0.180 |
| Year of release == 2017 | 1 | 0.00 | 0.042 |
| Year of release == 2019 | 39 | 0.07 | 0.253 |
| Year of release == 2022 | 1 | 0.00 | 0.042 |
| Observations | 570 | | |

Includes all identified (barcode merged) samples

Table 4: Year of Release among CG Varieties - Barcode Level

| | Freq | Mean | SD |
|---|---|---|---|
| Year of release | | 2007.84 | 3.090 |
| Year of release == 2002 | 2 | 0.01 | 0.076 |
| Year of release == 2006 | 239 | 0.68 | 0.465 |
| Year of release == 2009 | 22 | 0.06 | 0.243 |
| Year of release == 2012 | 60 | 0.17 | 0.378 |
| Year of release == 2013 | 19 | 0.05 | 0.227 |
| Year of release == 2019 | 7 | 0.02 | 0.140 |
| Observations | 349 | | |

Includes only CG samples.

Table 5: Total Number of Assigned Unique Varieties in Households* - HH Level

| | N | Mean | SD | Sum |
|---|---|---|---|---|
| Total number of unique varieties in HH | 264 | 1.27 | 0.446 | |
| Total unique varieties in HH == 1 | 264 | 0.73 | 0.446 | 192 |
| Total unique varieties in HH == 2 | 264 | 0.27 | 0.446 | 72 |

*The sample is only limited to the barcodes that are assigned, removing all the varieties that are ‘NA’.

Table 6: Crosstab with Farmer's Perception & Genetic Identities - Plot Level

| | % of Variety in the Plot | | |
|---|---|---|---|
| Number of Genetic Varieties in the Plot | <100% | 100% | Total |
| 1 | 50 | 95 | 145 |
| 2 | 38 | 56 | 94 |
| Total | 88 | 151 | 239 |

The sample is limited to the plots with even barcode samples.

Table 7: Crosstab of Planting Material and Genetic Identities - Barcode Level

| Planting Material == 100 % | Private Sector Hybrids | NARO Hybrids | NARO OPVs | Unassigned Varieties |
|---|---|---|---|---|
| No | 29 | 57 | 222 | 89 |
| Yes | 33 | 51 | 136 | 69 |
| Total | 62 | 108 | 358 | 158 |

In row, Yes if the % of new planting material of this variety obtained from outside own farm is 100%.

Table 8: Planting Material Recycled for Seasons - Barcode Level

| | All | | NARO Hybrids | | NARO OPVs | |
|---|---|---|---|---|---|---|
| Seasons | Freq | Percent | Freq | Percent | Freq | Percent |
| 0 | 7 | 0.02 | 2 | 0.04 | 4 | 0.02 |
| 1 | 26 | 0.06 | 6 | 0.11 | 9 | 0.04 |
| 2 | 133 | 0.33 | 19 | 0.33 | 69 | 0.31 |
| 3 | 91 | 0.22 | 11 | 0.19 | 58 | 0.26 |
| 4 | 89 | 0.22 | 12 | 0.21 | 45 | 0.20 |
| 5 | 15 | 0.04 | 2 | 0.04 | 10 | 0.05 |
| 6 | 9 | 0.02 | 1 | 0.02 | 5 | 0.02 |
| 8 | 7 | 0.02 | 0 | 0.00 | 5 | 0.02 |
| 10 | 16 | 0.04 | 1 | 0.02 | 7 | 0.03 |
| 14 | 1 | 0.00 | 1 | 0.02 | 0 | 0.00 |
| 15 | 6 | 0.01 | 0 | 0.00 | 6 | 0.03 |
| 16 | 1 | 0.00 | 0 | 0.00 | 1 | 0.00 |
| 100 | 7 | 0.02 | 2 | 0.04 | 3 | 0.01 |
| Total | 408 | | 57 | | 222 | |

For planting material obtained from own farm, for how many planting seasons this variety has been recycled/replanted since it was last acquired from outside

# 2 Cassava

Table 9: Types of Variety in Cassava

| | N | Sum | Mean | SD |
|---|---|---|---|---|
| HH has at least 1 Landrace Variety | 646 | 212 | 0.328 | 0.470 |
| HH has at least 1 CGIAR Related Variety | 646 | 227 | 0.351 | 0.478 |
| HH has all Unassigned Varieties | 646 | 233 | 0.361 | 0.481 |

The genetic identity is taken at 5% threshold level.

Table 10: Regional Distribution of Varieties in Cassava

| | N | Sum | Mean | SD |
|---|---|---|---|---|
| CENTRAL | | | | |
| HH has all Unassigned varieties | 137 | 39 | 0.285 | 0.453 |
| HH has at least 1 NAROCAS-1 variety | 137 | 3 | 0.022 | 0.147 |
| HH has at least 1 NASE-19 variety | 137 | 3 | 0.022 | 0.147 |
| HH has at least 1 Improved variety | 137 | 6 | 0.044 | 0.205 |
| EASTERN | | | | |
| HH has all Unassigned varieties | 203 | 55 | 0.271 | 0.446 |
| HH has at least 1 NAROCAS-1 variety | 203 | 75 | 0.369 | 0.484 |
| HH has at least 1 NASE-19 variety | 203 | 49 | 0.241 | 0.429 |
| HH has at least 1 Improved variety | 203 | 139 | 0.685 | 0.466 |
| NORTHERN | | | | |
| HH has all Unassigned varieties | 153 | 67 | 0.438 | 0.498 |
| HH has at least 1 NAROCAS-1 variety | 153 | 11 | 0.072 | 0.259 |
| HH has at least 1 NASE-19 variety | 153 | 27 | 0.176 | 0.382 |
| HH has at least 1 Improved variety | 153 | 54 | 0.353 | 0.479 |
| WESTERN | | | | |
| HH has all Unassigned varieties | 153 | 72 | 0.471 | 0.501 |
| HH has at least 1 NAROCAS-1 variety | 153 | 1 | 0.007 | 0.081 |
| HH has at least 1 NASE-19 variety | 153 | 4 | 0.026 | 0.160 |
| HH has at least 1 Improved variety | 153 | 6 | 0.039 | 0.195 |
| Total | | | | |
| HH has all Unassigned varieties | 646 | 233 | 0.361 | 0.481 |
| HH has at least 1 NAROCAS-1 variety | 646 | 90 | 0.139 | 0.347 |
| HH has at least 1 NASE-19 variety | 646 | 83 | 0.128 | 0.335 |
| HH has at least 1 Improved variety | 646 | 205 | 0.317 | 0.466 |

Table 11: Farmers' perception vs Genetic Identities - Barcode Level

| Farmers' Perception of Variety | CGIAR Varieties | Landrace Varieties | Unassigned Varieties |
|---|---|---|---|
| DON'T KNOW | 5 | 10 | 19 |
| TRADITIONAL | 159 | 272 | 508 |
| IMPROVED | 179 | 69 | 177 |
| Total | 343 | 351 | 704 |

Landrace includes both Landrace and Released Landrace.

Table 12: Comparison of UNOMA Covariates among Different Identities - Barcode Level

| | CGIAR-rel | | Landrace | | Unassigned | | (1) - (2) | | (1) - (3) | |
|---|---|---|---|---|---|---|---|---|---|---|
| | N | Mean | N | Mean | N | Mean | Diff. | p | Diff. | p |
| % of new planting material of this variety obtained from outside own farm | 343 | 58.45 | 351 | 36.17 | 703 | 45.06 | 22.29 | 0.00*** | 13.39 | 0.00*** |
| For planting material obtained from own farm, for how many planting seasons this variety has been recycled since it was last required from outside | 149 | 5.74 | 228 | 9.39 | 405 | 6.75 | -3.65 | 0.05* | -1.01 | 0.52 |
| **Destiny Of Harvest Of This Variety?** Sell | 343 | 24.20 | 351 | 19.66 | 704 | 25.00 | 4.54 | 0.15 | -0.80 | 0.78 |
| **Source Of The Planting Material:** | | | | | | | | | | |
| Another Farmer (Relative/Neighbor) | 343 | 86.01 | 351 | 89.74 | 704 | 90.77 | -3.74 | 0.13 | -4.76 | 0.03** |
| Self-reported name same as the Ref Library Name | 343 | 0.29 | 351 | 0.57 | 704 | 0.00 | -0.28 | 0.58 | 0.29 | 0.32 |
| **What Do You Like About This Variety?** | | | | | | | | | | |
| Yield (High) | 343 | 70.85 | 351 | 66.10 | 704 | 58.66 | 4.75 | 0.18 | 12.18 | 0.00*** |
| Taste (Good) | 343 | 67.93 | 351 | 63.53 | 704 | 65.06 | 4.40 | 0.22 | 2.87 | 0.35 |
| Cooking Properties | 343 | 21.57 | 351 | 27.07 | 704 | 26.28 | -5.49 | 0.09* | -4.70 | 0.09* |
| Disease Or Pest Resistance (Good) | 343 | 10.50 | 351 | 12.25 | 704 | 11.93 | -1.76 | 0.47 | -1.44 | 0.49 |
| Time To Maturation | 343 | 23.91 | 351 | 25.64 | 704 | 20.45 | -1.73 | 0.60 | 3.45 | 0.21 |
| **Dislike about this variety**: | | | | | | | | | | |
| Disease Or Pest Resistance (Susceptible) | 343 | 35.86 | 351 | 32.19 | 703 | 34.85 | 3.67 | 0.31 | 1.01 | 0.75 |
| Drought Tolerance (Susceptible) | 343 | 16.03 | 351 | 14.53 | 703 | 14.79 | 1.51 | 0.58 | 1.24 | 0.60 |
| Affected by any pests: Yes/No? | 335 | 74.63 | 349 | 80.80 | 694 | 70.32 | -6.18 | 0.34 | 4.31 | 0.42 |
| Affected by any diseases: Yes/No? | 335 | 69.25 | 349 | 84.24 | 694 | 72.48 | -14.99 | 0.01*** | -3.22 | 0.51 |

CGIAR-rel is the combination of Improved and Elite Clone varieties. Landrace is the combination of Landrace and Released Landrace varieties.

Table 13: Share of HH with CG Varieties - HH Level

| | Freq | Mean |
|---|---|---|
| IITA-TMS-IBA120067 | 11 | 0.05 |
| NAROCAS 1 | 90 | 0.40 |
| NASE 1 | 1 | 0.00 |
| NASE 13 | 8 | 0.04 |
| NASE 19 | 83 | 0.37 |
| NASE 3 | 34 | 0.15 |
| NASE 12 | 15 | 0.07 |
| TMEB14 | 11 | 0.05 |
| Observations | 227 | |

Table 14: Distribution of Year of Release - Barcode Level

| | All Sample | | | CGIAR | | |
|---|---|---|---|---|---|---|
| | Freq | Mean | SD | Freq | Mean | SD |
| Year of release | | 2005.30 | 15.85 | | 2010.88 | 7.89 |
| Year of release == 1970 | 49 | 0.14 | 0.34 | 0 | 0.00 | 0.00 |
| Year of release == 1994 | 45 | 0.13 | 0.33 | 45 | 0.15 | 0.35 |
| Year of release == 2000 | 20 | 0.06 | 0.23 | 20 | 0.06 | 0.25 |
| Year of release == 2011 | 8 | 0.02 | 0.15 | 8 | 0.03 | 0.16 |
| Year of release == 2015 | 237 | 0.66 | 0.47 | 237 | 0.76 | 0.42 |
| Observations | 359 | | | 310 | | |

# 3 Banana

Table 15: Farmers' Perception of the Variety - Variety Level

| | N | Sum | Mean | SD |
|---|---|---|---|---|
| Improved | 1073 | 106 | 0.099 | 0.299 |
| Traditional | 1073 | 1012 | 0.943 | 0.232 |
| Don't Know | 1073 | 20 | 0.019 | 0.135 |

Table 16: Summary of UNOMA Covariates Among Different Varieties - Barcode Level

| | Matooke | | Non-matooke | | Unassigned | |
|---|---|---|---|---|---|---|
| | Mean(%) | N | Mean(%) | N | Mean(%) | N |
| For planting material obtained from own farm, for how many planting seasons this variety has been recycled since acquired from outside | 12.42 | 986 | 6.11*** | 160 | 7.88 | 16 |
| Destiny Of Harvest Of This Variety? Sell | 32.50 | 1763 | 40.25*** | 323 | 38.78 | 49 |
| Source of the Planting Material: NAADS | 0.28 | 1777 | 1.23*** | 324 | 8.16*** | 49 |
| Source of the Planting Material: Gov'ment/OWC/MP | 0.17 | 1777 | 2.78*** | 324 | 2.04*** | 49 |
| Source of the Planting Material: Farmer Group/Local Multiplier | 2.59 | 1777 | 3.70 | 324 | 0.00 | 49 |
| Source of the Planting Material: Another Farmer (Relative/Neighbor) | 93.58 | 1777 | 90.12** | 324 | 87.76 | 49 |
| Type of variety: Improved | 6.81 | 1777 | 9.88* | 324 | 10.20 | 49 |
| Self-reported name same as the reference library name | 0.00 | 1777 | 0.06*** | 324 | 0.00 | 49 |
| Like About This Variety: Yield (High) | 60.41 | 1763 | 48.29*** | 321 | 46.94* | 49 |
| Like About This Variety: Taste (Good) | 75.16 | 1763 | 63.24*** | 321 | 79.59 | 49 |
| Like About This Variety: Nutrition (General) | 9.98 | 1763 | 18.38*** | 321 | 14.29 | 49 |
| Like About This Variety: Disease Or Pest Resistance (Good) | 9.53 | 1763 | 12.77* | 321 | 10.20 | 49 |
| Like About This Variety: Time To Maturation | 17.81 | 1763 | 5.30*** | 321 | 12.24 | 49 |
| Dislikes About This Variety: Yield (Low) | 10.49 | 1763 | 10.73 | 317 | 10.20 | 49 |
| Dislikes About This Variety: Disease Or Pest Resistance (Susceptible) | 33.35 | 1763 | 30.60 | 317 | 26.53 | 49 |
| Dislikes About This Variety: Time To Maturation (Long) | 19.80 | 1763 | 24.29** | 317 | 32.65* | 49 |
| Dislikes About This Variety: Drought Tolerance (Susceptible) | 21.21 | 1763 | 17.67 | 317 | 20.41 | 49 |
| Affected by any pests: Yes = 1 | 23.93 | 1003 | 31.86* | 226 | 50.00** | 10 |
| Affected by any diseases: Yes/No? | 43.47 | 1003 | 37.61 | 226 | 30.00 | 10 |

* p <0.1, ** p < 0.05, *** p <0.01. The variety Sukali Ndizi is reported as Ndizi by the farmers. The stars indicate the difference of each covariates for the column varieties with the Matooke variety.

# 4 Beans

Table 17: Distribution of Year of Release Beans - Barcode Level

| | All sample | | | CGIAR varieties | | |
|---|---|---|---|---|---|---|
| | Freq | Mean% | SD | Freq | Mean% | SD |
| Year of release | | 2009.95 | 5.54 | | 2010.42 | 6.19 |
| 1994 | 2 | 0.01 | 0.11 | 2 | 0.02 | 0.13 |
| 1995 | 9 | 0.06 | 0.24 | 9 | 0.08 | 0.27 |
| 1999 | 4 | 0.03 | 0.16 | 4 | 0.03 | 0.18 |
| 2003 | 4 | 0.03 | 0.16 | 4 | 0.03 | 0.18 |
| 2006 | 14 | 0.09 | 0.29 | 0 | 0.00 | 0.00 |
| 2010 | 30 | 0.19 | 0.40 | 7 | 0.06 | 0.24 |
| 2012 | 66 | 0.43 | 0.50 | 66 | 0.56 | 0.50 |
| 2016 | 23 | 0.15 | 0.36 | 23 | 0.20 | 0.40 |
| 2019 | 2 | 0.01 | 0.11 | 2 | 0.02 | 0.13 |
| Observations | 154 | | | 117 | | |

Table 18: CG Varieties Grown by Households - HH Level

| HH with at least 1 Variety of: | N | Sum | Mean | SD |
|---|---|---|---|---|
| K132 | 97 | 1 | 0.010 | 0.102 |
| NABE1 | 97 | 5 | 0.052 | 0.222 |
| NABE10C | 97 | 3 | 0.031 | 0.174 |
| NABE12C | 97 | 4 | 0.041 | 0.200 |
| NABE16 | 97 | 7 | 0.072 | 0.260 |
| NABE17 | 97 | 6 | 0.062 | 0.242 |
| NABE2 | 97 | 3 | 0.031 | 0.174 |
| NABE20 | 97 | 40 | 0.412 | 0.495 |
| NABE21 | 97 | 3 | 0.031 | 0.174 |
| NABE23 | 97 | 13 | 0.134 | 0.342 |
| NABE6 | 97 | 1 | 0.010 | 0.102 |
| NAROBEAN1 | 97 | 1 | 0.010 | 0.102 |
| NAROBEAN2 | 97 | 10 | 0.103 | 0.306 |
| NAROBEAN4C | 97 | 5 | 0.052 | 0.222 |
| NAROBEAN5C | 97 | 5 | 0.052 | 0.222 |
| NAROBEAN6 | 97 | 1 | 0.010 | 0.102 |
| NAROBEAN7 | 97 | 1 | 0.010 | 0.102 |

Table 19: Distribution of Unique Varieties Beans - HH Level

| | Sum | Mean% |
|---|---|---|
| Unique Varieties | | 1.43 |
| 1 Unique Variety in HH | 193 | 68.93 |
| 2 Unique Varieties in HH | 65 | 23.21 |
| 3 Unique Varieties in HH | 14 | 5.00 |
| 4 Unique Varieties in HH | 6 | 2.14 |
| 5 Unique Varieties in HH | 1 | 0.36 |
| 6 Unique Varieties in HH | 1 | 0.36 |
| Observations | 280 | |

Sample is limited to the Households with Assigned varieties.

Table 20: Farmers' Perception of Variety vs Genetic Identity - Barcode Level

| Farmers' Perception of Variety | Released Varieties | Landrace Varieties | Unmatched Varieties |
|---|---|---|---|
| DON'T KNOW | 2 | 8 | 5 |
| TRADITIONAL | 112 | 224 | 149 |
| IMPROVED | 40 | 52 | 51 |
| Total | 154 | 284 | 205 |

Table 21: Frequency of All Varieties

|  | Mean | Sum | N |
|---|---|---|---|
| K132 | 0.00 | 1 | 280 |
| Masindi Yellow Short | 0.01 | 2 | 280 |
| NABE1 | 0.02 | 5 | 280 |
| NABE10C | 0.01 | 3 | 280 |
| NABE12C | 0.01 | 4 | 280 |
| NABE13 | 0.05 | 14 | 280 |
| NABE15 | 0.07 | 19 | 280 |
| NABE16 | 0.03 | 7 | 280 |
| NABE17 | 0.02 | 6 | 280 |
| NABE2 | 0.01 | 3 | 280 |
| NABE20 | 0.14 | 40 | 280 |
| NABE21 | 0.01 | 3 | 280 |
| NABE23 | 0.05 | 13 | 280 |
| NABE6 | 0.00 | 1 | 280 |
| NAROBEAN1 | 0.00 | 1 | 280 |
| NAROBEAN2 | 0.04 | 10 | 280 |
| NAROBEAN4C | 0.02 | 5 | 280 |
| NAROBEAN5C | 0.02 | 5 | 280 |
| NAROBEAN6 | 0.00 | 1 | 280 |
| NAROBEAN7 | 0.00 | 1 | 280 |
| UGD.001 | 0.09 | 26 | 280 |
| UGD.003 | 0.00 | 1 | 280 |
| UGD.005 | 0.00 | 1 | 280 |
| UGD.007 | 0.05 | 15 | 280 |
| UGK10 | 0.01 | 2 | 280 |
| UGK107 | 0.00 | 1 | 280 |
| UGK119 | 0.01 | 3 | 280 |
| UGK121 | 0.00 | 1 | 280 |
| UGK122 | 0.01 | 3 | 280 |
| UGK129 | 0.01 | 2 | 280 |
| UGK130 | 0.01 | 3 | 280 |
| UGK139 | 0.00 | 1 | 280 |
| UGK145 | 0.01 | 3 | 280 |
| UGK166 | 0.04 | 11 | 280 |
| UGK22 | 0.01 | 3 | 280 |
| UGK24 | 0.01 | 3 | 280 |
| UGK28 | 0.03 | 7 | 280 |
| UGK44 | 0.00 | 1 | 280 |
| UGK59 | 0.03 | 8 | 280 |
| UGK71 | 0.12 | 34 | 280 |
| UGK99 | 0.04 | 10 | 280 |
| UNGB-133 | 0.03 | 7 | 280 |
| UNGB-149 | 0.00 | 1 | 280 |
| UNGB-1582 | 0.01 | 3 | 280 |
| UNGB-2443 | 0.00 | 1 | 280 |
| UNGB-361 | 0.00 | 1 | 280 |
| UNGB-3740 | 0.00 | 1 | 280 |
| UNGB-3861 | 0.00 | 1 | 280 |
| UNGB-3925 | 0.00 | 1 | 280 |
| UNGB-4170 | 0.00 | 1 | 280 |
| UNGB-4394 | 0.04 | 10 | 280 |
| UNGB-4399 | 0.01 | 2 | 280 |
| UNGB-4427 | 0.02 | 5 | 280 |
| UNGB-4428 | 0.03 | 7 | 280 |
| UNGB-4429 | 0.02 | 6 | 280 |
| UNGB-4431 | 0.05 | 13 | 280 |
| UNGB-4972 | 0.01 | 2 | 280 |
| UNGB-5049 | 0.00 | 1 | 280 |
| UNGB-5079 | 0.02 | 6 | 280 |
| UNGB-5142 | 0.00 | 1 | 280 |
| UNGB-5737 | 0.00 | 1 | 280 |
| UNGB-5741 | 0.12 | 34 | 280 |
| UNGB-5756 | 0.01 | 4 | 280 |
| UNGB-5763 | 0.00 | 1 | 280 |
| UNGB-741 | 0.00 | 1 | 280 |
| UNGB-770 | 0.01 | 2 | 280 |
| UNGB-857 | 0.01 | 4 | 280 |

Table 22: Comparison of HH Covariates between Different Genetic Identities - Barcode Level

| | CGIAR | | Released | | Landrace | | Unmatched | | (1)-(2) | | (1)-(3) | | (1)-(4) | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | N | Mean | N | Mean | N | Mean | N | Mean | Diff. | P-val | Diff. | P-val | Diff. | P-val |
| **Destiny Of Harvest** | | | | | | | | | | | | | | |
| Sell | 117 | 0.56 | 154 | 0.56 | 284 | 0.55 | 205 | 0.53 | 0.02 | 0.80 | 0.01 | 0.84 | 0.04 | 0.52 |
| All HH | 117 | 0.97 | 154 | 0.94 | 284 | 0.92 | 205 | 0.90 | 0.16** | 0.02 | 0.05** | 0.02 | 0.07*** | 0.00 |
| Children | 117 | 0.01 | 154 | 0.01 | 284 | 0.01 | 205 | 0.00 | 0.01 | 0.32 | 0.00 | 0.88 | 0.00 | 0.71 |
| Adult Men | 117 | 0.01 | 154 | 0.01 | 284 | 0.01 | 205 | 0.01 | -0.02 | 0.52 | 0.00 | 0.88 | -0.01 | 0.61 |
| Adult Women | 117 | 0.01 | 154 | 0.01 | 284 | 0.00 | 205 | 0.00 | 0.01 | 0.32 | 0.01 | 0.59 | 0.00 | 0.71 |
| Give It Away | 117 | 0.03 | 154 | 0.03 | 284 | 0.02 | 205 | 0.02 | -0.00 | 0.96 | 0.00 | 0.95 | 0.01 | 0.73 |
| Animal Feed | 117 | 0.00 | 154 | 0.00 | 284 | 0.00 | 205 | 0.00 | 0.00 | . | 0.00 | . | 0.00 | . |
| Other | 117 | 0.06 | 154 | 0.06 | 284 | 0.09 | 205 | 0.11 | -0.02 | 0.68 | -0.03 | 0.31 | -0.05 | 0.13 |
| Don't Know | 117 | 0.00 | 154 | 0.00 | 284 | 0.00 | 205 | 0.00 | 0.00 | . | 0.00 | . | 0.00 | . |
| **Like About This Variety** | | | | | | | | | | | | | | |
| Yield (High) | 117 | 0.72 | 154 | 0.72 | 284 | 0.68 | 205 | 0.72 | -0.01 | 0.89 | 0.04 | 0.45 | 0.00 | 0.99 |
| Taste (Good) | 117 | 0.72 | 154 | 0.68 | 284 | 0.69 | 205 | 0.65 | 0.15 | 0.11 | 0.03 | 0.53 | 0.07 | 0.20 |
| Nutrition (General) | 117 | 0.19 | 154 | 0.16 | 284 | 0.15 | 205 | 0.19 | 0.11* | 0.07 | 0.04 | 0.34 | -0.00 | 0.96 |
| Nutrition (Specifies Iron or Zinc) | 117 | 0.04 | 154 | 0.03 | 284 | 0.01 | 205 | 0.01 | 0.04** | 0.02 | 0.03 | 0.15 | 0.03 | 0.17 |
| Cooking Properties | 117 | 0.18 | 154 | 0.15 | 284 | 0.14 | 205 | 0.17 | 0.13** | 0.02 | 0.04 | 0.31 | 0.01 | 0.84 |
| Disease Or Pest Resistance (Good) | 117 | 0.08 | 154 | 0.08 | 284 | 0.06 | 205 | 0.07 | -0.00 | 0.94 | 0.01 | 0.64 | 0.01 | 0.78 |
| Time To Maturation | 117 | 0.14 | 154 | 0.15 | 284 | 0.13 | 205 | 0.14 | -0.05 | 0.47 | 0.01 | 0.86 | 0.00 | 1.00 |
| Drought Tolerance (Good) | 117 | 0.07 | 154 | 0.10 | 284 | 0.11 | 205 | 0.07 | -0.15** | 0.05 | -0.04 | 0.14 | -0.00 | 0.87 |
| Good All-Round | 117 | 0.05 | 154 | 0.04 | 284 | 0.04 | 205 | 0.03 | 0.05** | 0.01 | 0.02 | 0.49 | 0.02 | 0.35 |
| Market (Good) | 117 | 0.13 | 154 | 0.19 | 284 | 0.14 | 205 | 0.11 | -0.25*** | 0.01 | -0.01 | 0.81 | 0.02 | 0.67 |
| Crop Management Aspects | 117 | 0.02 | 154 | 0.03 | 284 | 0.04 | 205 | 0.02 | -0.06 | 0.18 | -0.02 | 0.27 | -0.01 | 0.65 |
| Storage (Keeps Well) | 117 | 0.02 | 154 | 0.01 | 284 | 0.02 | 205 | 0.03 | 0.02 | 0.16 | -0.00 | 0.97 | -0.01 | 0.47 |
| Other(Specify) | 117 | 0.03 | 154 | 0.03 | 284 | 0.02 | 205 | 0.00 | -0.00 | 0.96 | 0.00 | 0.79 | 0.03* | 0.08 |
| **Dislikes About This Variety** | | | | | | | | | | | | | | |
| Yield (Low) | 117 | 0.02 | 154 | 0.02 | 284 | 0.04 | 205 | 0.03 | -0.01 | 0.74 | -0.02 | 0.19 | -0.02 | 0.33 |
| Taste (Not Good) | 117 | 0.01 | 154 | 0.05 | 284 | 0.06 | 205 | 0.04 | -0.15** | 0.02 | -0.05*** | 0.00 | -0.04** | 0.04 |
| Not Nutritious | 117 | 0.01 | 154 | 0.01 | 284 | 0.01 | 205 | 0.03 | -0.02 | 0.52 | -0.01 | 0.62 | -0.02 | 0.16 |
| Doesn't Contain Extra Zinc or Iron | 117 | 0.01 | 154 | 0.01 | 284 | 0.00 | 205 | 0.02 | 0.01 | 0.32 | 0.01 | 0.59 | -0.01 | 0.40 |
| Cooking Properties (Bad) | 117 | 0.05 | 154 | 0.08 | 284 | 0.06 | 205 | 0.08 | -0.11* | 0.09 | -0.01 | 0.84 | -0.03 | 0.34 |
| Disease Pest Resist. (Susceptible) | 117 | 0.33 | 154 | 0.29 | 284 | 0.28 | 205 | 0.28 | 0.17** | 0.03 | 0.05 | 0.32 | 0.06 | 0.31 |
| Time To Maturation (Long) | 117 | 0.17 | 154 | 0.16 | 284 | 0.12 | 205 | 0.16 | 0.06 | 0.32 | 0.05 | 0.24 | 0.01 | 0.73 |
| Drought Tolerance (Susceptible) | 117 | 0.25 | 154 | 0.23 | 284 | 0.26 | 205 | 0.19 | 0.06 | 0.45 | -0.02 | 0.74 | 0.06 | 0.20 |
| Not Good All-Round | 117 | 0.03 | 154 | 0.03 | 284 | 0.05 | 205 | 0.05 | -0.03 | 0.49 | -0.02 | 0.30 | -0.02 | 0.27 |
| Market (Poor) | 117 | 0.14 | 154 | 0.14 | 284 | 0.13 | 205 | 0.10 | 0.00 | 0.98 | 0.01 | 0.79 | 0.03 | 0.37 |
| Crop Management Aspects | 117 | 0.10 | 154 | 0.14 | 284 | 0.06 | 205 | 0.15 | -0.14* | 0.07 | 0.05 | 0.14 | -0.04 | 0.24 |
| Storage (Does Not Keep Well) | 117 | 0.11 | 154 | 0.11 | 284 | 0.10 | 205 | 0.08 | 0.00 | 0.96 | 0.02 | 0.64 | 0.03 | 0.34 |
| Other(Specify) | 117 | 0.13 | 154 | 0.12 | 284 | 0.19 | 205 | 0.16 | 0.05 | 0.40 | -0.06 | 0.11 | -0.03 | 0.49 |
| **Source Of Planting Material:** | | | | | | | | | | | | | | |
| NGO/Relief | 117 | 0.00 | 154 | 0.01 | 284 | 0.00 | 205 | 0.00 | -0.03 | 0.32 | -0.00 | 0.32 | 0.00 | . |
| NAADS | 117 | 0.01 | 154 | 0.02 | 284 | 0.03 | 205 | 0.04 | -0.05 | 0.25 | -0.02 | 0.13 | -0.04** | 0.04 |
| Gov'ment/OWC/MP | 117 | 0.00 | 154 | 0.01 | 284 | 0.01 | 205 | 0.01 | -0.03 | 0.32 | -0.01* | 0.08 | -0.01* | 0.08 |
| Farmer Group/Local Multiplier | 117 | 0.07 | 154 | 0.09 | 284 | 0.04 | 205 | 0.03 | -0.09 | 0.16 | 0.03 | 0.20 | 0.04 | 0.14 |
| Research Centre | 117 | 0.01 | 154 | 0.01 | 284 | 0.00 | 205 | 0.00 | 0.01 | 0.32 | 0.01 | 0.59 | 0.00 | 0.71 |
| Another Farmer (Relative/Neighbor) | 117 | 0.45 | 154 | 0.43 | 284 | 0.45 | 205 | 0.45 | 0.10 | 0.27 | 0.01 | 0.92 | 0.00 | 0.94 |
| Market | 117 | 0.44 | 154 | 0.44 | 284 | 0.47 | 205 | 0.46 | 0.04 | 0.68 | -0.03 | 0.62 | -0.01 | 0.81 |
| Don't Know | 117 | 0.02 | 154 | 0.01 | 284 | 0.01 | 205 | 0.01 | 0.02 | 0.16 | 0.01 | 0.63 | 0.00 | 0.87 |
| NAADS or Gov'ment/OWC/MP | 117 | 0.00 | 154 | 0.00 | 284 | 0.00 | 205 | 0.00 | 0.00 | . | 0.00 | . | 0.00 | . |
| **Payment of Planting Material:** | | | | | | | | | | | | | | |
| Cash Purchase | 117 | 0.62 | 154 | 0.60 | 284 | 0.57 | 205 | 0.60 | 0.05 | 0.61 | 0.05 | 0.37 | 0.02 | 0.79 |
| Gift | 117 | 0.27 | 154 | 0.31 | 284 | 0.37 | 205 | 0.25 | -0.13 | 0.16 | -0.09* | 0.07 | 0.02 | 0.70 |
| Vouchers | 117 | 0.00 | 154 | 0.00 | 284 | 0.00 | 205 | 0.00 | 0.00 | . | 0.00 | . | 0.00 | . |
| In-kind Payment | 117 | 0.06 | 154 | 0.05 | 284 | 0.01 | 205 | 0.09 | 0.06*** | 0.01 | 0.05** | 0.05 | -0.03 | 0.35 |
| Exchange | 117 | 0.03 | 154 | 0.03 | 284 | 0.04 | 205 | 0.04 | 0.01 | 0.82 | -0.01 | 0.70 | -0.00 | 0.82 |
| Other (Specify) | 117 | 0.00 | 154 | 0.00 | 284 | 0.00 | 205 | 0.00 | 0.00 | . | 0.00 | . | -0.00 | 0.32 |
| **What type of variety is this:** | | | | | | | | | | | | | | |
| Improved | 117 | 0.24 | 154 | 0.26 | 284 | 0.18 | 205 | 0.25 | -0.09 | 0.34 | 0.06 | 0.22 | -0.01 | 0.85 |
| Traditional | 117 | 0.74 | 154 | 0.73 | 284 | 0.79 | 205 | 0.73 | 0.07 | 0.44 | -0.05 | 0.34 | 0.02 | 0.74 |
| Don't Know | 117 | 0.02 | 154 | 0.01 | 284 | 0.03 | 205 | 0.02 | 0.02 | 0.16 | -0.01 | 0.48 | -0.01 | 0.65 |
| Type of Improved seed/planting material used: Certified+ | 113 | 0.05 | 144 | 0.06 | 267 | 0.03 | 196 | 0.03 | -0.01 | 0.82 | 0.02 | 0.42 | 0.02 | 0.36 |

In (1)-(2), the variable for comparison is defined by assigning value 1 if Released & 0 if CGIAR, and similarly in (1)-(3) and (1)-(4).
+ In 'type of improved seed/planting material used: Certified' variable, the variable takes value of 0 for all observations for which the household declares that the bean is not improved.

Table 23: Comparison of UNOMA Diseases & Pests Between Different Genetic Identities - Barcode Level

| | CGIAR | | Released | | Landrace | | Unmatched | | (1)-(2) | | (1)-(3) | | (1)-(4) | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | N | Mean | N | Mean | N | Mean | N | Mean | Diff. | P-val | Diff. | P-val | Diff. | P-val |
| **PESTS:** | | | | | | | | | | | | | | |
| **Affected by any pests:** Yes/No? | 117 | 0.44 | 154 | 0.43 | 283 | 0.46 | 205 | 0.40 | 0.03 | 0.75 | -0.02 | 0.72 | 0.04 | 0.48 |
| **Might affect the crop in future:** | | | | | | | | | | | | | | |
| Cutworms | 66 | 0.26 | 88 | 0.28 | 154 | 0.27 | 124 | 0.31 | -0.11 | 0.38 | -0.02 | 0.82 | -0.06 | 0.41 |
| Bean fly (Bean stem maggot) | 66 | 0.14 | 88 | 0.11 | 154 | 0.08 | 124 | 0.16 | 0.09 | 0.15 | 0.05 | 0.28 | -0.02 | 0.64 |
| Flower Thrips | 66 | 0.05 | 88 | 0.05 | 154 | 0.08 | 124 | 0.06 | 0.00 | 1.00 | -0.03 | 0.34 | -0.02 | 0.58 |
| Aphids | 66 | 0.30 | 88 | 0.30 | 154 | 0.29 | 124 | 0.25 | 0.03 | 0.79 | 0.01 | 0.87 | 0.05 | 0.44 |
| Flower beetles | 66 | 0.09 | 88 | 0.07 | 154 | 0.06 | 124 | 0.06 | 0.09** | 0.01 | 0.03 | 0.42 | 0.03 | 0.53 |
| Foliage beetles | 66 | 0.03 | 88 | 0.05 | 154 | 0.03 | 124 | 0.02 | -0.06 | 0.37 | -0.00 | 0.93 | 0.01 | 0.56 |
| Pod borers | 66 | 0.11 | 88 | 0.11 | 154 | 0.12 | 124 | 0.07 | -0.03 | 0.72 | -0.02 | 0.71 | 0.03 | 0.46 |
| Pod sucking bugs | 66 | 0.06 | 88 | 0.06 | 154 | 0.06 | 124 | 0.05 | 0.02 | 0.78 | 0.00 | 0.95 | 0.01 | 0.73 |
| **Currently affects plot production:** | | | | | | | | | | | | | | |
| Cutworms | 51 | 0.49 | 66 | 0.48 | 129 | 0.40 | 81 | 0.42 | 0.02 | 0.88 | 0.09 | 0.30 | 0.07 | 0.43 |
| Bean fly (Bean stem maggot) | 51 | 0.14 | 66 | 0.14 | 129 | 0.22 | 81 | 0.11 | 0.00 | 0.97 | -0.09 | 0.15 | 0.03 | 0.66 |
| Flower Thrips | 51 | 0.04 | 66 | 0.03 | 129 | 0.08 | 81 | 0.04 | 0.04 | 0.16 | -0.04 | 0.29 | 0.00 | 0.95 |
| Aphids | 51 | 0.41 | 66 | 0.39 | 129 | 0.34 | 81 | 0.47 | 0.08 | 0.59 | 0.07 | 0.39 | -0.06 | 0.52 |
| Flower beetles | 51 | 0.20 | 66 | 0.18 | 129 | 0.12 | 81 | 0.14 | 0.06 | 0.56 | 0.07 | 0.26 | 0.06 | 0.38 |
| Foliage beetles | 51 | 0.04 | 66 | 0.05 | 129 | 0.09 | 81 | 0.04 | -0.03 | 0.71 | -0.05 | 0.15 | 0.00 | 0.95 |
| Pod borers | 51 | 0.10 | 66 | 0.11 | 129 | 0.14 | 81 | 0.16 | -0.04 | 0.73 | -0.04 | 0.43 | -0.06 | 0.29 |
| Pod sucking bugs | 51 | 0.06 | 66 | 0.05 | 129 | 0.05 | 81 | 0.06 | 0.06* | 0.08 | 0.01 | 0.75 | -0.00 | 0.95 |
| How many weeks after planting the pest present was noticed? | 51 | 4.20 | 66 | 4.18 | 129 | 4.11 | 81 | 3.94 | 0.06 | 0.91 | 0.09 | 0.76 | 0.26 | 0.39 |
| **DISEASES:** | | | | | | | | | | | | | | |
| **Affected by any diseases:** Yes/No? | 117 | 0.43 | 154 | 0.43 | 283 | 0.44 | 205 | 0.43 | -0.01 | 0.96 | -0.01 | 0.84 | -0.01 | 0.91 |
| **Might affect the crop in future:** | | | | | | | | | | | | | | |
| Common blight | 67 | 0.42 | 88 | 0.50 | 159 | 0.51 | 116 | 0.47 | -0.34*** | 0.00 | -0.09 | 0.21 | -0.05 | 0.53 |
| Halo blight | 67 | 0.27 | 88 | 0.26 | 159 | 0.33 | 116 | 0.26 | 0.03 | 0.78 | -0.06 | 0.33 | 0.01 | 0.88 |
| Bean Common Mosaic Virus (BCMV) | 67 | 0.09 | 88 | 0.08 | 159 | 0.04 | 116 | 0.05 | 0.04 | 0.48 | 0.05 | 0.24 | 0.04 | 0.36 |
| Bean Anthracnose | 67 | 0.15 | 88 | 0.11 | 159 | 0.15 | 116 | 0.19 | 0.15*** | 0.00 | -0.00 | 0.97 | -0.04 | 0.48 |
| Bean rust | 67 | 0.18 | 88 | 0.15 | 159 | 0.14 | 116 | 0.22 | 0.13* | 0.05 | 0.04 | 0.46 | -0.05 | 0.46 |
| Fusarium Wilt/ Fusarium Yellows | 67 | 0.06 | 88 | 0.07 | 159 | 0.06 | 116 | 0.02 | -0.04 | 0.62 | -0.00 | 0.93 | 0.04 | 0.18 |
| Fusarium root rot | 67 | 0.01 | 88 | 0.01 | 159 | 0.03 | 116 | 0.04 | 0.01 | 0.32 | -0.01 | 0.60 | -0.03 | 0.24 |
| Pythium | 67 | 0.00 | 88 | 0.00 | 159 | 0.00 | 116 | 0.00 | 0.00 | . | 0.00 | . | 0.00 | . |
| Sclerotium Root Rot (white mold) | 67 | 0.00 | 88 | 0.00 | 159 | 0.01 | 116 | 0.00 | 0.00 | . | -0.01 | 0.32 | 0.00 | . |
| **Currently affects plot production:** | | | | | | | | | | | | | | |
| Common blight | 50 | 0.62 | 66 | 0.64 | 124 | 0.57 | 89 | 0.66 | -0.07 | 0.63 | 0.05 | 0.57 | -0.04 | 0.62 |
| Halo blight | 50 | 0.40 | 66 | 0.44 | 124 | 0.44 | 89 | 0.49 | -0.16 | 0.28 | -0.04 | 0.67 | -0.09 | 0.29 |
| Bean Common Mosaic Virus (BCMV) | 50 | 0.14 | 66 | 0.12 | 124 | 0.11 | 89 | 0.15 | 0.08 | 0.34 | 0.03 | 0.64 | -0.01 | 0.92 |
| Bean Anthracnose | 50 | 0.06 | 66 | 0.05 | 124 | 0.12 | 89 | 0.09 | 0.06* | 0.08 | -0.06 | 0.18 | -0.03 | 0.51 |
| Bean rust | 50 | 0.28 | 66 | 0.21 | 124 | 0.19 | 89 | 0.12 | 0.28*** | 0.00 | 0.09 | 0.24 | 0.16** | 0.04 |
| Fusarium Wilt/ Fusarium Yellows | 50 | 0.04 | 66 | 0.03 | 124 | 0.10 | 89 | 0.10 | 0.04 | 0.16 | -0.06 | 0.14 | -0.06 | 0.15 |
| Fusarium root rot | 50 | 0.04 | 66 | 0.03 | 124 | 0.04 | 89 | 0.03 | 0.04 | 0.16 | -0.00 | 0.99 | 0.01 | 0.85 |
| Pythium | 50 | 0.10 | 66 | 0.09 | 124 | 0.12 | 89 | 0.10 | 0.04 | 0.62 | -0.02 | 0.69 | -0.00 | 0.98 |
| Sclerotium Root Rot (white mold) | 50 | 0.02 | 66 | 0.05 | 124 | 0.02 | 89 | 0.01 | -0.10 | 0.25 | 0.00 | 0.87 | 0.01 | 0.70 |
| How many weeks after planting disease present was noticed? | 50 | 4.66 | 66 | 4.52 | 124 | 4.59 | 89 | 4.76 | 0.60 | 0.30 | 0.07 | 0.85 | -0.10 | 0.79 |

* p < .10, ** p < .05, p < *** .01. In (1)-(2), the variable for comparison is defined by assigning value 1 if Released & 0 if CGIAR, and similarly in (1)-(3) and (1)-(4).

# 5 Sweetpotato

Table 24: CG Varieties Grown by Households - HH Level

| HH with at least 1 Variety of: | N | Sum | Mean | SD |
|---|---|---|---|---|
| KAKAMEGA | 41 | 1 | 0.024 | 0.156 |
| NAROSPOT 1 | 41 | 32 | 0.780 | 0.419 |
| NAROSPOT 12O | 41 | 1 | 0.024 | 0.156 |
| NASPOT 8 | 41 | 7 | 0.171 | 0.381 |

Table 25: Distribution of Unique Varieties in Sweetpotato - HH Level

| | Sum | Mean | SD |
|---|---|---|---|
| Average number of unique varieties in HH | | 1.70 | 0.736 |
| Total unique varieties in HH == 1 | 269 | 0.46 | 0.498 |
| Total unique varieties in HH == 2 | 237 | 0.40 | 0.491 |
| Total unique varieties in HH == 3 | 79 | 0.13 | 0.341 |
| Total unique varieties in HH == 4 | 4 | 0.01 | 0.082 |
| Total unique varieties in HH == 4 | 1 | 0.00 | 0.041 |
| Total HH | 590 | | |

Includes unidentified NA as 1 unique varieties.

Table 26: Distribution of Samples Collected - HH Level

| | Sum | Mean | SD |
|---|---|---|---|
| Number of Samples Collected | 1644 | 2.09 | 1.040 |
| HH with Total number of Samples Collected == 1 | 254 | 0.32 | 0.468 |
| HH with Total number of Samples Collected == 2 | 289 | 0.37 | 0.482 |
| HH with Total number of Samples Collected == 3 | 204 | 0.26 | 0.438 |
| HH with Total number of Samples Collected == 4 | 16 | 0.02 | 0.141 |
| HH with Total number of Samples Collected == 5 | 10 | 0.01 | 0.112 |
| HH with Total number of Samples Collected == 6 | 13 | 0.02 | 0.128 |
| HH with Total number of Samples Collected == 8 | 1 | 0.00 | 0.036 |
| Observations | 787 | | |

Table 27: Intra-plot Heterogeneity Limited to Even Barcode Samples - Plot Level

| | N | Sum | Mean | SD |
|---|---|---|---|---|
| Total Barcodes = 2 × Distinct Genetic Varieties | 245 | 59 | 0.241 | 0.428 |
| Intentionally Planted Single Varieties | 245 | 58 | 0.237 | 0.426 |
| Intentionally Planted Multiple & Dups. Matched | 245 | 0 | 0.000 | 0.000 |
| Intentionally Planted Multiple & Dups. Not Matched | 245 | 1 | 0.004 | 0.064 |
| Unintentionally Planted Single Varieties | 245 | 0 | 0.000 | 0.000 |
| Unintentionally Planted Multiple Varieties | 245 | 12 | 0.049 | 0.216 |

There are 241 HHs and 245 plots with even number of barcodes. In 245 plots, 59 plots have matches where the total number of barcodes is twice the number of genetic identities of the sweetpotato present in the plot. Duplicates matched considered for the farmers' self-reported variety names.

Table 28: Distribution of Unique Varieties in Households - HH Level

| | Sum | Mean | SD |
|---|---|---|---|
| Unique varieties in HH | | 1.43 | 0.602 |
| Total unique varieties in HH == 1 | 268 | 0.63 | 0.484 |
| Total unique varieties in HH == 2 | 135 | 0.32 | 0.466 |
| Total unique varieties in HH == 3 | 22 | 0.05 | 0.222 |
| Total unique varieties in HH == 4 | 1 | 0.00 | 0.048 |
| Observations | 426 | | |

The sample is limited to the identified households that are assigned, removing all the NA varieties.

Table 29: Farmers' Perception of the Variety vs Genetic Identity - Barcode Level

| Farmers' Perception of the Variety | Released | Landraces | Unassigned |
|---|---|---|---|
| DON'T KNOW | 3 | 14 | 13 |
| TRADITIONAL | 37 | 446 | 490 |
| IMPROVED | 21 | 109 | 88 |
| | 61 | 569 | 591 |

Table 30: Distribution of Year of Release Only Among CG Varieties - Barcode Level

| | Released Varieties | | | CG Varieties | | |
|---|---|---|---|---|---|---|
| | Freq | Mean | SD | Freq | Mean | SD |
| Year of release | | 2009.25 | 9.250 | | 2014.93 | 4.146 |
| 1995 | 11 | 0.18 | 0.388 | 0 | 0.00 | 0.000 |
| 1999 | 8 | 0.13 | 0.340 | 0 | 0.00 | 0.000 |
| 2004 | 1 | 0.02 | 0.128 | 1 | 0.02 | 0.154 |
| 2007 | 7 | 0.11 | 0.321 | 7 | 0.17 | 0.377 |
| 2013 | 1 | 0.02 | 0.128 | 1 | 0.02 | 0.154 |
| 2017 | 33 | 0.54 | 0.502 | 33 | 0.79 | 0.415 |
| Observations | 61 | | | 42 | | |

The sample is limited only among identified barcode samples.

Table 31: Summary of UNOMA Variety Covariates Among Different Varieties - Barcode Level

| | Released | | Landraces | | Unassigned | |
|---|---|---|---|---|---|---|
| | Mean(%) | N | Mean(%) | N | Mean(%) | N |
| For planting material obtained from own farm, for how many planting seasons this variety has been recycled/replanted since it was last acquired from outside | 9.60 | 35 | 11.09 | 290 | 11.65 | 307 |
| Destiny Of Harvest Of This Variety? Sell | 19.67 | 61 | 18.10 | 569 | 18.61 | 591 |
| Source of the Planting Material: NAADS | 1.64 | 61 | 0.70 | 569 | 0.85 | 591 |
| Source of the Planting Material: Gov'ment/OWC/MP | 1.64 | 61 | 1.05 | 569 | 0.68 | 591 |
| Source of the Planting Material: Farmer Group/Local Multiplier | 3.28 | 61 | 1.41 | 569 | 2.88 | 591 |
| Source of the Planting Material: Another Farmer (Relative/Neighbor) | 86.89 | 61 | 91.74 | 569 | 90.86 | 591 |
| Type of variety: Improved | 34.43 | 61 | 19.16*** | 569 | 14.89*** | 591 |
| Self-reported name same as the reference library name | 0.00 | 61 | 0.04 | 569 | 0.00 | 591 |
| Like About This Variety: Yield (High) | 67.21 | 61 | 68.31 | 568 | 60.07 | 591 |
| Like About This Variety: Taste (Good) | 63.93 | 61 | 70.95 | 568 | 73.10 | 591 |
| Like About This Variety: Nutrition (General) | 24.59 | 61 | 14.96* | 568 | 16.07* | 591 |
| Like About This Variety: Disease Or Pest Resistance (Good) | 6.56 | 61 | 6.16 | 568 | 6.43 | 591 |
| Like About This Variety: Time To Maturation | 31.15 | 61 | 23.24 | 568 | 23.01* | 591 |
| Dislikes About This Variety: Yield (Low) | 6.56 | 61 | 6.71 | 566 | 6.61 | 590 |
| Dislikes About This Variety: Disease Or Pest Resistance (Susceptible) | 37.70 | 61 | 33.39 | 566 | 30.17 | 590 |
| Dislikes About This Variety: Time To Maturation (Long) | 3.28 | 61 | 9.19 | 566 | 12.71** | 590 |
| Dislikes About This Variety: Drought Tolerance (Susceptible) | 29.51 | 61 | 24.73 | 566 | 23.73 | 590 |
| Affected by any pests: Yes = 1 | 40.00 | 60 | 42.88 | 569 | 44.58 | 590 |
| Pests currently affecting the plot production: Sweetpotato weevils (SPW | 41.94 | 31 | 40.64 | 283 | 31.66 | 319 |
| Diseases currently affecting plot production: Leaf spot and stem blight | 25.00 | 28 | 59.19*** | 223 | 58.23*** | 249 |
| Pox Streptomyces ipomoea | 25.00 | 28 | 11.21** | 223 | 15.26 | 249 |
| Sweet potato virus disease (SPVD) | 28.57 | 28 | 18.83 | 223 | 22.49 | 249 |

The stars indicate the difference of each covariates for the column variable with the Released variable.
* p <0.1, ** p < 0.05, *** p <0.01

# 6 Groundnuts

Table 32: Year of Release Only Among CG Varieties - Barcode Level

| | All Sample | | | Released | | | CGIAR | | |
|---|---|---|---|---|---|---|---|---|---|
| | Freq | Mean | SD | Freq | Mean | SD | Freq | Mean | SD |
| Year of release | | 1996.40 | 19.42 | | 1996.47 | 19.61 | | 2008.07 | 5.20 |
| Year of release == 1966 | 33 | 0.28 | 0.45 | 32 | 0.28 | 0.45 | 0 | 0.00 | 0.00 |
| Year of release == 1998 | 16 | 0.13 | 0.34 | 16 | 0.14 | 0.35 | 16 | 0.19 | 0.39 |
| Year of release == 2002 | 4 | 0.03 | 0.18 | 0 | 0.00 | 0.00 | 4 | 0.05 | 0.21 |
| Year of release == 2010 | 8 | 0.07 | 0.25 | 8 | 0.07 | 0.26 | 8 | 0.09 | 0.29 |
| Year of release == 2011 | 58 | 0.49 | 0.50 | 58 | 0.51 | 0.50 | 58 | 0.67 | 0.47 |
| Observations | 119 | | | 114 | | | 86 | | |

The average year of Release of CG varieties among Groundnuts is 2008.

Table 33: Unique Varieties in the HH - HH Level

| | Freq | Mean% | N |
|---|---|---|---|
| Unique Varieties | | 1.39 | 101 |
| 1 Unique Variety in HH | 68 | 67.33 | 101 |
| 2 Unique Varieties in HH | 27 | 26.73 | 101 |
| 3 Unique Varieties in HH | 6 | 5.94 | 101 |

The average number of unique varieties per HH is 1.39. There are 67.33% HH with just 1 unique variety.

Table 34: Farmers' Perception vs Genetic Identity - Barcode Level

| Farmers' perception of Variety | CGIAR Varieties | Assigned, but not CG | Unassigned Varieties |
|---|---|---|---|
| DON'T KNOW | 3 | 3 | 0 |
| TRADITIONAL | 56 | 77 | 78 |
| IMPROVED | 27 | 45 | 23 |
| Total | 86 | 125 | 101 |

Table 35: Comparison of Covariates among Different Genetic Identities - Barcode Level

| | CGIAR | | Assigned, not CG | | Unassigned | | (1) - (2) | | (1)-(3) | |
|---|---|---|---|---|---|---|---|---|---|---|
| | N | Mean | N | Mean | N | Mean | Diff. | p | Diff. | p |
| Destiny Of Harvest Of This Variety? Sell | 86 | 0.43 | 125 | 0.51 | 101 | 0.25 | -0.08 | 0.24 | 0.18 | 0.01*** |
| **What Do You Like About This Variety?** | | | | | | | | | | |
| Yield (High) | 86 | 0.67 | 125 | 0.66 | 101 | 0.75 | 0.02 | 0.78 | -0.08 | 0.24 |
| Taste (Good) | 86 | 0.73 | 125 | 0.64 | 101 | 0.67 | 0.09 | 0.15 | 0.06 | 0.38 |
| Nutrition (General) | 86 | 0.30 | 125 | 0.21 | 101 | 0.32 | 0.09 | 0.13 | -0.01 | 0.83 |
| Nutrition (Specifies Iron or Zinc) | 86 | 0.00 | 125 | 0.02 | 101 | 0.04 | -0.02 | 0.16 | -0.04 | 0.04** |
| Cooking Properties | 86 | 0.41 | 125 | 0.15 | 101 | 0.16 | 0.25 | 0.00*** | 0.25 | 0.00*** |
| Disease Or Pest Resistance (Good) | 86 | 0.02 | 125 | 0.10 | 101 | 0.04 | -0.07 | 0.02** | -0.02 | 0.52 |
| Time To Maturation | 86 | 0.06 | 125 | 0.13 | 101 | 0.12 | -0.07 | 0.08* | -0.06 | 0.14 |
| Drought Tolerance (Good) | 86 | 0.13 | 125 | 0.10 | 101 | 0.13 | 0.02 | 0.60 | -0.00 | 0.99 |
| Good All-Round | 86 | 0.03 | 125 | 0.03 | 101 | 0.07 | 0.00 | 0.91 | -0.03 | 0.29 |
| Market (Good) | 86 | 0.03 | 125 | 0.11 | 101 | 0.13 | -0.08 | 0.03** | -0.09 | 0.02** |
| Crop Management Aspects | 86 | 0.03 | 125 | 0.02 | 101 | 0.03 | 0.01 | 0.65 | 0.01 | 0.84 |
| Storage (Keeps Well) | 86 | 0.00 | 125 | 0.00 | 101 | 0.00 | 0.00 | . | 0.00 | . |
| Other(Specify) | 86 | 0.00 | 125 | 0.00 | 101 | 0.00 | 0.00 | . | 0.00 | . |
| **Dislikes About This Variety?** | | | | | | | | | | |
| Yield (Low) | 86 | 0.02 | 125 | 0.04 | 101 | 0.03 | -0.02 | 0.49 | -0.01 | 0.78 |
| Taste (Not Good) | 86 | 0.00 | 125 | 0.02 | 101 | 0.03 | -0.02 | 0.08* | -0.03 | 0.08* |
| Not Nutritious | 86 | 0.00 | 125 | 0.00 | 101 | 0.02 | 0.00 | . | -0.02 | 0.16 |
| Doesn't Contain Extra Zinc or Iron | 86 | 0.00 | 125 | 0.00 | 101 | 0.00 | 0.00 | . | 0.00 | . |
| Cooking Properties (Bad) | 86 | 0.00 | 125 | 0.01 | 101 | 0.00 | -0.01 | 0.32 | 0.00 | . |
| Disease Or Pest Resistance (Susceptible) | 86 | 0.24 | 125 | 0.23 | 101 | 0.46 | 0.01 | 0.84 | -0.21 | 0.00*** |
| Time To Maturation (Long) | 86 | 0.03 | 125 | 0.10 | 101 | 0.17 | -0.06 | 0.07* | -0.13 | 0.00*** |
| Drought Tolerance (Susceptible) | 86 | 0.34 | 125 | 0.45 | 101 | 0.50 | -0.11 | 0.10 | -0.16 | 0.03** |
| Not Good All-Round | 86 | 0.00 | 125 | 0.00 | 101 | 0.10 | 0.00 | . | -0.10 | 0.00*** |
| Market (Poor) | 86 | 0.02 | 125 | 0.05 | 101 | 0.06 | -0.02 | 0.33 | -0.04 | 0.21 |
| Crop Management Aspects | 86 | 0.51 | 125 | 0.23 | 101 | 0.10 | 0.28 | 0.00*** | 0.41 | 0.00*** |
| Storage (Does Not Keep Well) | 86 | 0.00 | 125 | 0.00 | 101 | 0.02 | 0.00 | . | -0.02 | 0.16 |
| Other(Specify) | 86 | 0.05 | 125 | 0.11 | 101 | 0.04 | -0.07 | 0.07* | 0.01 | 0.82 |
| **Source Of The Planting Material**: NGO/Relief | 86 | 0.00 | 125 | 0.01 | 101 | 0.00 | -0.01 | 0.32 | 0.00 | . |
| NAADS | 86 | 0.00 | 125 | 0.00 | 101 | 0.00 | 0.00 | . | 0.00 | . |
| Gov'ment/OWC/MP | 86 | 0.00 | 125 | 0.00 | 101 | 0.00 | 0.00 | . | 0.00 | . |
| Farmer Group/Local Multiplier | 86 | 0.01 | 125 | 0.00 | 101 | 0.01 | 0.01 | 0.32 | 0.00 | 0.91 |
| Research Centre | 86 | 0.00 | 125 | 0.00 | 101 | 0.00 | 0.00 | . | 0.00 | . |
| Another Farmer (Relative/Neighbor) | 86 | 0.35 | 125 | 0.40 | 101 | 0.54 | -0.05 | 0.45 | -0.20 | 0.01*** |
| Market | 86 | 0.64 | 125 | 0.56 | 101 | 0.45 | 0.08 | 0.25 | 0.19 | 0.01*** |
| Don't Know | 86 | 0.00 | 125 | 0.03 | 101 | 0.00 | -0.03 | 0.05** | 0.00 | . |
| Affected by any pests: Yes/No? | 86 | 0.40 | 125 | 0.31 | 101 | 0.51 | 0.08 | 0.22 | -0.12 | 0.10 |
| **Pests currently affecting the plot production**: | | | | | | | | | | |
| Aphids: Aphis craccivora | 34 | 0.24 | 39 | 0.13 | 52 | 0.15 | 0.11 | 0.25 | 0.08 | 0.37 |
| Termites: Odontotermes and Microtermes spp | 34 | 0.44 | 39 | 0.18 | 52 | 0.35 | 0.26 | 0.02** | 0.10 | 0.39 |
| Affected by any diseases: Yes/No? | 86 | 0.65 | 125 | 0.45 | 101 | 0.63 | 0.20 | 0.00*** | 0.02 | 0.80 |
| **Diseases currently affecting the plot production:** | | | | | | | | | | |
| Groundnut rosette dis | 56 | 0.64 | 56 | 0.54 | 64 | 0.11 | 0.11 | 0.25 | 0.53 | 0.00*** |
| Early and late leaf spots | 56 | 0.43 | 56 | 0.46 | 64 | 0.73 | -0.04 | 0.71 | -0.31 | 0.00*** |
| Groundnut rusts | 56 | 0.30 | 56 | 0.43 | 64 | 0.28 | -0.12 | 0.17 | 0.02 | 0.79 |

The stars indicate the difference of covariates across the column specified. * $p < 0.1$, ** $p < 0.05$, *** $p < 0.01$

# Appendix T. Sample selectivity and testing for robustness through calibration

## Problem Identification: sample selectivity

The Uganda Household Integrated Survey (UHIS) has a sampling frame allowing to calculate nationally representative estimates of innovations measured at the household or community level. In addition, as explained in the main report, a targeted random subset of households was targeted for sampling of grain and leaf samples for DNA analysis of 6 crops, with the objective of estimating adoption rates of improved varieties of those crops. A number of difficulties during data collection and field implementation unfortunately led to the lack of DNA information for a relatively large share of households targeted for the DNA analysis. As a result, the sample of households for which final DNA results are available are no longer a random subset of Ugandan households. To understand the resulting selectivity of the sample, we compared different household covariates for those households for which the DNA data were successfully collected and identified with the full set of households. We find the selection correlates to observable characteristics for all 6 crops, which makes it likely that the households for whom DNA is available are also different from others along other (unobserved) characteristics. By way of illustration, Table 1 shows for maize, how the households of the full UNOMA sample differ from the selected sample for some important covariates.

Table 1: Illustration: Selection along selected covariates for Maize

| | Full Sample (Unweighted) | Selected Sample (Unweighted) | Difference |
|---|---|---|---|
| Value of assets owned by HH (UGX million) | 4.99<br>(11.16) | 7.10<br>(15.24) | 2.11***<br>(0.68) |
| HH members working in the HH farms | 1.69<br>(1.47) | 1.82<br>(1.48) | 0.13*<br>(0.07) |
| Total area of parcels owned by HH | 3.34<br>(3.44) | 3.95<br>(3.58) | 0.61***<br>(0.21) |
| Distance to nearest road (km) | 1.14<br>(1.96) | 1.32<br>(2.13) | 0.18*<br>(0.10) |
| Female share of family labor > 50% | 0.44<br>(0.50) | 0.40<br>(0.50) | -0.04*<br>(0.02) |
| HH has some Chicken | 0.48<br>(0.50) | 0.55<br>(0.50) | 0.07***<br>(0.02) |

Standard errors in parentheses.

A fuller set of differences in observable household characteristics and regions is documented in tables 14 to 19 at the end of this appendix, for each of the 6 crops. These demonstrate that the sample of households included in the DNA analysis (because DNA samples were collected for them and could be merged into the reference library) varies along a number of dimensions from the nationally-representative set of households growing the crop. Selectivity based on household characteristics differs by crop, and selectivity is also different for different regions and subregions. Selectivity on household characteristics is relatively the least important for cassava and sweet potato.

### Calibration Method and Robustness results

To evaluate to what extent the selectivity in the sample could be affecting the estimates of adoption rates, we conducted two sets of calibrations. The first set of calibrations starts from the sample of households for whom the detailed crop variety data for the targeted crops was collected in the UNOMA module, and compares this with the final subset (selected subsample) of households for whom DNA data is available. The second set of calibrations starts from the full sample of households cultivating the specific targeted crop, and compares this with the final subset (selected subsample) of households for whom DNA data is available, while only including DNA data collected in the trip and visit as per the research design explained in the main text.

Both calibrations aim to rebalance the samples by using information regarding the differences between the selected samples and the full samples. They provide a set of weights that we can apply to the adoption rate estimates, to evaluate their robustness to two alternative corrections for selectivity. While we acknowledge that this only allows testing robustness for selectivity on observables, the variability in the estimates arguably allows to gauge the importance of the non-random selection of the DNA samples.

The results of this robustness test are presented in Table 2 below. The table presents adoption rates of CGIAR varieties of each of the 6 crops with DNA using the population weights (corresponding to estimates presented in the main report) in the first column; adoption rates using the weights calibrated based on the first set of calibrations (from comparing UNOMA module households with the subsample with DNA) in the second column; and adoption rates using the weights calibrated based on the second set of calibrations (from comparing all households growing a crop with the subsample with DNA) in the third column. The third column does not include estimates for banana as the calibration model did not converge.

Results are presented separately by region, and then for the total sample in the bottom panel. Focusing on the bottom panel, results show that using the calibration weights leads to relatively small differences in the estimated rates of adoption of CGIAR varieties for each of the six crops (with differences smaller than 2.5 percentage points for all crops).

We therefore conclude that the main estimates in the report are robust to different corrections for the selectivity of the sample. As a result, while the point estimates should be interpreted with caution, the table provides some assurance on the broader conclusions regarding adoption rates.

Table 2: Adoption of CGIAR Varieties using Population Weights and Calibrated Weights

| | Mean(%) Using Population Weights | Mean(%) Using Calibrated Weights starting from HHs with UNOMA module | Mean (/%) Using Calibrated Weights starting from all HHs growing the specific crop |
|---|---|---|---|
| CENTRAL | | | |
| CGIAR Varieties in Maize | 46.37 | 43.54 | 40.20 |
| CGIAR Varieties in Banana | 1.56 | 1.46 | . |
| CGIAR Varieties in Beans | 37.4 | 35.80 | 37.92 |
| CGIAR Varieties in Cassava | 7.61 | 7.72 | 8.23 |
| CGIAR Varieties in Groundnuts | 0.00 | 0.00 | 0.00 |
| CGIAR Varieties in Sweetpotato | 29.42 | 26.78 | 26.48 |
| EASTERN | | | |
| CGIAR Varieties in Maize | 57.86 | 58.54 | 58.14 |
| CGIAR Varieties in Banana | 0.00 | 0.00 | . |
| CGIAR Varieties in Beans | 16.27 | 18.35 | 20.06 |
| CGIAR Varieties in Cassava | 73.00 | 72.20 | 73.17 |
| CGIAR Varieties in Groundnuts | 58.44 | 51.55 | 53.75 |
| CGIAR Varieties in Sweetpotato | 1.17 | 1.32 | 1.27 |
| NORTHERN | | | |
| CGIAR Varieties in Maize | 66.24 | 67.58 | 66.00 |
| CGIAR Varieties in Banana | 0.00 | 0.00 | . |
| CGIAR Varieties in Beans | 19.86 | 13.88 | 15.90 |
| CGIAR Varieties in Cassava | 38.40 | 37.09 | 35.26 |
| CGIAR Varieties in Groundnuts | 18.26 | 16.49 | 23.46 |
| CGIAR Varieties in Sweetpotato | 2.50 | 2.60 | 2.40 |
| WESTERN | | | |
| CGIAR Varieties in Maize | 55.08 | 53.86 | 51.75 |
| CGIAR Varieties in Banana | 0.00 | 0.00 | . |
| CGIAR Varieties in Beans | 17.17 | 19.07 | 9.64 |
| CGIAR Varieties in Cassava | 11.00 | 11.72 | 12.24 |
| CGIAR Varieties in Groundnuts | 0.00 | 0.00 | 0.00 |
| CGIAR Varieties in Sweetpotato | 4.68 | 4.47 | 5.04 |
| TOTAL | | | |
| CGIAR Varieties in Maize | 57.17 | 56.81 | 55.14 |
| CGIAR Varieties in Banana | 0.43 | 0.35 | . |
| CGIAR Varieties in Beans | 20.77 | 20.07 | 21.25 |
| CGIAR Varieties in Cassava | 34.44 | 36.41 | 36.93 |
| CGIAR Varieties in Groundnuts | 27.97 | 25.17 | 25.46 |
| CGIAR Varieties in Sweetpotato | 7.39 | 7.44 | 7.69 |

Covariates that did not allow for convergence of calibration module were excluded from calibrations of weights.

The calibration failed to converge for Banana in Column 3, meaning that with the set of covariates mentioned below, the selected sample failed to reflect the population sample.

### Details on the Calibration Method

We use ReGenesees package in Rstudio to calibrate the population weights using a set of household covariates (Zardetto, 2015). The overall intuition of the calibration is to define a set of weights, so that analysis on the selected sample better represents the full population. Therefore, after identifying the full sample and the selected sample, we predict the probability of a household to be selected using post-double-selection (PDSLasso) method starting from for 50 household covariates[1] and enumerator fixed effects, while clustering the standard errors at the EA level (Belloni et al. 2016).

To run the calibration model, we assign the original population weights to the full sample, whereas for the selected sample, we adjust the weights by dividing the original population weights by the probability of selection. In other words, the sampling design for the selected sample includes inverse probability weights adjusted to the original population weights.

Using the ReGenesees package in Rstudio, we specify the calibration model using a rich set of household covariates representing demographic composition, labor market participation, and assets. This allows to obtain calibrated weights adjusting for the selection of the household based on this set of covariates. We then compare the full sample using original population weights and the selected sample using the calibrated weights for each of the covariates used in the calibration. We find that the calibration eliminates any difference between the two samples. This confirms that the calibration adjusts for differences across observables. See upper panel in tables below.

A key question for this calibration exercise is whether it also allows to reduce differences for variables not used in the calibration. If so, it will make it more likely that using the calibrated weights also helps correct for some of the differences in unobservables. To strengthen the validation, we therefore extend the comparison of the full sample and the selected sample (adjusted with the calibrated weights) to covariates that were not used in computing the calibrated weights. The bottom panel in the tables below shows that the differences between the full sample and the selected sample are generally smaller also for these variables that were not used for the calibration, confirming that the calibrated weights help adjust for wider differences between the selected and the full sample.

The tables below show these comparisons for each of the 6 crops, for both calibration exercises explained above (Tables 3 to 8 and Tables 9 to 13 respectively). Each of the tables only includes a selected set of variables for readability, with Tables 14 to 19 showing the fuller selectivity issues on the non-calibrated samples.

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[1] The household covariates are cleaned before processing into the PDSlasso. This is done to adjust for the missing values, remove perfectly collinear variables, create indicator variables, etc.

## References

Belloni, A., Chernozhukov, V., Hansen, C., & Kozbur, D. (2016). Inference in High-Dimensional Panel Models With an Application to Gun Control. Journal of Business & Economic Statistics, 34(4), 590–605. https://doi.org/10.1080/07350015.2015.1102733

Zardetto, D. (2015). ReGenesees: An Advanced R System for Calibration, Estimation and Sampling Error Assessment in Complex Sample Surveys. Journal of Official Statistics, 31(2), 177-203. https://sciendo.com/article/10.1515/jos-2015-0013.

## Tables with results of calibration on balance of covariates starting from households with UNOMA modules

Table 3: Comparison of Covariates across Calibrated and Non-calibrated Variables - Maize

| | 1 | | | 2 | | |
|---|---|---|---|---|---|---|
| | Full Sample (Unweighted) | Selected Sample (Unweighted) | Difference | Full Sample (Pop. Wgted) | Selected Sample (Calib. Wgted) | Difference |
| **Selected Calibrated Variables** | | | | | | |
| Value of assets owned by HH (UGX million) | 4.99 | 7.10 | 2.11*** | 5.30 | 5.30 | 0.00 |
| | (11.16) | (15.24) | (0.68) | (11.80) | (11.65) | (0.43) |
| HH members working in HH farms | 1.69 | 1.82 | 0.13* | 1.70 | 1.70 | 0.00 |
| | (1.47) | (1.48) | (0.07) | (1.42) | (1.43) | (0.08) |
| Total area of parcels owned by HH | 3.34 | 3.95 | 0.61*** | 3.19 | 3.19 | 0.00 |
| | (3.44) | (3.58) | (0.21) | (3.02) | (2.81) | (0.16) |
| Female share of family labor > 50% | 0.44 | 0.40 | -0.04* | 0.43 | 0.43 | 0.00 |
| | (0.50) | (0.50) | (0.02) | (0.50) | (0.50) | (0.03) |
| **Non-calibrated Variables** | | | | | | |
| Age of hh head | 47.1147 | 46.8508 | -0.2639 | 47.1138 | 47.0945 | -0.0193 |
| | (15.7008) | (14.9490) | (0.8214) | (15.9471) | (15.6625) | (0.9875) |
| PCA1 of assets owned by HH | -0.1619 | -0.1716 | -0.0098 | -0.1628 | -0.1973 | -0.0345 |
| | (0.5156) | (0.2071) | (0.0217) | (0.4944) | (0.1743) | (0.0233) |
| Area of plots in HH in acres (s2) | 0.6246 | 0.7048 | 0.0801 | 0.6596 | 0.6856 | 0.0260 |
| | (0.6325) | (0.6828) | (0.0347)** | (0.6453) | (0.6988) | (0.0410) |
| Distance to road is not reported | 0.1608 | 0.1460 | -0.0148 | 0.1807 | 0.1865 | 0.0058 |
| | (0.3675) | (0.3537) | (0.0170) | (0.3850) | (0.3901) | (0.0210) |
| Distance to market is not reported | 0.2392 | 0.2095 | -0.0297 | 0.2721 | 0.2575 | -0.0146 |
| | (0.4268) | (0.4076) | (0.0202) | (0.4453) | (0.4380) | (0.0256) |
| HH has some Large Ruminants | 0.3010 | 0.3238 | 0.0228 | 0.2487 | 0.2207 | -0.0280 |
| | (0.4589) | (0.4687) | (0.0241) | (0.4325) | (0.4154) | (0.0212) |
| HH has some Small Ruminants | 0.4078 | 0.4381 | 0.0303 | 0.3969 | 0.3797 | -0.0172 |
| | (0.4917) | (0.4969) | (0.0215) | (0.4895) | (0.4861) | (0.0288) |
| HH has some Chicken | 0.4755 | 0.5492 | 0.0737 | 0.4624 | 0.4915 | 0.0291 |
| | (0.4996) | (0.4984) | (0.0246)*** | (0.4988) | (0.5007) | (0.0263) |
| HH has some Pigs | 0.1657 | 0.2000 | 0.0343 | 0.1777 | 0.1824 | 0.0047 |
| | (0.3720) | (0.4006) | (0.0196)* | (0.3825) | (0.3868) | (0.0249) |
| Distance to nearest market (km) | 3.4912 | 3.7124 | 0.2212 | 3.2615 | 3.3141 | 0.0526 |
| | (3.4264) | (3.2516) | (0.1974) | (3.1663) | (3.0173) | (0.1909) |
| Distance to nearest road (km) | 1.1416 | 1.3225 | 0.1809 | 1.0438 | 1.1231 | 0.0793 |
| | (1.9558) | (2.1301) | (0.1033)* | (1.7695) | (1.9537) | (0.1054) |

Standard errors in parentheses.

## Table 4: Comparison of Covariates Across Calibrated and Non-calibrated Variables: Cassava

| | 1 | | | 2 | | |
|---|---|---|---|---|---|---|
| | Full Sample (Unweighted) | Selected Sample (Unweighted) | Difference | Full Sample (Pop. Wgted) | Selected Sample (Calib. Wgted) | Difference |
| **Selected Calibrated Variables** | | | | | | |
| Value of assets owned by HH (UGX million) | 6.50 | 6.83 | 0.3318 | 6.58 | 6.58 | 0.00 |
| | (12.62) | (13.64) | (0.29) | (12.18) | (12.51) | (0.25) |
| HH members working in farms (7d) | 1.77 | 1.85 | 0.08 | 1.7722 | 1.77 | 0.00 |
| | (1.48) | (1.52) | (0.03)** | (1.47) | (1.50) | (0.03) |
| Total area of parcels owned by HH (acres) | 2.95 | 2.91 | -0.04 | 2.82 | 2.82 | 0.00 |
| | (3.14) | (2.49) | (0.09) | (2.67) | (2.38) | (0.06) |
| HH labor force (7d) | 1.98 | 2.06 | 0.08** | 1.99 | 1.99 | 0.00 |
| | (1.47) | (1.51) | (0.03) | (1.46) | (1.49) | (0.03) |
| Female HH members in the labor force | 1.01 | 1.04 | 0.04* | 1.01 | 1.01 | 0.00 |
| | (0.88) | (0.91) | (0.02) | (0.87) | (0.90) | (0.02) |
| **Non-calibrated Variables** | | | | | | |
| HH has some livestock | 0.6979 | 0.7059 | 0.0080 | 0.6776 | 0.6888 | 0.0112 |
| | (0.4594) | (0.4560) | (0.0108) | (0.4676) | (0.4633) | (0.0118) |
| Age of hh head | 46.6784 | 47.1935 | 0.5151 | 46.6081 | 46.5810 | -0.0271 |
| | (15.3856) | (15.5783) | (0.3304) | (15.2944) | (15.5075) | (0.3476) |
| PCA1 of assets owned by HH ∼N(0,1) | -0.0680 | -0.0385 | 0.0295 | -0.0771 | -0.0525 | 0.0246 |
| | (0.9332) | (1.0185) | (0.0166)* | (0.8857) | (0.9833) | (0.0175) |
| Area of plots in HH in acres (s2) | 0.5975 | 0.6076 | 0.0100 | 0.6090 | 0.6055 | -0.0034 |
| | (0.5507) | (0.5676) | (0.0125) | (0.5833) | (0.5996) | (0.0134) |
| Distance to road is not reported | 0.0168 | 0.0212 | 0.0043 | 0.0127 | 0.0127 | 0.0000 |
| | (0.1287) | (0.1440) | (0.0035) | (0.1122) | (0.1122) | (0.0015) |
| Distance to market is not reported | 0.1527 | 0.1596 | 0.0070 | 0.1466 | 0.1444 | -0.0022 |
| | (0.3599) | (0.3666) | (0.0103) | (0.3539) | (0.3518) | (0.0095) |
| HH has some Large Ruminants | 0.2411 | 0.2353 | -0.0058 | 0.2252 | 0.2114 | -0.0139 |
| | (0.4279) | (0.4245) | (0.0096) | (0.4180) | (0.4086) | (0.0097) |
| HH has some Small Ruminants | 0.3832 | 0.3793 | -0.0039 | 0.3830 | 0.3787 | -0.0044 |
| | (0.4864) | (0.4856) | (0.0119) | (0.4864) | (0.4854) | (0.0125) |
| HH has some Chicken | 0.4884 | 0.4938 | 0.0054 | 0.4758 | 0.4870 | 0.0112 |
| | (0.5001) | (0.5003) | (0.0117) | (0.4997) | (0.5002) | (0.0116) |
| HH has some Pigs | 0.1968 | 0.2090 | 0.0121 | 0.2065 | 0.2024 | -0.0041 |
| | (0.3978) | (0.4069) | (0.0091) | (0.4050) | (0.4021) | (0.0095) |
| Distance to nearest market (km) | 2.9302 | 3.0939 | 0.1637 | 2.8891 | 3.0056 | 0.1164 |
| | (2.7280) | (2.8573) | (0.0708)** | (2.7130) | (2.7480) | (0.0766) |
| Distance to nearest road (km) | 1.0678 | 1.1492 | 0.0814 | 1.0324 | 1.0313 | -0.0011 |
| | (1.9219) | (2.1105) | (0.0453)* | (1.8377) | (1.8695) | (0.0522) |

## Table 5: Comparison of Covariates Across Calibrated and Non-calibrated Variables: Banana

| | 1 | | | 2 | | |
|---|---|---|---|---|---|---|
| | Full Sample (Unweighted) | Selected Sample (Unweighted) | Difference | Full Sample (Pop. Wgted) | Selected Sample (Calib. Wgted) | Difference |
| **Selected Calibrated Variables** | | | | | | |
| Value of assets owned by HH (UGX million) | 7.8806 | 8.4513 | 0.5707 | 7.9634 | 7.9634 | 0.0000 |
| | (14.5350) | (15.0630) | (0.3115)* | (14.3973) | (14.1938) | (0.4275) |
| HH members working in the HH farms | 1.6667 | 1.7037 | 0.0370 | 1.6941 | 1.6941 | 0.0000 |
| | (1.3275) | (1.3198) | (0.0282) | (1.3015) | (1.2910) | (0.0360) |
| Total area of parcels owned by HH (acres) | 2.7386 | 2.7006 | -0.0380 | 2.7855 | 2.7855 | 0.0000 |
| | (2.7368) | (2.6556) | (0.0542) | (2.6688) | (2.6618) | (0.0863) |
| HH has female member listed on a parcel title | 0.5677 | 0.5281 | -0.0396 | 0.5674 | 0.5674 | 0.0000 |
| | (0.4954) | (0.4996) | (0.0117)*** | (0.4955) | (0.4958) | (0.0157) |
| Female HH members in the labor force | 1.0179 | 1.0576 | 0.0397 | 1.0297 | 1.0297 | 0.0000 |
| | (0.8443) | (0.8408) | (0.0167)** | (0.8159) | (0.7816) | (0.0205) |
| **Non-calibrated Variables** | | | | | | |
| HH has some livestock | 0.7035 | 0.7177 | 0.0142 | 0.6996 | 0.7026 | 0.0029 |
| | (0.4569) | (0.4504) | (0.0099) | (0.4587) | (0.4574) | (0.0171) |
| Age of hh head | 48.9930 | 49.2893 | 0.2963 | 48.7496 | 48.5948 | -0.1548 |
| | (15.9435) | (16.3945) | (0.3050) | (15.7181) | (15.5557) | (0.4565) |
| PCA1 of assets owned by HH ∼N(0,1) | -0.0404 | -0.0476 | -0.0072 | -0.0223 | 0.0092 | 0.0315 |
| | (0.9698) | (0.9660) | (0.0204) | (1.0087) | (1.1042) | (0.0333) |
| Area of plots in HH in acres (s2) | 0.5878 | 0.5805 | -0.0073 | 0.6228 | 0.6188 | -0.0039 |
| | (0.6164) | (0.6360) | (0.0132) | (0.6443) | (0.6997) | (0.0230) |
| Distance to road is not reported | 0.1980 | 0.2135 | 0.0155 | 0.2199 | 0.2358 | 0.0159 |
| | (0.3987) | (0.4101) | (0.0092)* | (0.4144) | (0.4248) | (0.0114) |
| Distance to market is not reported | 0.3652 | 0.3750 | 0.0098 | 0.3873 | 0.3875 | 0.0002 |
| | (0.4817) | (0.4845) | (0.0116) | (0.4874) | (0.4875) | (0.0172) |
| HH has some Large Ruminants | 0.2289 | 0.2388 | 0.0099 | 0.2168 | 0.2185 | 0.0017 |
| | (0.4203) | (0.4266) | (0.0099) | (0.4122) | (0.4135) | (0.0133) |
| HH has some Small Ruminants | 0.3572 | 0.3624 | 0.0051 | 0.3525 | 0.3429 | -0.0096 |
| | (0.4794) | (0.4810) | (0.0104) | (0.4780) | (0.4750) | (0.0151) |
| HH has some Chicken | 0.4627 | 0.4775 | 0.0148 | 0.4721 | 0.4864 | 0.0143 |
| | (0.4989) | (0.4998) | (0.0116) | (0.4995) | (0.5002) | (0.0171) |
| HH has some Pigs | 0.2338 | 0.2598 | 0.0260 | 0.2436 | 0.2525 | 0.0089 |
| | (0.4235) | (0.4389) | (0.0092)*** | (0.4295) | (0.4347) | (0.0147) |
| Distance to nearest market (km) | 2.8662 | 2.8610 | -0.0052 | 2.9658 | 2.9944 | 0.0286 |
| | (2.8793) | (2.9931) | (0.0718) | (2.8784) | (3.1154) | (0.1084) |
| Distance to nearest road (km) | 0.8878 | 0.9139 | 0.0261 | 0.9999 | 1.1200 | 0.1201 |
| | (1.7721) | (1.8900) | (0.0401) | (1.8619) | (2.1220) | (0.0667)* |

Table 6: Comparison of Covariates Across Calibrated and Non-calibrated Variables: Beans

| | | 1 | | | 2 | |
|---|---|---|---|---|---|---|
| | Full Sample (Unweighted) | Selected Sample (Unweighted) | Difference | Full Sample (Pop. Wgted) | Selected Sample (Calib. Wgted) | Difference |
| **Selected Calibrated Variables** | | | | | | |
| Value of assets owned by HH (UGX million) | 7.6283 | 8.9762 | 1.3478 | 7.4729 | 7.4729 | 0.0000 |
| | (14.1201) | (16.5158) | (0.7132)* | (13.2877) | (14.5104) | (0.8440) |
| HH members working in the HH farms | 1.7119 | 1.7541 | 0.0422 | 1.7504 | 1.7504 | 0.0000 |
| | (1.3126) | (1.3364) | (0.0599) | (1.2988) | (1.3466) | (0.0995) |
| HH has female member listed on a parcel title | 0.5361 | 0.4522 | -0.0840 | 0.5260 | 0.5260 | 0.0000 |
| | (0.4981) | (0.4977) | (0.0226)*** | (0.4988) | (0.4994) | (0.0342) |
| Female share of family labor > 50% | 0.4217 | 0.4426 | 0.0209 | 0.4132 | 0.4132 | 0.0000 |
| | (0.4941) | (0.4974) | (0.0201) | (0.4927) | (0.4931) | (0.0316) |
| Female HH members in the labor force | 1.0296 | 1.0710 | 0.0415 | 1.0425 | 1.0425 | 0.0000 |
| | (0.8166) | (0.8212) | (0.0367) | (0.7906) | (0.8487) | (0.0571) |
| **Non-calibrated Variables** | | | | | | |
| HH has some livestock | 0.6605 | 0.6913 | 0.0308 | 0.6451 | 0.7006 | 0.0555 |
| | (0.4738) | (0.4626) | (0.0202) | (0.4787) | (0.4586) | (0.0293)* |
| Age of hh head | 46.7114 | 47.3538 | 0.6424 | 46.6239 | 46.9225 | 0.2986 |
| | (15.3645) | (15.4891) | (0.6502) | (15.3959) | (16.3054) | (1.2403) |
| PCA1 of assets owned by HH ∼N(0,1) | 0.0070 | 0.0847 | 0.0776 | 0.0050 | 0.2236 | 0.2187 |
| | (1.0947) | (1.2876) | (0.0515) | (1.0788) | (1.5943) | (0.1294)* |
| Area of plots in HH in acres (s2) | 0.5894 | 0.5855 | -0.0040 | 0.6216 | 0.5733 | -0.0484 |
| | (0.6024) | (0.6153) | (0.0300) | (0.6241) | (0.5463) | (0.0317) |
| Distance to road is not reported | 0.2738 | 0.3060 | 0.0322 | 0.3134 | 0.3052 | -0.0082 |
| | (0.4462) | (0.4615) | (0.0211) | (0.4641) | (0.4611) | (0.0337) |
| Distance to market is not reported | 0.3877 | 0.4426 | 0.0549 | 0.4115 | 0.4319 | 0.0204 |
| | (0.4875) | (0.4974) | (0.0241)** | (0.4924) | (0.4960) | (0.0351) |
| HH has some Large Ruminants | 0.1950 | 0.1776 | -0.0174 | 0.1881 | 0.1881 | 0.0000 |
| | (0.3964) | (0.3827) | (0.0170) | (0.3910) | (0.3913) | (0.0282) |
| HH has some Small Ruminants | 0.3636 | 0.3634 | -0.0002 | 0.3477 | 0.3476 | -0.0001 |
| | (0.4813) | (0.4816) | (0.0228) | (0.4765) | (0.4769) | (0.0336) |
| HH has some Chicken | 0.4337 | 0.4617 | 0.0280 | 0.4357 | 0.4701 | 0.0344 |
| | (0.4959) | (0.4992) | (0.0235) | (0.4961) | (0.4998) | (0.0289) |
| HH has some Pigs | 0.2388 | 0.2896 | 0.0508 | 0.2515 | 0.2934 | 0.0419 |
| | (0.4266) | (0.4542) | (0.0227)** | (0.4341) | (0.4559) | (0.0332) |
| Distance to nearest market (km) | 2.8603 | 2.6275 | -0.2328 | 3.0499 | 2.6236 | -0.4263 |
| | (3.1882) | (3.0222) | (0.1996) | (3.5857) | (2.8870) | (0.3138) |
| Distance to nearest road (km) | 0.8854 | 0.8095 | -0.0759 | 1.0006 | 0.8858 | -0.1149 |
| | (1.7658) | (1.7444) | (0.1430) | (1.8474) | (1.7527) | (0.1637) |

Table 7: Comparison of Covariates Across Calibrated and Non-calibrated Variables: Sweetpotato

| | | 1 | | | 2 | |
|---|---|---|---|---|---|---|
| | Full Sample (Unweighted) | Selected Sample (Unweighted) | Difference | Full Sample (Pop. Wgted) | Selected Sample (Calib. Wgted) | Difference |
| **Selected Calibrated Variables** | | | | | | |
| Head is Female | 0.2913 | 0.3085 | 0.0171 | 0.2840 | 0.2840 | 0.0000 |
| | (0.4547) | (0.4623) | (0.0089)* | (0.4512) | (0.4513) | (0.0147) |
| HH has motor vehicle | 0.0089 | 0.0119 | 0.0030 | 0.0099 | 0.0099 | 0.0000 |
| | (0.0940) | (0.1084) | (0.0011)*** | (0.0990) | (0.0990) | (0.0007) |
| HH has mobile phone | 0.8569 | 0.8398 | -0.0170 | 0.8754 | 0.8754 | 0.0000 |
| | (0.3491) | (0.3653) | (0.0061)*** | (0.3292) | (0.3290) | (0.0071) |
| Female share of family labor >50% | 0.4389 | 0.4237 | -0.0152 | 0.4457 | 0.4457 | 0.0000 |
| | (0.4966) | (0.4946) | (0.0105) | (0.4974) | (0.4975) | (0.0169) |
| Total area of parcels owned by HH (acres) | 2.8951 | 2.9446 | 0.0496 | 2.7156 | 2.7156 | 0.0000 |
| | (2.6265) | (2.6592) | (0.0558) | (2.5144) | (2.4923) | (0.0696) |
| **Non-calibrated Variables** | | | | | | |
| HH has some livestock | 0.6883 | 0.7034 | 0.0151 | 0.6314 | 0.6436 | 0.0122 |
| | (0.4635) | (0.4572) | (0.0117) | (0.4827) | (0.4794) | (0.0176) |
| Age of hh head | 47.5331 | 47.7695 | 0.2364 | 47.4455 | 47.4037 | -0.0418 |
| | (15.6488) | (15.8291) | (0.3141) | (15.8225) | (15.8429) | (0.4269) |
| PCA1 of assets owned by HH ∼N(0,1) | -0.0241 | -0.0127 | 0.0114 | -0.0152 | -0.0141 | 0.0011 |
| | (1.0707) | (1.1063) | (0.0204) | (1.0798) | (1.0934) | (0.0391) |
| Area of plots in HH in acres (s2) | 0.5365 | 0.5251 | -0.0114 | 0.5349 | 0.5258 | -0.0091 |
| | (0.5122) | (0.4608) | (0.0142) | (0.5200) | (0.4658) | (0.0206) |
| Distance to road is not reported | 0.2341 | 0.2237 | -0.0104 | 0.2966 | 0.2805 | -0.0160 |
| | (0.4237) | (0.4171) | (0.0095) | (0.4570) | (0.4496) | (0.0172) |
| Distance to market is not reported | 0.3308 | 0.3085 | -0.0223 | 0.3898 | 0.3783 | -0.0114 |
| | (0.4708) | (0.4623) | (0.0100)** | (0.4880) | (0.4854) | (0.0162) |
| HH has some Large Ruminants | 0.2417 | 0.2729 | 0.0312 | 0.2244 | 0.2322 | 0.0078 |
| | (0.4284) | (0.4458) | (0.0087)*** | (0.4175) | (0.4226) | (0.0129) |
| HH has some Small Ruminants | 0.4160 | 0.4254 | 0.0094 | 0.3731 | 0.3747 | 0.0016 |
| | (0.4932) | (0.4948) | (0.0108) | (0.4839) | (0.4845) | (0.0141) |
| HH has some Chicken | 0.4517 | 0.4678 | 0.0161 | 0.4245 | 0.4260 | 0.0015 |
| | (0.4980) | (0.4994) | (0.0108) | (0.4946) | (0.4949) | (0.0152) |
| HH has some Pigs | 0.1858 | 0.1814 | -0.0044 | 0.1806 | 0.1811 | 0.0005 |
| | (0.3892) | (0.3856) | (0.0086) | (0.3849) | (0.3854) | (0.0108) |
| Distance to nearest market (km) | 2.8764 | 2.9921 | 0.1157 | 2.7108 | 2.8556 | 0.1448 |
| | (2.8906) | (2.8645) | (0.0624)* | (2.8013) | (2.8938) | (0.0754)* |
| Distance to nearest road (km) | 1.0208 | 1.1014 | 0.0806 | 0.9799 | 1.0791 | 0.0991 |
| | (2.0784) | (2.1890) | (0.0422)* | (2.0034) | (2.1569) | (0.0471)** |

Table 8: Comparison of Covariates Across Calibrated and Non-calibrated Variables: Groundnuts

| | 1 | | | 2 | | |
|---|---|---|---|---|---|---|
| | Full Sample (Unweighted) | Selected Sample (Unweighted) | Difference | Full Sample (Pop. Wgted) | Selected Sample (Calib. Wgted) | Difference |
| **Selected Calibrated Variables** | | | | | | |
| Maximum years of schooling in HH | 7.6414 | 7.1172 | -0.5242 | 7.8231 | 7.8231 | 0.0000 |
| | (3.8359) | (3.7890) | (0.2899)* | (3.7077) | (3.5149) | (0.3343) |
| Value of assets owned by HH (UGX million) | 5.6707 | 5.1186 | -0.5522 | 5.7596 | 5.7596 | 0.0000 |
| | (10.3053) | (11.1678) | (0.7440) | (10.4458) | (10.9414) | (0.9942) |
| HH has female member listed on a parcel title | 0.7286 | 0.6563 | -0.0723 | 0.7625 | 0.7625 | 0.0000 |
| | (0.4453) | (0.4768) | (0.0348)** | (0.4262) | (0.4272) | (0.0449) |
| Female share of family labor >50% | 0.4857 | 0.4688 | -0.0170 | 0.4621 | 0.4621 | 0.0000 |
| | (0.5005) | (0.5010) | (0.0319) | (0.4993) | (0.5005) | (0.0591) |
| HH has furniture | 0.9343 | 0.8906 | -0.0437 | 0.9291 | 0.9291 | 0.0000 |
| | (0.2481) | (0.3133) | (0.0177)** | (0.2570) | (0.2576) | (0.0268) |
| **Non-calibrated Variables** | | | | | | |
| HH has some livestock | 0.7943 | 0.7891 | -0.0052 | 0.7616 | 0.7909 | 0.0294 |
| | (0.4048) | (0.4096) | (0.0297) | (0.4267) | (0.4082) | (0.0457) |
| Age of hh head | 49.7114 | 51.4531 | 1.7417 | 49.8930 | 50.0734 | 0.1804 |
| | (15.0319) | (15.9467) | (1.1078) | (15.3897) | (15.8362) | (1.7094) |
| PCA1 of assets owned by HH ∼N(0,1) | -0.1872 | -0.2237 | -0.0365 | -0.1830 | -0.2034 | -0.0204 |
| | (0.1930) | (0.1501) | (0.0116)*** | (0.1973) | (0.1603) | (0.0169) |
| Area of plots in HH in acres (s2) | 0.7420 | 0.7273 | -0.0146 | 0.7761 | 0.6739 | -0.1022 |
| | (0.7618) | (0.6758) | (0.0537) | (0.8523) | (0.7136) | (0.0872) |
| Distance to road is not reported | 0.1314 | 0.1328 | 0.0014 | 0.1433 | 0.1129 | -0.0304 |
| | (0.3384) | (0.3407) | (0.0331) | (0.3509) | (0.3177) | (0.0381) |
| Distance to market is not reported | 0.1943 | 0.1172 | -0.0771 | 0.2239 | 0.1820 | -0.0419 |
| | (0.3962) | (0.3229) | (0.0298)*** | (0.4174) | (0.3874) | (0.0583) |
| HH has some Large Ruminants | 0.3371 | 0.3672 | 0.0300 | 0.2705 | 0.3261 | 0.0556 |
| | (0.4734) | (0.4839) | (0.0371) | (0.4449) | (0.4706) | (0.0561) |
| HH has some Small Ruminants | 0.4429 | 0.4141 | -0.0288 | 0.3860 | 0.4584 | 0.0725 |
| | (0.4974) | (0.4945) | (0.0356) | (0.4875) | (0.5002) | (0.0603) |
| HH has some Chicken | 0.5029 | 0.5313 | 0.0284 | 0.5139 | 0.5926 | 0.0786 |
| | (0.5007) | (0.5010) | (0.0341) | (0.5005) | (0.4933) | (0.0519) |
| HH has some Pigs | 0.2343 | 0.2500 | 0.0157 | 0.2504 | 0.2791 | 0.0287 |
| | (0.4242) | (0.4347) | (0.0296) | (0.4339) | (0.4503) | (0.0484) |
| Distance to nearest market (km) | 3.5232 | 3.7677 | 0.2445 | 3.3414 | 3.7382 | 0.3968 |
| | (3.1941) | (3.2089) | (0.3031) | (3.0437) | (3.3964) | (0.3938) |
| Distance to nearest road (km) | 1.0931 | 1.7735 | 0.6805 | 0.9934 | 1.5641 | 0.5708 |
| | (2.0870) | (2.8869) | (0.2096)*** | (1.9265) | (2.7495) | (0.2425)** |

## Tables with results of calibration on balance of covariates starting from all households growing the targeted crop

Table 9: Comparison of Covariates Across Calibrated and Non-Calibrated Variables: Maize

| | 1 | | | 2 | | |
|---|---|---|---|---|---|---|
| | Full Sample (Unweighted) | Selected Sample (Unweighted) | Diff. | Full Sample (Pop. Wgted) | Selected Sample (Calib. Wgted) | Diff. |
| **Selected Calibrated Variables** | | | | | | |
| Value of assets owned by HH (UGX million) | 5.0810 | 7.1130 | 2.0310 *** | 5.2160 | 5.2160 | 0.0000 |
| | (3.3070) | (3.9070) | (0.7410) | (3.3580) | (3.5740) | (0.7960) |
| HH members working in the HH farms | 1.6250 | 1.8250 | 0.2000 ** | 1.6100 | 1.6100 | 0.0000 |
| | (1.1930) | (1.2200) | (0.0820) | (1.1740) | (1.1570) | (0.0710) |
| Total area of parcels owned by HH | 3.1270 | 3.9610 | 0.8340 *** | 3.0150 | 3.0150 | 0.0000 |
| | (1.8040) | (1.8930) | (0.2290) | (1.7090) | (1.6270) | (0.1990) |
| HH has motor cycle | 0.0920 | 0.1210 | 0.0290 | 0.0960 | 0.0960 | 0.0000 |
| | (0.5380) | (0.5720) | (0.0150)** | (0.5420) | (0.5430) | (0.0200) |
| **Non-calibrated Variables** | | | | | | |
| HH has some livestock | 0.6660 | 0.7580 | 0.0920 *** | 0.6370 | 0.5890 | -0.0480 |
| | (0.6870) | (0.6550) | (0.0230) | (0.6930) | (0.7020) | (0.0330) |
| Area of plots in HH | 0.6720 | 0.7700 | 0.0970 *** | 0.6870 | 0.7190 | 0.0320 |
| | (0.7770) | (0.7980) | (0.0370) | (0.7980) | (0.8210) | (0.0410) |
| Distance to nearest road (km) | 0.9090 | 1.1760 | 0.2670 *** | 0.8470 | 0.9270 | 0.0800 |
| | (1.3370) | (1.4410) | (0.0980) | (1.2730) | (1.3180) | (0.0510) |
| Distance to road is not reported | 0.0300 | 0.0450 | 0.0150 | 0.0270 | 0.0290 | 0.0020 |
| | (0.4120) | (0.4550) | (0.0120) | (0.4020) | (0.4090) | (0.0100) |
| HH has some Large Ruminants | 0.2620 | 0.3250 | 0.0630 *** | 0.2240 | 0.1800 | -0.0450 ** |
| | (0.6630) | (0.6850) | (0.0260) | (0.6460) | (0.6200) | (0.0170) |
| HH has some Small Ruminants | 0.3860 | 0.4390 | 0.0530 | 0.3640 | 0.3260 | -0.0380 |
| | (0.6980) | (0.7050) | (0.0230)** | (0.6940) | (0.6850) | (0.0340) |

Table 10: Comparison of Covariates Across Calibrated and Non-Calibrated Variables: Cassava

| | 1 | | | 2 | | |
|---|---|---|---|---|---|---|
| | Full Sample (Unweighted) | Selected Sample (Unweighted) | Diff. | Full Sample (Pop. Wgted) | Selected Sample (Calib. Wgted) | Diff. |
| **Selected Calibrated Variables** | | | | | | |
| Female share of labor >50% | 0.4280 | 0.3990 | -0.0290** | 0.4180 | 0.4180 | 0.0000 |
| | (0.7040) | (0.7000) | (0.0140) | (0.7020) | (0.7030) | (0.0130) |
| Value of assets owned by HH (UGX million) | 6.1260 | 6.8490 | 0.7240* | 6.3670 | 6.3670 | 0.0000 |
| | (3.5280) | (3.7010) | (0.3740) | (3.5420) | (3.4900) | (0.3910) |
| HH has motor vehicle | 0.0110 | 0.0160 | 0.0050* | 0.0140 | 0.0140 | 0.0000 |
| | (0.3200) | (0.3530) | (0.0030) | (0.3410) | (0.3410) | (0.0030) |
| HH labor force | 1.9300 | 2.0600 | 0.1300*** | 1.9240 | 1.9240 | 0.0000 |
| | (1.1950) | (1.2320) | (0.0400) | (1.1890) | (1.2010) | (0.0580) |
| **Non-calibrated Variables** | | | | | | |
| HH has some livestock | 0.6740 | 0.7060 | 0.0320** | 0.6530 | 0.6800 | 0.0270* |
| | (0.6850) | (0.6750) | (0.0130) | (0.6900) | (0.6830) | (0.0150) |
| Distance to nearest market (km) | 2.9600 | 3.1120 | 0.1520* | 2.9790 | 3.0300 | 0.0510 |
| | (1.6970) | (1.7050) | (0.0890) | (1.7360) | (1.6930) | (0.0860) |
| Distance to nearest road (km) | 1.0820 | 1.1550 | 0.0730 | 1.0340 | 1.0470 | 0.0120 |
| | (1.4050) | (1.4610) | (0.0520) | (1.3690) | (1.3850) | (0.0640) |
| HH has some Chicken | 0.4630 | 0.4940 | 0.0300** | 0.4500 | 0.4780 | 0.0280 |
| | (0.7060) | (0.7070) | (0.0140) | (0.7050) | (0.7070) | (0.0170) |
| HH has some Pigs | 0.1840 | 0.2090 | 0.0250** | 0.1940 | 0.2040 | 0.0100 |
| | (0.6220) | (0.6380) | (0.0110) | (0.6290) | (0.6350) | (0.0100) |
| Distance to road is not reported | 0.0260 | 0.0210 | -0.0040 | 0.0190 | 0.0150 | -0.0040 |
| | (0.3970) | (0.3810) | (0.0050) | (0.3690) | (0.3490) | (0.0030) |

## Tables with results of calibration on balance of covariates starting from all households growing the targeted crop

Table 11: Comparison of Covariates Across Calibrated and Non-Calibrated Variables: Beans

| | 1 | | | 2 | | |
|---|---|---|---|---|---|---|
| | Full Sample (Unweighted) | Selected Sample (Unweighted) | Diff. | Full Sample (Pop. Wgted) | Selected Sample (Calib. Wgted) | Diff. |
| **Selected Calibrated Variables** | | | | | | |
| Female member listed on parcel | 0.5510 | 0.4550 | -0.0960*** | 0.5450 | 0.5450 | 0.0000 |
| | (0.7040) | (0.7050) | (0.0260) | (0.7050) | (0.7050) | (0.0400) |
| Value of assets owned by HH (UGX million) | 6.8560 | 8.9780 | 2.1210** | 6.9860 | 6.9860 | 0.0000 |
| | (3.6680) | (4.0640) | (0.8190) | (3.6510) | (3.8220) | (0.8190) |
| HH labor force | 1.8780 | 1.9970 | 0.1200* | 1.9110 | 1.9110 | 0.0000 |
| | (1.1730) | (1.1560) | (0.0650) | (1.1660) | (1.1630) | (0.0740) |
| Female HH members in the labor force | 0.9870 | 1.0710 | 0.0840** | 1.0020 | 1.0020 | 0.0000 |
| | (0.9140) | (0.9060) | (0.0410) | (0.9000) | (0.9290) | (0.0410) |
| **Non-calibrated Variables** | | | | | | |
| HH has some livestock | 0.6550 | 0.6910 | 0.0360 | 0.6330 | 0.7040 | 0.0710* |
| | (0.6900) | (0.6800) | (0.0230) | (0.6940) | (0.6760) | (0.0400) |
| Area of plots in HH in acres | 0.5940 | 0.5850 | -0.0080 | 0.6210 | 0.5500 | -0.0710** |
| | (0.7710) | (0.7840) | (0.0320) | (0.7850) | (0.7210) | (0.0260) |
| Distance to market not reported | 0.1810 | 0.2270 | 0.0460** | 0.1750 | 0.1880 | 0.0140 |
| | (0.6210) | (0.6480) | (0.0230) | (0.6160) | (0.6260) | (0.0280) |
| Distance to nearest market (km) | 3.0540 | 2.6020 | -0.4520** | 3.1560 | 2.6380 | -0.5180 |
| | (1.8050) | (1.7300) | (0.2040) | (1.8660) | (1.7340) | (0.3640) |
| HH has some Large Ruminants | 0.2210 | 0.1780 | -0.0430** | 0.2000 | 0.2130 | 0.0140 |
| | (0.6440) | (0.6190) | (0.0200) | (0.6320) | (0.6400) | (0.0380) |
| HH has some Pigs | 0.2090 | 0.2900 | 0.0810*** | 0.2190 | 0.2680 | 0.0490 |
| | (0.6380) | (0.6740) | (0.0250) | (0.6430) | (0.6660) | (0.0360) |

Table 12: Comparison of Covariates Across Calibrated and Non-Calibrated Variables: Sweetpotato

| | 1 | | | 2 | | |
|---|---|---|---|---|---|---|
| | Full Sample (Unweighted) | Selected Sample (Unweighted) | Diff. | Full Sample (Pop. Wgted) | Selected Sample (Calib. Wgted) | Diff. |
| **Selected Calibrated Variables** | | | | | | |
| HH has mobile phone | 0.8560 | 0.8410 | -0.0150* | 0.8730 | 0.8730 | 0.0000 |
| | (0.5910) | (0.6030) | (0.0080) | (0.5760) | (0.5750) | (0.0080) |
| Value of assets owned by HH (UGX million) | 6.4560 | 6.2050 | -0.2510 | 6.3840 | 6.3840 | 0.0000 |
| | (3.5220) | (3.3790) | (0.2960) | (3.4050) | (3.3390) | (0.3380) |
| Area of parcels owned (acres) | 2.7780 | 2.9450 | 0.1660** | 2.6060 | 2.6060 | 0.0000 |
| | (1.6000) | (1.6310) | (0.0650) | (1.5590) | (1.5320) | (0.0440) |
| Head is Female | 0.2930 | 0.3080 | 0.0160 | 0.2910 | 0.2910 | 0.0000 |
| | (0.6750) | (0.6800) | (0.0100) | (0.6740) | (0.6740) | (0.0160) |
| **Non-calibrated Variables** | | | | | | |
| HH has some livestock | 0.6810 | 0.7030 | 0.0220* | 0.6330 | 0.6430 | 0.0100 |
| | (0.6830) | (0.6760) | (0.0130) | (0.6950) | (0.6920) | (0.0160) |
| Age of hh head | 47.1030 | 47.7690 | 0.6660* | 47.0370 | 47.1100 | 0.0730 |
| | (3.9350) | (3.9790) | (0.3550) | (3.9540) | (3.9740) | (0.3860) |
| Distance to road not reported | 0.0210 | 0.0270 | 0.0060* | 0.0170 | 0.0220 | 0.0050 |
| | (0.3740) | (0.4000) | (0.0030) | (0.3530) | (0.3810) | (0.0060) |
| Distance to market not reported | 0.1540 | 0.1460 | -0.0090 | 0.1530 | 0.1720 | 0.0190* |
| | (0.6000) | (0.5930) | (0.0080) | (0.5990) | (0.6140) | (0.0100) |
| Distance to nearest market (km) | 2.8680 | 3.0160 | 0.1480** | 2.7400 | 2.9080 | 0.1680 |
| | (1.6980) | (1.6880) | (0.0710) | (1.6600) | (1.6930) | (0.1500) |
| HH has some Large Ruminants | 0.2400 | 0.2730 | 0.0330*** | 0.2230 | 0.2310 | 0.0080 |
| | (0.6540) | (0.6680) | (0.0110) | (0.6460) | (0.6500) | (0.0130) |

Table 13: Comparison of Covariates Across Calibrated and Non-Calibrated Variables: Groundnuts

| | 1 | | | 2 | | |
|---|---|---|---|---|---|---|
| | Full Sample (Unweighted) | Selected Sample (Unweighted) | Diff. | Full Sample (Pop. Wgted) | Selected Sample (Calib. Wgted) | Diff. |
| **Selected Calibrated Variables** | | | | | | |
| Max. years of schooling in HH | 7.6220 | 7.0330 | -0.5890* | 7.7050 | 7.7050 | 0.0000 |
| | (1.9250) | (1.9570) | (0.3380) | (1.9030) | (1.8850) | (0.2940) |
| Value of assets owned | 5.8920 | 5.2950 | -0.5970 | 5.9490 | 5.9490 | 0.0000 |
| by HH (UGX million) | (3.2130) | (3.3830) | (0.8700) | (3.2090) | (3.6350) | (1.7020) |
| Female member listed on parcel | 0.7570 | 0.6690 | -0.0880** | 0.7750 | 0.7750 | 0.0000 |
| | (0.6550) | (0.6870) | (0.0380) | (0.6470) | (0.6480) | (0.0570) |
| Head is Female | 0.3600 | 0.3800 | 0.0200 | 0.3600 | 0.3600 | 0.0000 |
| | (0.6930) | (0.6980) | (0.0400) | (0.6930) | (0.6940) | (0.0600) |
| **Non-calibrated Variables** | | | | | | |
| HH has some livestock | 0.7460 | 0.7930 | 0.0480 | 0.7110 | 0.8060 | 0.0940 |
| | (0.6600) | (0.6380) | (0.0370) | (0.6730) | (0.6300) | (0.0580) |
| Distance to market not reported | 0.1430 | 0.0870 | -0.0560** | 0.1610 | 0.1270 | -0.0340 |
| | (0.5860) | (0.5280) | (0.0260) | (0.5970) | (0.5790) | (0.0570) |
| Distance to nearest road (km) | 0.9790 | 1.7650 | 0.7860*** | 0.9460 | 1.5420 | 0.5960* |
| | (1.3720) | (1.7090) | (0.2590) | (1.3390) | (1.6590) | (0.2940) |
| HH has furniture | 0.9400 | 0.8840 | -0.0560*** | 0.9340 | 0.9050 | -0.0300 |
| | (0.4850) | (0.5670) | (0.0210) | (0.4940) | (0.5430) | (0.0330) |
| HH has access to internet | 0.0160 | 0.0000 | -0.0160*** | 0.0150 | 0.0000 | -0.0150** |
| | (0.3540) | (0.0000) | (0.0060) | (0.3430) | (0.0000) | (0.0050) |
| HH has some Large Ruminants | 0.2910 | 0.3880 | 0.0970** | 0.2410 | 0.3340 | 0.0930 |
| | (0.6740) | (0.7000) | (0.0420) | (0.6540) | (0.6880) | (0.0670) |

## Tables comparing households with DNA analysis (selected sample) with all survey households (full sample) growing each crop, before calibration (all covariates)

Table 14: Comparison of HH Covariates from all Maize growing households from HH Survey and the HH with at least 1 Barcode Identified Sample

| | Full HH Sample | | | Selected Sample | | | Difference | | |
|---|---|---|---|---|---|---|---|---|---|
| | N | Mean | SD | N | Mean | SD | N | Diff | tstats |
| Head is female | 1444 | 0.305 | 0.460 | 315 | 0.267 | 0.443 | 1759 | -0.038 | (-1.371) |
| Age of hh head | 1444 | 46.697 | 15.384 | 315 | 46.851 | 14.949 | 1759 | 0.153 | (0.164) |
| Head completed primary school | 1360 | 0.384 | 0.486 | 305 | 0.410 | 0.493 | 1665 | 0.026 | (0.835) |
| Maximum years of schooling in HH | 1374 | 7.153 | 3.785 | 308 | 7.195 | 3.769 | 1682 | 0.042 | (0.176) |
| Female HH members with main work | 1445 | 0.898 | 0.886 | 315 | 0.943 | 0.861 | 1760 | 0.045 | (0.828) |
| HH members working in the HH farms (7d) | 1445 | 1.625 | 1.423 | 315 | 1.822 | 1.487 | 1760 | 0.197** | (2.150) |
| Female % of labor in farm >50% | 1445 | 0.552 | 0.498 | 315 | 0.473 | 0.500 | 1760 | -0.079** | (-2.528) |
| HH labor force (7d) | 1445 | 1.819 | 1.434 | 315 | 1.978 | 1.481 | 1760 | 0.158* | (1.730) |
| Female HH members in the labor force | 1445 | 0.935 | 0.890 | 315 | 0.971 | 0.861 | 1760 | 0.036 | (0.677) |
| Female share of labor > 50% | 1445 | 0.448 | 0.497 | 315 | 0.400 | 0.491 | 1760 | -0.048 | (-1.561) |
| Female member listed on a parcel title | 1408 | 0.705 | 0.456 | 308 | 0.679 | 0.468 | 1716 | -0.026 | (-0.887) |
| HH owned assets value(UGX mil.) | 1378 | 5.262 | 11.169 | 308 | 7.239 | 15.387 | 1686 | 1.977** | (2.133) |
| Value of assets owned by HH (ihs) | 1378 | 1.377 | 1.318 | 308 | 1.589 | 1.396 | 1686 | 0.212** | (2.437) |
| PCA1 of assets owned by HH N(0,1) | 1372 | -0.151 | 0.549 | 308 | -0.170 | 0.209 | 1680 | -0.018 | (-0.966) |
| Distance to nearest road (km) | 1153 | 1.051 | 1.970 | 315 | 1.322 | 2.130 | 1468 | 0.271** | (2.034) |
| Distance to road is not reported | 1196 | 0.036 | 0.186 | 315 | 0.146 | 0.354 | 1511 | 0.110*** | (5.332) |
| Road distance from dist/subreg/reg | 1005 | 0.024 | 0.153 | 315 | 0.006 | 0.080 | 1320 | -0.018*** | (-2.664) |
| Distance to nearest market (km) | 1015 | 3.438 | 3.567 | 315 | 3.712 | 3.252 | 1330 | 0.274 | (1.278) |
| Distance to market is not reported | 1196 | 0.151 | 0.359 | 315 | 0.210 | 0.408 | 1511 | 0.058** | (2.309) |
| Market distance from dist/subreg/reg | 1005 | 0.032 | 0.176 | 315 | 0.016 | 0.125 | 1320 | -0.016* | (-1.780) |
| Area of parcels owned by HH (acres) | 1445 | 3.127 | 3.255 | 315 | 3.951 | 3.584 | 1760 | 0.825*** | (3.760) |
| Total area of parcels owned by HH (ihs) | 1445 | 1.579 | 0.739 | 315 | 1.810 | 0.743 | 1760 | 0.231*** | (5.004) |
| Area of plots in HH in acres (s2) | 1302 | 0.691 | 0.632 | 315 | 0.705 | 0.683 | 1617 | 0.014 | (0.334) |
| Area of Plot is Missing | 1005 | 0.126 | 0.332 | 315 | 0.124 | 0.330 | 1320 | -0.003 | (-0.120) |
| Western | 1445 | 0.277 | 0.448 | 315 | 0.200 | 0.401 | 1760 | -0.077*** | (-3.017) |
| Eastern | 1445 | 0.302 | 0.459 | 315 | 0.292 | 0.455 | 1760 | -0.010 | (-0.365) |
| Northern | 1445 | 0.275 | 0.447 | 315 | 0.356 | 0.479 | 1760 | 0.081*** | (2.743) |
| Central | 1445 | 0.138 | 0.345 | 315 | 0.152 | 0.360 | 1760 | 0.014 | (0.629) |
| ACHOLI | 1445 | 0.058 | 0.234 | 315 | 0.117 | 0.322 | 1760 | 0.059*** | (3.092) |
| ANKOLE | 1445 | 0.051 | 0.219 | 315 | 0.038 | 0.192 | 1760 | -0.012 | (-1.015) |
| BUKEDI | 1445 | 0.067 | 0.250 | 315 | 0.060 | 0.238 | 1760 | -0.007 | (-0.455) |
| BUNYORO | 1445 | 0.071 | 0.257 | 315 | 0.108 | 0.311 | 1760 | 0.037* | (1.952) |
| BUSOGA | 1445 | 0.089 | 0.284 | 315 | 0.073 | 0.261 | 1760 | -0.016 | (-0.945) |
| ELGON | 1445 | 0.078 | 0.267 | 315 | 0.063 | 0.244 | 1760 | -0.014 | (-0.907) |
| KAMPALA | 1445 | 0.000 | 0.000 | 315 | 0.051 | 0.220 | 1760 | 0.051*** | (4.099) |
| KARAMOJA | 1445 | 0.058 | 0.234 | 315 | 0.006 | 0.080 | 1760 | -0.052*** | (-6.799) |
| KIGEZI | 1445 | 0.105 | 0.307 | 315 | 0.095 | 0.294 | 1760 | -0.010 | (-0.540) |
| LANGO | 1445 | 0.084 | 0.278 | 315 | 0.086 | 0.280 | 1760 | 0.001 | (0.074) |
| NORTH BUGANDA | 1445 | 0.087 | 0.281 | 315 | 0.067 | 0.250 | 1760 | -0.020 | (-1.248) |
| SOUTH BUGANDA | 1445 | 0.054 | 0.226 | 315 | 0.095 | 0.294 | 1760 | 0.041** | (2.344) |
| TESO | 1445 | 0.070 | 0.255 | 315 | 0.048 | 0.213 | 1760 | -0.022 | (-1.618) |
| TOORO | 1445 | 0.055 | 0.227 | 315 | 0.092 | 0.290 | 1760 | 0.037** | (2.152) |

Table 15: Comparison of HH Covariates from all Cassava growing Households from HH Survey and the HH with at least 1 Barcode Identified Sample

| | Full HH Sample | | | Selected Sample | | | Difference | | |
|---|---|---|---|---|---|---|---|---|---|
| | N | Mean | SD | N | Mean | SD | N | Diff | tstats |
| Head is female | 1221 | 0.301 | 0.459 | 645 | 0.299 | 0.458 | 1866 | -0.001 | (-0.060) |
| Age of hh head | 1221 | 46.809 | 15.522 | 645 | 47.206 | 15.587 | 1866 | 0.397 | (0.524) |
| Head completed primary school | 1143 | 0.363 | 0.481 | 615 | 0.366 | 0.482 | 1758 | 0.003 | (0.115) |
| Maximum years of schooling in HH | 1156 | 6.984 | 3.721 | 621 | 6.921 | 3.650 | 1777 | -0.063 | (-0.346) |
| Female HH members with main work: crop/livestock | 1224 | 0.953 | 0.873 | 646 | 0.997 | 0.912 | 1870 | 0.044 | (1.014) |
| HH members working in the HH farms (7d) | 1224 | 1.723 | 1.446 | 646 | 1.851 | 1.527 | 1870 | 0.128* | (1.760) |
| Female share of labor in the farm >50% | 1224 | 0.538 | 0.499 | 646 | 0.511 | 0.500 | 1870 | -0.028 | (-1.134) |
| HH labor force (7d) | 1224 | 1.930 | 1.427 | 646 | 2.060 | 1.512 | 1870 | 0.131* | (1.811) |
| Female HH members in the labor force | 1224 | 1.006 | 0.867 | 646 | 1.045 | 0.906 | 1870 | 0.039 | (0.902) |
| Female share of labor > 50% | 1224 | 0.428 | 0.495 | 646 | 0.396 | 0.490 | 1870 | -0.032 | (-1.331) |
| Female member listed on a parcel title | 1171 | 0.523 | 0.500 | 629 | 0.518 | 0.500 | 1800 | -0.004 | (-0.176) |
| Value of assets owned by HH (UGX mil.) | 1175 | 6.279 | 12.670 | 628 | 6.968 | 13.807 | 1803 | 0.688 | (1.038) |
| Value of assets owned by HH (ihs) | 1175 | 1.591 | 1.318 | 628 | 1.676 | 1.345 | 1803 | 0.085 | (1.292) |
| PCA1 of assets owned by HH N(0,1) | 1169 | -0.028 | 1.064 | 625 | -0.038 | 1.018 | 1794 | -0.010 | (-0.202) |
| Distance to nearest road (km) | 1224 | 1.109 | 2.020 | 646 | 1.125 | 2.099 | 1870 | 0.016 | (0.158) |
| Distance to road is not reported | 1224 | 0.222 | 0.416 | 646 | 0.212 | 0.409 | 1870 | -0.010 | (-0.507) |
| Road distance from dist/subreg/reg | 1224 | 0.017 | 0.130 | 646 | 0.025 | 0.156 | 1870 | 0.008 | (1.063) |
| Distance to nearest market (km) | 1224 | 2.944 | 2.885 | 646 | 3.121 | 2.910 | 1870 | 0.177 | (1.255) |
| Distance to market is not reported | 1224 | 0.328 | 0.470 | 646 | 0.324 | 0.468 | 1870 | -0.005 | (-0.215) |
| Market distance from dist/subreg/reg | 1224 | 0.038 | 0.190 | 646 | 0.087 | 0.282 | 1870 | 0.049*** | (3.979) |
| Area of parcels owned by HH (acres) | 1224 | 2.861 | 3.181 | 646 | 2.913 | 2.485 | 1870 | 0.052 | (0.391) |
| Total area of parcels owned by HH (ihs) | 1224 | 1.495 | 0.739 | 646 | 1.549 | 0.712 | 1870 | 0.054 | (1.552) |
| Area of plots in HH in acres (s2) | 1224 | 0.597 | 0.552 | 646 | 0.598 | 0.568 | 1870 | 0.001 | (0.055) |
| Area of Plot is Missing | 1224 | 0.000 | 0.000 | 646 | 0.015 | 0.124 | 1870 | 0.015*** | (3.185) |
| Western | 1224 | 0.200 | 0.400 | 646 | 0.237 | 0.425 | 1870 | 0.037* | (1.809) |
| Eastern | 1224 | 0.341 | 0.474 | 646 | 0.314 | 0.465 | 1870 | -0.026 | (-1.162) |
| Northern | 1224 | 0.252 | 0.434 | 646 | 0.237 | 0.425 | 1870 | -0.015 | (-0.710) |
| Central | 1224 | 0.177 | 0.382 | 646 | 0.212 | 0.409 | 1870 | 0.035* | (1.788) |
| ACHOLI | 1224 | 0.029 | 0.169 | 646 | 0.020 | 0.141 | 1870 | -0.009 | (-1.265) |
| ANKOLE | 1224 | 0.029 | 0.169 | 646 | 0.031 | 0.173 | 1870 | 0.002 | (0.185) |
| BUKEDI | 1224 | 0.113 | 0.316 | 646 | 0.115 | 0.319 | 1870 | 0.002 | (0.117) |
| BUNYORO | 1224 | 0.071 | 0.257 | 646 | 0.082 | 0.275 | 1870 | 0.011 | (0.839) |
| BUSOGA | 1224 | 0.100 | 0.301 | 646 | 0.079 | 0.270 | 1870 | -0.022 | (-1.577) |
| ELGON | 1224 | 0.043 | 0.204 | 646 | 0.023 | 0.151 | 1870 | -0.020** | (-2.417) |
| KAMPALA | 1224 | 0.000 | 0.000 | 646 | 0.006 | 0.079 | 1870 | 0.006** | (2.005) |
| KARAMOJA | 1224 | 0.011 | 0.103 | 646 | 0.062 | 0.241 | 1870 | 0.051*** | (5.165) |
| KIGEZI | 1224 | 0.056 | 0.229 | 646 | 0.105 | 0.307 | 1870 | 0.050*** | (3.616) |
| LANGO | 1224 | 0.105 | 0.306 | 646 | 0.091 | 0.288 | 1870 | -0.013 | (-0.924) |
| NORTH BUGANDA | 1224 | 0.092 | 0.290 | 646 | 0.121 | 0.326 | 1870 | 0.028* | (1.862) |
| SOUTH BUGANDA | 1224 | 0.089 | 0.285 | 646 | 0.098 | 0.297 | 1870 | 0.008 | (0.595) |
| TESO | 1224 | 0.090 | 0.286 | 646 | 0.062 | 0.241 | 1870 | -0.028** | (-2.231) |
| TOORO | 1224 | 0.063 | 0.243 | 646 | 0.105 | 0.307 | 1870 | 0.042*** | (3.039) |

Table 16: Comparison of HH Covariates from all Banana growing Households from HH Survey and the HH with at least 1 Barcode Identified Sample

| | Full HH Sample | | | Selected Sample | | | Difference | | |
|---|---|---|---|---|---|---|---|---|---|
| | N | Mean | SD | N | Mean | SD | N | Diff | tstats |
| Head is female | 1108 | 0.310 | 0.463 | 710 | 0.324 | 0.468 | 1818 | 0.014 | (0.642) |
| Age of hh head | 1108 | 48.436 | 15.961 | 710 | 49.289 | 16.418 | 1818 | 0.853 | (1.092) |
| Head completed primary school | 1030 | 0.374 | 0.484 | 684 | 0.386 | 0.487 | 1714 | 0.012 | (0.508) |
| Maximum years of schooling in HH | 1044 | 7.189 | 3.806 | 694 | 7.320 | 3.802 | 1738 | 0.131 | (0.704) |
| Female HH members with main work | 1112 | 0.961 | 0.860 | 712 | 0.996 | 0.849 | 1824 | 0.034 | (0.841) |
| HH members working in the HH farms | 1112 | 1.689 | 1.384 | 712 | 1.704 | 1.320 | 1824 | 0.015 | (0.229) |
| Female % of labor in the farm >50% | 1112 | 0.557 | 0.497 | 712 | 0.551 | 0.498 | 1824 | -0.006 | (-0.255) |
| HH labor force (7d) | 1112 | 1.904 | 1.391 | 712 | 1.965 | 1.326 | 1824 | 0.061 | (0.942) |
| Female HH members in the labor force | 1112 | 1.009 | 0.857 | 712 | 1.058 | 0.841 | 1824 | 0.049 | (1.195) |
| Female share of labor > 50% | 1112 | 0.446 | 0.497 | 712 | 0.430 | 0.495 | 1824 | -0.016 | (-0.683) |
| Female member on a parcel title | 1069 | 0.544 | 0.498 | 700 | 0.524 | 0.500 | 1769 | -0.020 | (-0.830) |
| HH assets owned value (UGX mil.) | 1065 | 7.533 | 13.909 | 704 | 8.474 | 15.133 | 1769 | 0.941 | (1.322) |
| Value of assets owned by HH (ihs) | 1065 | 1.785 | 1.349 | 704 | 1.929 | 1.346 | 1769 | 0.144** | (2.196) |
| PCA1 of assets owned by HH N(0,1) | 1062 | -0.001 | 1.094 | 703 | -0.048 | 0.966 | 1765 | -0.047 | (-0.947) |
| Distance to nearest road (km) | 1112 | 0.903 | 1.698 | 712 | 0.914 | 1.890 | 1824 | 0.011 | (0.121) |
| Distance to road is not reported | 1112 | 0.265 | 0.442 | 712 | 0.213 | 0.410 | 1824 | -0.052** | (-2.553) |
| Road distance from dist/subreg/reg | 1112 | 0.021 | 0.142 | 712 | 0.004 | 0.065 | 1824 | -0.016*** | (-3.353) |
| Distance to nearest market (km) | 1111 | 2.786 | 2.816 | 712 | 2.861 | 2.993 | 1823 | 0.075 | (0.533) |
| Distance to market is not reported | 1112 | 0.409 | 0.492 | 712 | 0.375 | 0.484 | 1824 | -0.034 | (-1.461) |
| Market distance from dist/subreg/reg | 1112 | 0.042 | 0.201 | 712 | 0.035 | 0.184 | 1824 | -0.007 | (-0.780) |
| Area of parcels owned by HH (acres) | 1112 | 2.700 | 3.160 | 712 | 2.701 | 2.656 | 1824 | 0.001 | (0.005) |
| Total area of HH parcels (ihs) | 1112 | 1.426 | 0.755 | 712 | 1.457 | 0.721 | 1824 | 0.031 | (0.879) |
| Area of plots in HH in acres (s2) | 1112 | 0.587 | 0.633 | 712 | 0.580 | 0.636 | 1824 | -0.006 | (-0.199) |
| Area of Plot is Missing | 1112 | 0.000 | 0.000 | 712 | 0.000 | 0.000 | 1824 | 0.000 | (.) |
| Western | 1112 | 0.353 | 0.478 | 712 | 0.431 | 0.496 | 1824 | 0.078*** | (3.314) |
| Eastern | 1112 | 0.279 | 0.449 | 712 | 0.284 | 0.451 | 1824 | 0.005 | (0.228) |
| Northern | 1112 | 0.089 | 0.285 | 712 | 0.059 | 0.236 | 1824 | -0.030** | (-2.444) |
| Central | 1112 | 0.201 | 0.401 | 712 | 0.226 | 0.419 | 1824 | 0.026 | (1.295) |
| ACHOLI | 1112 | 0.017 | 0.130 | 712 | 0.014 | 0.118 | 1824 | -0.003 | (-0.517) |
| ANKOLE | 1112 | 0.087 | 0.282 | 712 | 0.077 | 0.267 | 1824 | -0.010 | (-0.761) |
| BUKEDI | 1112 | 0.073 | 0.260 | 712 | 0.052 | 0.222 | 1824 | -0.021* | (-1.830) |
| BUNYORO | 1112 | 0.058 | 0.233 | 712 | 0.066 | 0.248 | 1824 | 0.008 | (0.726) |
| BUSOGA | 1112 | 0.090 | 0.286 | 712 | 0.093 | 0.290 | 1824 | 0.003 | (0.200) |
| ELGON | 1112 | 0.105 | 0.307 | 712 | 0.122 | 0.328 | 1824 | 0.017 | (1.106) |
| KAMPALA | 1112 | 0.000 | 0.000 | 712 | 0.003 | 0.053 | 1824 | 0.003 | (1.415) |
| KARAMOJA | 1112 | 0.000 | 0.000 | 712 | 0.221 | 0.415 | 1824 | 0.221*** | (14.182) |
| KIGEZI | 1112 | 0.171 | 0.377 | 712 | 0.031 | 0.173 | 1824 | -0.140*** | (-10.746) |
| LANGO | 1112 | 0.050 | 0.219 | 712 | 0.097 | 0.296 | 1824 | 0.047*** | (3.612) |
| NORTH BUGANDA | 1112 | 0.103 | 0.303 | 712 | 0.129 | 0.336 | 1824 | 0.027* | (1.719) |
| SOUTH BUGANDA | 1112 | 0.109 | 0.312 | 712 | 0.017 | 0.129 | 1824 | -0.092*** | (-8.745) |
| TESO | 1112 | 0.014 | 0.119 | 712 | 0.067 | 0.251 | 1824 | 0.053*** | (5.271) |
| TOORO | 1112 | 0.101 | 0.301 | 712 | 0.011 | 0.105 | 1824 | -0.089*** | (-9.079) |

Table 17: Comparison of HH Covariates from all Beans growing Households from HH Survey and the HH with at least 1 Barcode Identified Sample

| | Full HH Sample | | | Selected Sample | | | Difference | |
|---|---|---|---|---|---|---|---|---|
| | N | Mean | SD | N | Mean | SD | N | Diff | tstats |
| Head is female | 1272 | 0.320 | 0.467 | 365 | 0.337 | 0.473 | 1637 | 0.017 | (0.607) |
| Age of hh head | 1272 | 46.681 | 15.549 | 365 | 47.334 | 15.506 | 1637 | 0.653 | (0.709) |
| Head completed primary school | 1188 | 0.401 | 0.490 | 343 | 0.426 | 0.495 | 1531 | 0.025 | (0.825) |
| Maximum years of schooling in HH | 1202 | 7.209 | 3.818 | 349 | 7.321 | 3.927 | 1551 | 0.112 | (0.472) |
| Female HH members with main work | 1274 | 0.936 | 0.836 | 366 | 1.022 | 0.847 | 1640 | 0.086* | (1.722) |
| HH members working in the HH farms (7d) | 1274 | 1.647 | 1.358 | 366 | 1.754 | 1.336 | 1640 | 0.107 | (1.349) |
| Female share of labor in the farm >50% | 1274 | 0.560 | 0.497 | 366 | 0.557 | 0.497 | 1640 | -0.002 | (-0.077) |
| HH labor force (7d) | 1274 | 1.878 | 1.376 | 366 | 1.997 | 1.335 | 1640 | 0.120 | (1.501) |
| Female HH members in the labor force | 1274 | 0.987 | 0.835 | 366 | 1.071 | 0.821 | 1640 | 0.084* | (1.726) |
| Female share of labor > 50% | 1274 | 0.440 | 0.497 | 366 | 0.443 | 0.497 | 1640 | 0.003 | (0.104) |
| Female member listed on a parcel title | 1214 | 0.552 | 0.498 | 352 | 0.455 | 0.499 | 1566 | -0.097*** | (-3.227) |
| Value of assets owned by HH (UGX mil.) | 1223 | 7.029 | 13.684 | 357 | 9.146 | 16.685 | 1580 | 2.117** | (2.192) |
| Value of assets owned by HH (ihs) | 1223 | 1.680 | 1.360 | 357 | 1.998 | 1.348 | 1580 | 0.319*** | (3.921) |
| PCA1 of assets owned by HH N(0,1) | 1218 | 0.003 | 1.112 | 356 | 0.085 | 1.288 | 1574 | 0.081 | (1.078) |
| Distance to nearest road (km) | 1274 | 0.956 | 1.753 | 366 | 0.810 | 1.744 | 1640 | -0.147 | (-1.415) |
| Distance to road is not reported | 1274 | 0.255 | 0.436 | 366 | 0.306 | 0.461 | 1640 | 0.051* | (1.883) |
| Road distance from dist/subreg/reg | 1274 | 0.014 | 0.118 | 366 | 0.014 | 0.116 | 1640 | -0.000 | (-0.068) |
| Distance to nearest market (km) | 1274 | 3.021 | 3.210 | 366 | 2.627 | 3.022 | 1640 | -0.393** | (-2.163) |
| Distance to market is not reported | 1274 | 0.372 | 0.484 | 366 | 0.443 | 0.497 | 1640 | 0.071** | (2.407) |
| Market distance from dist/subreg/reg | 1274 | 0.031 | 0.172 | 366 | 0.030 | 0.171 | 1640 | -0.001 | (-0.055) |
| Area of parcels owned by HH (acres) | 1274 | 2.798 | 3.124 | 366 | 2.863 | 2.855 | 1640 | 0.065 | (0.376) |
| Total area of parcels owned by HH (ihs) | 1274 | 1.466 | 0.748 | 366 | 1.490 | 0.755 | 1640 | 0.023 | (0.519) |
| Area of plots in HH in acres (s2) | 1274 | 0.557 | 0.593 | 366 | 0.585 | 0.615 | 1640 | 0.029 | (0.798) |
| Area of Plot is Missing | 1274 | 0.000 | 0.000 | 366 | 0.000 | 0.000 | 1640 | 0.000 | (.) |
| Western | 1274 | 0.374 | 0.484 | 366 | 0.489 | 0.501 | 1640 | 0.115*** | (3.917) |
| Eastern | 1274 | 0.230 | 0.421 | 366 | 0.164 | 0.371 | 1640 | -0.066*** | (-2.912) |
| Northern | 1274 | 0.152 | 0.359 | 366 | 0.079 | 0.270 | 1640 | -0.073*** | (-4.208) |
| Central | 1274 | 0.179 | 0.383 | 366 | 0.268 | 0.443 | 1640 | 0.089*** | (3.476) |
| ACHOLI | 1274 | 0.016 | 0.124 | 366 | 0.008 | 0.090 | 1640 | -0.008 | (-1.279) |
| ANKOLE | 1274 | 0.072 | 0.259 | 366 | 0.112 | 0.316 | 1640 | 0.040** | (2.208) |
| BUKEDI | 1274 | 0.052 | 0.222 | 366 | 0.046 | 0.211 | 1640 | -0.005 | (-0.424) |
| BUNYORO | 1274 | 0.082 | 0.275 | 366 | 0.057 | 0.233 | 1640 | -0.025* | (-1.738) |
| BUSOGA | 1274 | 0.078 | 0.269 | 366 | 0.071 | 0.257 | 1640 | -0.007 | (-0.484) |
| ELGON | 1274 | 0.098 | 0.298 | 366 | 0.046 | 0.211 | 1640 | -0.052*** | (-3.740) |
| KAMPALA | 1274 | 0.000 | 0.000 | 366 | 0.000 | 0.000 | 1640 | 0.000 | (.) |
| KARAMOJA | 1274 | 0.042 | 0.200 | 366 | 0.232 | 0.423 | 1640 | 0.191*** | (8.361) |
| KIGEZI | 1274 | 0.159 | 0.365 | 366 | 0.055 | 0.228 | 1640 | -0.104*** | (-6.621) |
| LANGO | 1274 | 0.062 | 0.241 | 366 | 0.098 | 0.298 | 1640 | 0.036** | (2.140) |
| NORTH BUGANDA | 1274 | 0.097 | 0.295 | 366 | 0.169 | 0.376 | 1640 | 0.073*** | (3.419) |
| SOUTH BUGANDA | 1274 | 0.090 | 0.287 | 366 | 0.000 | 0.000 | 1640 | -0.090*** | (-11.239) |
| TESO | 1274 | 0.005 | 0.074 | 366 | 0.087 | 0.283 | 1640 | 0.082*** | (5.488) |
| TOORO | 1274 | 0.113 | 0.317 | 366 | 0.016 | 0.127 | 1640 | -0.097*** | (-8.716) |

Table 18: Comparison of HH Covariates from all Sweet Potato growing households from HH Survey and the HH with at least 1 Barcode Identified Sample

| | Full HH Sample | | | Selected Sample | | | Difference | | |
|---|---|---|---|---|---|---|---|---|---|
| | N | Mean | SD | N | Mean | SD | N | Diff | tstats |
| Head is female | 889 | 0.294 | 0.456 | 590 | 0.308 | 0.462 | 1479 | 0.015 | (0.610) |
| Age of hh head | 889 | 47.105 | 15.503 | 590 | 47.769 | 15.829 | 1479 | 0.665 | (0.798) |
| Head completed primary school | 815 | 0.393 | 0.489 | 546 | 0.390 | 0.488 | 1361 | -0.003 | (-0.094) |
| Maximum years of schooling in HH | 826 | 7.450 | 3.698 | 551 | 7.475 | 3.695 | 1377 | 0.025 | (0.124) |
| Female HH members with main work | 891 | 0.981 | 0.889 | 590 | 0.980 | 0.880 | 1481 | -0.001 | (-0.027) |
| HH members working in the HH farms | 891 | 1.746 | 1.472 | 590 | 1.769 | 1.502 | 1481 | 0.023 | (0.293) |
| Female % of labor in the farm >50% | 891 | 0.547 | 0.498 | 590 | 0.539 | 0.499 | 1481 | -0.008 | (-0.287) |
| HH labor force (7d) | 891 | 1.957 | 1.472 | 590 | 1.985 | 1.484 | 1481 | 0.027 | (0.349) |
| Female HH members in the labor force | 891 | 1.020 | 0.879 | 590 | 1.019 | 0.867 | 1481 | -0.002 | (-0.034) |
| Female share of labor > 50% | 891 | 0.433 | 0.496 | 590 | 0.424 | 0.495 | 1481 | -0.009 | (-0.361) |
| Female member on a parcel title | 850 | 0.548 | 0.498 | 570 | 0.537 | 0.499 | 1420 | -0.011 | (-0.422) |
| HH assets owned value (UGX mil.) | 846 | 6.652 | 12.685 | 564 | 6.375 | 11.634 | 1410 | -0.277 | (-0.423) |
| Value of assets owned by HH (ihs) | 846 | 1.654 | 1.343 | 564 | 1.635 | 1.323 | 1410 | -0.019 | (-0.256) |
| PCA1 of assets owned by HH N(0,1) | 842 | 0.015 | 1.176 | 560 | -0.002 | 1.134 | 1402 | -0.017 | (-0.265) |
| Distance to nearest road (km) | 891 | 0.996 | 1.990 | 590 | 1.101 | 2.189 | 1481 | 0.106 | (0.943) |
| Distance to road is not reported | 891 | 0.238 | 0.426 | 590 | 0.224 | 0.417 | 1481 | -0.014 | (-0.636) |
| Road distance from dist/subreg/reg | 891 | 0.028 | 0.165 | 590 | 0.042 | 0.202 | 1481 | 0.014 | (1.435) |
| Distance to nearest market (km) | 890 | 2.821 | 2.875 | 590 | 2.992 | 2.864 | 1480 | 0.171 | (1.122) |
| Distance to market is not reported | 891 | 0.337 | 0.473 | 590 | 0.308 | 0.462 | 1481 | -0.028 | (-1.140) |
| Market distance from dist/subreg/reg | 891 | 0.051 | 0.219 | 590 | 0.068 | 0.252 | 1481 | 0.017 | (1.362) |
| Area of parcels owned by HH (acres) | 891 | 2.778 | 2.559 | 590 | 2.945 | 2.659 | 1481 | 0.166 | (1.196) |
| Total area of HH parcels (ihs) | 891 | 1.498 | 0.711 | 590 | 1.555 | 0.710 | 1481 | 0.057 | (1.509) |
| Area of plots in HH in acres (s2) | 891 | 0.531 | 0.507 | 590 | 0.525 | 0.461 | 1481 | -0.006 | (-0.218) |
| Area of Plot is Missing | 891 | 0.000 | 0.000 | 590 | 0.000 | 0.000 | 1481 | 0.000 | (.) |
| Western | 891 | 0.302 | 0.459 | 590 | 0.305 | 0.461 | 1481 | 0.003 | (0.130) |
| Eastern | 891 | 0.327 | 0.469 | 590 | 0.342 | 0.475 | 1481 | 0.016 | (0.629) |
| Northern | 891 | 0.162 | 0.368 | 590 | 0.208 | 0.407 | 1481 | 0.047** | (2.253) |
| Central | 891 | 0.167 | 0.373 | 590 | 0.144 | 0.351 | 1481 | -0.023 | (-1.211) |
| ACHOLI | 891 | 0.040 | 0.197 | 590 | 0.051 | 0.220 | 1481 | 0.010 | (0.932) |
| ANKOLE | 891 | 0.034 | 0.180 | 590 | 0.022 | 0.147 | 1481 | -0.012 | (-1.361) |
| BUKEDI | 891 | 0.090 | 0.286 | 590 | 0.092 | 0.289 | 1481 | 0.002 | (0.114) |
| BUNYORO | 891 | 0.072 | 0.258 | 590 | 0.071 | 0.257 | 1481 | -0.001 | (-0.047) |
| BUSOGA | 891 | 0.121 | 0.327 | 590 | 0.103 | 0.305 | 1481 | -0.018 | (-1.071) |
| ELGON | 891 | 0.026 | 0.159 | 590 | 0.029 | 0.167 | 1481 | 0.003 | (0.345) |
| KAMPALA | 891 | 0.000 | 0.000 | 590 | 0.005 | 0.071 | 1481 | 0.005* | (1.735) |
| KARAMOJA | 891 | 0.007 | 0.082 | 590 | 0.173 | 0.378 | 1481 | 0.166*** | (10.502) |
| KIGEZI | 891 | 0.169 | 0.375 | 590 | 0.086 | 0.281 | 1481 | -0.083*** | (-4.857) |
| LANGO | 891 | 0.065 | 0.247 | 590 | 0.078 | 0.268 | 1481 | 0.013 | (0.933) |
| NORTH BUGANDA | 891 | 0.098 | 0.297 | 590 | 0.066 | 0.249 | 1481 | -0.032** | (-2.209) |
| SOUTH BUGANDA | 891 | 0.074 | 0.262 | 590 | 0.119 | 0.324 | 1481 | 0.045*** | (2.793) |
| TESO | 891 | 0.093 | 0.291 | 590 | 0.039 | 0.194 | 1481 | -0.054*** | (-4.302) |
| TOORO | 891 | 0.056 | 0.230 | 590 | 0.066 | 0.249 | 1481 | 0.010 | (0.779) |

Table 19: Comparison of HH Covariates from all Groundnut growing households from HH Survey and the HH with at least 1 Barcode Identified Sample

| | Full HH Sample | | | Selected Sample | | | Difference | | |
|---|---|---|---|---|---|---|---|---|---|
| | N | Mean | SD | N | Mean | SD | N | Diff | tstats |
| Head is female | 518 | 0.359 | 0.480 | 128 | 0.359 | 0.482 | 646 | 0.000 | (0.006) |
| Age of hh head | 518 | 49.002 | 15.046 | 128 | 51.453 | 15.947 | 646 | 2.451 | (1.574) |
| Head completed primary school | 498 | 0.426 | 0.495 | 126 | 0.429 | 0.497 | 624 | 0.003 | (0.058) |
| Maximum years of schooling in HH | 504 | 7.615 | 3.748 | 128 | 7.117 | 3.789 | 632 | -0.498 | (-1.331) |
| Female HH members with main work | 519 | 0.954 | 0.844 | 128 | 0.961 | 0.846 | 647 | 0.007 | (0.086) |
| HH members working in the HH farms | 519 | 1.645 | 1.380 | 128 | 1.734 | 1.455 | 647 | 0.089 | (0.625) |
| Female % of labor in the farm >50% | 519 | 0.574 | 0.495 | 128 | 0.539 | 0.500 | 647 | -0.035 | (-0.713) |
| HH labor force (7d) | 519 | 1.830 | 1.385 | 128 | 1.891 | 1.459 | 647 | 0.060 | (0.422) |
| Female HH members in the labor force | 519 | 0.983 | 0.839 | 128 | 0.969 | 0.851 | 647 | -0.014 | (-0.166) |
| Female share of labor > 50% | 519 | 0.476 | 0.500 | 128 | 0.469 | 0.501 | 647 | -0.007 | (-0.145) |
| Female member on a parcel title | 507 | 0.751 | 0.433 | 126 | 0.651 | 0.479 | 633 | -0.101** | (-2.153) |
| HH assets owned value (UGX mil.) | 504 | 5.940 | 10.428 | 128 | 5.119 | 11.168 | 632 | -0.821 | (-0.753) |
| Value of assets owned by HH (ihs) | 504 | 1.648 | 1.281 | 128 | 1.474 | 1.236 | 632 | -0.174 | (-1.409) |
| PCA1 of assets owned by HH N(0,1) | 501 | -0.184 | 0.210 | 126 | -0.223 | 0.151 | 627 | -0.039** | (-2.359) |
| Distance to nearest road (km) | 519 | 0.980 | 1.878 | 128 | 1.774 | 2.887 | 647 | 0.793*** | (2.959) |
| Distance to road is not reported | 519 | 0.164 | 0.370 | 128 | 0.133 | 0.341 | 647 | -0.031 | (-0.905) |
| Road distance from dist/subreg/reg | 519 | 0.000 | 0.000 | 128 | 0.008 | 0.088 | 647 | 0.008 | (1.000) |
| Distance to nearest market (km) | 519 | 3.385 | 3.267 | 128 | 3.768 | 3.209 | 647 | 0.383 | (1.204) |
| Distance to market is not reported | 519 | 0.241 | 0.428 | 128 | 0.117 | 0.323 | 647 | -0.124*** | (-3.619) |
| Market distance from dist/subreg/reg | 519 | 0.010 | 0.098 | 128 | 0.023 | 0.152 | 647 | 0.014 | (0.979) |
| Area of parcels owned by HH (acres) | 519 | 3.792 | 3.978 | 128 | 3.562 | 3.218 | 647 | -0.230 | (-0.690) |
| Total area of HH parcels (ihs) | 519 | 1.764 | 0.735 | 128 | 1.739 | 0.687 | 647 | -0.024 | (-0.354) |
| Area of plots in HH in acres (s2) | 519 | 0.720 | 0.725 | 128 | 0.727 | 0.676 | 647 | 0.008 | (0.116) |
| Area of Plot is Missing | 519 | 0.000 | 0.000 | 128 | 0.000 | 0.000 | 647 | 0.000 | (.) |
| Western | 519 | 0.295 | 0.456 | 128 | 0.125 | 0.332 | 647 | -0.170*** | (-4.779) |
| Eastern | 519 | 0.295 | 0.456 | 128 | 0.516 | 0.502 | 647 | 0.221*** | (4.538) |
| Northern | 519 | 0.285 | 0.452 | 128 | 0.250 | 0.435 | 647 | -0.035 | (-0.813) |
| Central | 519 | 0.123 | 0.329 | 128 | 0.109 | 0.313 | 647 | -0.014 | (-0.446) |
| ACHOLI | 519 | 0.091 | 0.287 | 128 | 0.039 | 0.195 | 647 | -0.051** | (-2.415) |
| ANKOLE | 519 | 0.052 | 0.222 | 128 | 0.008 | 0.088 | 647 | -0.044*** | (-3.537) |
| BUKEDI | 519 | 0.071 | 0.258 | 128 | 0.070 | 0.257 | 647 | -0.001 | (-0.039) |
| BUNYORO | 519 | 0.102 | 0.303 | 128 | 0.055 | 0.228 | 647 | -0.047* | (-1.963) |
| BUSOGA | 519 | 0.052 | 0.222 | 128 | 0.016 | 0.125 | 647 | -0.036** | (-2.475) |
| ELGON | 519 | 0.042 | 0.202 | 128 | 0.055 | 0.228 | 647 | 0.012 | (0.558) |
| KAMPALA | 519 | 0.000 | 0.000 | 128 | 0.047 | 0.212 | 647 | 0.047** | (2.499) |
| KARAMOJA | 519 | 0.025 | 0.156 | 128 | 0.008 | 0.088 | 647 | -0.017* | (-1.657) |
| KIGEZI | 519 | 0.073 | 0.261 | 128 | 0.094 | 0.293 | 647 | 0.021 | (0.726) |
| LANGO | 519 | 0.081 | 0.273 | 128 | 0.086 | 0.281 | 647 | 0.005 | (0.182) |
| NORTH BUGANDA | 519 | 0.075 | 0.264 | 128 | 0.023 | 0.152 | 647 | -0.052*** | (-2.916) |
| SOUTH BUGANDA | 519 | 0.048 | 0.214 | 128 | 0.375 | 0.486 | 647 | 0.327*** | (7.432) |
| TESO | 519 | 0.129 | 0.336 | 128 | 0.055 | 0.228 | 647 | -0.074*** | (-2.978) |
| TOORO | 519 | 0.069 | 0.254 | 128 | 0.070 | 0.257 | 647 | 0.001 | (0.038) |

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