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Progress Narrative First Year SweetGAINS

Use this form to provide updates to your foundation program officer regarding progress made toward achieving your project's stated outputs and outcomes.

The Progress Narrative must be submitted in Word, as PDFs will not be accepted.

General Information

Investment Title	SweetGAINS: Genetic Advances and Innovative Seed Systems for Sweet Potato		
Grantee/Vendor	International Potato Center		
Primary Contact	Hugo Campos	**Investment Start Date**	September 6, 2019
Feedback Contact[1]		**Investment End Date**	September 30, 2022
Feedback Email[1]		**Reporting Period Start Date**	September 6, 2019
Program Officer	Jim Lorenzen	**Reporting Period End Date**	September 30, 2020
Program Coordinator	Randy Shigetani	**Reporting Due Date**	October 31, 2020
Investment Total	$15,000,000.00	**Opportunity/Contract ID**	OPP1213329/INV-002971
Scheduled Payment Amount (If applicable)	$4,852,618.00		

[1] Feedback Contact/Email: The full name and email of the contact whom foundation staff queries for various surveys.

Submission Information

By submitting this report, I declare that I am authorized to certify, on behalf of the grantee or vendor identified on page 1, that I have examined the following statements and related attachments, and that to the best of my knowledge, they are true, correct and complete. I hereby also confirm that the grantee or vendor identified on page 1 has complied with all of the terms and conditions of the Grant Agreement or Contract for Services, as applicable, including but not limited to the clauses contained therein regarding Use of Funds, Anti-Terrorism, Subgrants and Subcontracts, and Regulated Activities.

Date Submitted	[October 31, 2020]	**Submitted by Contact Name**	Hugo Campos
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Acronyms

BLUPs	Best Linear Unbiased Predictions
BMGF	Bill & Melinda Gates Foundation
BrAPI	Breeding Application Programming
BTI	Boyce Thompson Institute
CIP	International Potato Center
CoP	Community of Practice
CSIR	The Council for Scientific and Industrial Research
DARS	Department of Agricultural Research Services
DDBIO	Development and delivery of Biofortified crops at scale
DFID	Department for International Development of the United Kingdom
DM	Dry matter
DNA	Deoxyribonucleic acid
DVM	Decentralized Vine Multiplier
EAB	External Advisory Board
EGS	Early Generation Seed
EiB	Excellence in Breeding
FCG	Focus Group Discussion
Fe	Iron
GP	Genomic Prediction
GS	Genomic Selection
GT4SP	Genomic Tools for Sweetpotato
IIAM	Mozambique Institute of Agricultural Research
INERA	Institut de l'Environnement et du Recherches Agricoles de Burkina Faso
KEPHIS	Kenya Plant Health Inspectorate Service
MDP	Mwanga Diversity Panel
MEL	Monitoring, Evaluation and Learning
MET	Multi environment Testing
NaCRRI	National Agricultural Crop Resources Research Institute
NARI	National Agricultural Research Institute
NaSARRI	National Semi Arid Resources Research Institute
NCSU	North Carolina State University
NGO	Non-governmental organization
NGO	Non-governmental organization
NIR	Near infrared spectroscopy
NRCRI	National Root Crops Research Institute Umudike
OFSP	Orange-fleshed Sweetpotato
PEARL	Program for Emerging Agricultural Research Leaders
QA	Quality Assurance
QC	Quality control
RAB	Rwanda Agriculture and Animal Resources Development Board
RTB	Roots, Tubers and Bananas
SARI	South Agricultural Research Institute
SASHA	Sweetpotato Action for Security and Health in Africa
SNP	Single-Nucleotide Polymorphism
SOPs	Standard Operating Procedures
SPBase	Sweetpotato Base
SPCSV	Sweetpotato Chlorotic Stunt Crinivirus
SPFMV	Sweetpotato Feathery Mottle Virus
SPVD	Sweetpotato Virus Disease
SPW	Sweetpotato weevil
SSA	Sub-Saharan Africa
SST	SweetPotato Tracker
SweetGAINS	Genetic Advances and Innovative Seed Systems for sweetpotato
TARI	Tanzania Agricultural Research Institute
TPEs	Target population of environments
WP	Work Package
Zn	Zinc

1. Progress Details

Provide information regarding the current period's progress toward achieving the investment outputs and outcomes as well as the work planned or anticipated for the next period. In addition, submit the Results Tracker with actual results as requested.

Executive Summary and main highlights

SweetGAINS's Primary Outcome is the modernization of breeding programs at International Potato Center (CIP) and at least 4 NARIs in Africa by 2022. It is an ambitious, yet attainable goal, which would require not only the upgrade and expansion of current breeding operations, but also to organize the way work is organized so that such breeding programs become high-performing teams. To achieve this, not only several breeding technology aspects will be upgraded and/or incorporated, but also change management aspects as well. This Bill & Melinda Gates Foundation (BMGF) investment builds upon previous, successful ones, namely SASHA I and II, and GT4SP, led by CIP and North Carolina State University (NCSU), respectively. SweetGAINS is organized around 4 Work Packages, which address multiple aspects of both breeding and seed research, since in order to increase genetic gains and the turnover of varieites at the smallholder level, not only effective breeding programs are required, but also equally effective seed delivery pathways.

This reports provides an account of research activities carried out between September 2019 and September 2020. It describes and connects activities carried out and main findings, and also deviations. Furthermore, it provides, on an outcome basis, a summary of COVID-19 impacts and ensuing work. The impact of COVID-19 has on the ability to implement field, and some lab activities, has been substantial because of country lockdowns, travel bans, and the constraints on conducting field work. A full account about the impact of COVID-19 on SweetGAINS operations, and mitigation measures taken, is provided in **Annex 0**.

A much more detailed accout of activities carried out, and technical details, is provided through multiple Annexes, which expand and deepen the science/technology narrative provided on this report. Despite this being SweetGAINS's first year of execution, and although scientific publications and presentations are not a priority outcome, several papers were published and presentations delivered, all of which are available in the ensuing links:

Workpackage 1

Workpackage 2

Workpackage 3

Workpackage 4

Work Package 1 (WP1)

WP1 is focused upon providing governance and project management for SweetGAINS. In addition, it is accountable for instilling an operational excellence/continuous improvement mindset, including the systematic calculation of genetic gains, akin to that already existing in most private breeding organizations. Breeding programs in the One CG centers are becoming more customer-driven, and more focused on designing Product Profiles[1] and ancillary activities upon which breeding pipelines and priorities are established. WP1 also provides the training and tools needed for these objectives to participant NARIs (National Agricultural Research Institutes) from Zambia, Mozambique, Rwanda, Malawi, Tanzania, Uganda, Ethiopia, Ghana, Nigeria and Burkina Faso, so sweetpotato breeding operations become much more customer-driven. WP1 is also accountable for research focused on varietal preference and gender, and for analyzing the Target Population of Environments (TPEs) targeted by SweetGAINS. WP1 is led by Hugo Campos from CIP.

During SweetGAINS's first year of execution, statistical approaches to analyze and establish TPEs have been gathered and discussed, and these will be implemented during the second and third years of SweetGAINS's life cycle. Briefly, linear mixed models with appropriate variance/covariance matrices have been identified already, which will be implemented, and legacy breeding datasets identified which will be used to further refine TPEs. In collaboration with WPs, extensive curation of previous breeding datasets has been nearly completed. Similar work has been conducted with updated statistical approaches to estimate genetic gains from datasets encompassing varieties from different decades and breeding legacy datasets, which will be implemented during the second year of project execution.

[1] Throughout this document, by product profile we will refer to the description of an individual product created based on the product concept definition. In turn, each product concept is identified and defined by the relevant set of key traits with minimum trait scores for each key trait required in a new product for a specific market segment to meet and/or exceed "customer" needs. Each product will have a unique product profile that will be used to describe and position the unique new product. These are current definitions from the Excellence in Breeding initiative (https://excellenceinbreeding.org/)

Field surveys have been conducted in targeted regions of Uganda and Mozambique to gain insight about which are the most preferred varieties, taking into account a gender perspective. As an example, in Uganda significant differences were observed between male and female preferences. For example, in Kamuli about 67% and 100% of men and women grew NASPOT 9 O, respectively. A similar situation was observed in Tanzania: In Butiama, 50% and 100% of male and female farmers prefer the variety Polista, respectively. In addition, using tools developed by the RTB Gender Platform and Excellence in Breeding, the first set of gender responsive Product Profiles is being developed. Surveys could not be conducted in Mozambique, and will be executed during the reminder of the year.

As a joint activity with Work Package 2, substantial progress has been achieved in operational excellence, as the first set of SOP (Standard Operational Procedures) targeting several aspects of data management such as phenotyping data management, crossing data management, and genotyping project management and tracking among others, have been developed and shared with NARIs (National Agricultural Research Institutes). An intensive training effort is being currently deployed to achieve full implementation of such SOPs across all CIP and NARIs sweetpotato breeding operations in Africa.

Agreements have been established with all participant NARIs but TARI (Tanzania), has been already agreed upon and awaits signatures in Tanzania. Such agreements will not only provide the resources needed, but also will drive the modernization of breeding operations at such NARIs. We anticipate to sign the agreement with TARI within the next few weeks.

A communications plan was developed and its implementation inittiatied, both within SweetGAINS and toward external stakeholders. An effective governance system has been established at several levels: at the more tactical one, Microsoft Project was chosen as the software to support project management and to link activities with financial resources. At a more strategic level, the SLT (SweetGAINS's Leadership Team) provides the analysis and decision making required at the SweetGAINS level, and an External Advisory Board (EAB) provides an external strategic perspective to ensure SweetGAINS is able to achieve its goals beyond expectations. EAB includes members from industry, private consultants with extensive experience in Africa, academics and NaCRRI's DG. Moreover, a MEL (Monitoring, Evaluation and Learning) system has been established, which is compliant with BMGF expectations.

WP1 Main achievements

- Insights gained about preferences of sweetpotato varieties more systematically and objectively, across different stakeholder groups. For example, in a targeted Ugandan region, despite NASPOT 8 having high levels of beta-carotene, its poor taste has made it less preferred among producers and consumers.
- Governance structures have been established at several levels, from establishing a functional External Advisory Board (EAB) to implementing Microsoft Project for a better monitoring of both activities and financial aspects.
- Operational Excellence progress with several SOPs developed and in the process of full implementation. Such SOPs will in addition facilitate data workflows towards SPBase (Sweetpotato database, managed from Boyce Thmpson Institute) as a central data management system
- Formal agreements with NARIs have been established, driving the modernization of breeding operations and providing the support required.

Work Package 2 (WP2)

WP2 represents the genetic improvement engine of SweetGAINS, and it is led by Maria Andrade from CIP. The major breeding hubs during the First Year were Mozambique (led by Maria Andrade), Uganda (led by Robert Mwanga until September 2020, and by Jolien Swanckaert from October 2020 onwards), and Ghana (led by Reuben Ssali), and a wide network of 10 NARIs. Ghana/West Africa breeding operations were terminated on September 2020.

In order to accelerate breeding activities related to improved cooking quality, and building on progress achieved by BMGF's RTBFood investment in Uganda, SOPs were established. Large genotypic differences were observed in terms of cooking time and dry matter after cooking in Mozambique. Similar activities are underway in Uganda, focused on the Mwanga Diversity Panel, a large diallel population established from several elite parents and key founders that encompasses 16 parents and 64 families. Large surveys to develop gender-aware sensory descriptors were carried out in Mozambique. Sex disaggregated market/trader, farmer and restaurant/consumer preferred traits were identified. SweetGAINS enabled the purchase of equipment to assess sensorial and texture characteristics,and also to upgrade kitchen facilities in order to achieve the high throughput needed for sensory quality selection purposes. The taste and aroma of boiled roots were the two most important sensory quality traits identified by consumers of sweetpotato, both women and men, respondents.

Progress towards developing hybrid sweetpotato varieties was also attained. In Uganda, 20 elite parents from either populations A and B were selected on the basis of BLUPs/GCA for key traits such as commercial storage root yield and sweetpotato virus disease (SPVD). Over 260,000 and 75,000 botanical seeds were harvested as polycrosses from population A and B, respectively. Similar progress was achieved in Mozambique, and hybrid progenies are currently in observation nurseries at two locations. Refocused breeding efforts in

Mozambique are making towards high enough levels of Fe content so as to develop stacked (Vitamin A + High Fe) biofortified sweetpotatoes, since current Fe levels ones does not support product development.

Excellent progress was achieved in terms of data management and operational excellence, with a set of Standard Operational Procedures (SOPs) developed through the data management Community of Practice (CoP), aggressive rolling out of novel statistical designs across CIP and NARI partners, and extensive curation of breeding datasets. Quality control of data has been improved as well, and training provided to NARIs on the use of the Field Book App and SPBase.

TARI in Tanzania identified nearly 90 clones out of which new varieties will be developed, and SARI in Ethiopia conducted several on-farm trials at highland areas in the Gedeo zone, and also large breeders seed multiplication of three newly released varieties, one OFSP (Orange Fleshed Sweetpotato) and two white fleshed varieties. RAB at Rwanda continued the multiplication of clones through tissue culture and started breeding trials with botanical seed from Uganda and Mozambique. In Ghana, four new varieties were released (SARI-Suyolo (PGA14008-9), SARI-Janlow (PGA14011-43), SARI-Tiemeh (PGA14372-3) and SARI-Nyoriberi-gu (PGA14398-4). In Ghana, a key focus remained on developing less sweet types of sweetpotato, the preferred option among West African consumers. As breeding operations were discontinuated in Ghana on September 2020, a proper handover to the local NARI, CSRI (Council For Scientific and Industrial Research) was conducted, and key advanced genotypes and parents were sent to KEPHIS in Kenya for maintenance under *in vitro* culture conditions.. NaCRRI in Uganda developed a product profile including sweetpotato weevil (SPW) tolerance as a value-added trait. INERA in Burkina Fasso initiated Multi EnvironmentalTrials with 25 clones (17 clones from Ghana, 5 elite clones and 3 local checks). Apart from conducting preliminary yield trials, advanced yield trials, IIAM in Mozambique, DARS in Malawi and ZARI in Zambia hosted regional trials with 20 elite genotypes (18 elite clones common in all countries & 2 check clones/popular varieties in each country). Each NARI established these trials at three locations in their respective countries following the novel resolvable design of row-column. In addition, ZARI and DARS had crossing blocks from which polycross true seed were harvested.Also IIAM in collaboration with CIP released 5 varieties with good quality in Mozambique.

WP2 Main achievements

- Despite COVID-19, over 95% of breeding germplasm was properly stored and managed, thus ensuring both the continuity and genetic representativeness of breeding operations.
- Publications and deployment of several SOPs were finalized to improve operational excellence and data management.
- Over 80% of the NARI breeding trials were designed and planted as resolvable or augmented row column designs, and we expect to achieve 100% during Year Two.
- The AbacusBIO-CIP study conducted in Uganda, which was focused on increasing our understanding about what gender disaggregated farmers and the market expect from new sweetpotato varieties was completed. Women in general, within and across supply chain segments, preferred quality traits and also had more diverse trait preferences, while men preferred agronomic or production traits. The implication of this is that a broad range of traits must be considered, to capture the appropriate balance of traits for women and men.
- The screening in Mozambique of key quality traits such as cooking time and dry matter after cooking was initiated.
- Running, jointly with Work package 4, a joint Breeding-Seed Research Community of Practice, with the main purpose of achieve pollination between these two key areas and to increase the understanding of participant scientists across the value chain from genetic crosses and new variety release, to seed delivery to multipliers. More work is needed though to achieve a full integration of breeding and seed research activities. Minutes of meetings held at Rwanda and Ghana (online) are available at (**Annex 1**).

Work Package 3 (WP3)

WP3 is focused on proofing the concept for Genomic Selection and Genomic Prediction for key traits in Uganda, both at CIP and in NaCRRI, and builds on the success of a previous BMGF investment, namely GT4SP. It is led by Craig Yencho from North Carolina State University, and it includes several US-based research organizations, such as Michigan State University, Boyce Thompson Institute, the University of Tennessee-Knoxville, and NaCRRI (Uganda). Its long term goals are not only to use Genomic Selection for the purpose of selecting superior clones, but also to reduce the breeding cycle via an accelerated elite parent recycling. During this first year, progress has been achieved towards the sequencing of two 6X varieties, namely Beaugard and Tanzania, and transcriptome datasets have been developed to support annotation of these genotypes.

Many operational and logistical aspects of Genomic Selection has been identified and discussed, and CIP, NaCRRI and NCSU are developing large training populations upon which to launch proof of concept studies from Year 2 onwards. On a related front, and because of the limited availability of mapping software able to address issues such as ploidy and heterogeneity, linkage analysis and haplotype identification methods are being expanded from a full-sib family basis into a multiple inter-connected family structure, such as in the MDP population already described.

Since the quality of any Genomic Seletion effort is strongly related to the quality of its phenotype, a large and detailed field effort is being conducted to increase the heritability and reliability of SPW (Sweetpotato Weevil) tolerance field datasets. In addition, significant progress has been achieved with the incorporation of linear mixed model capabilities to SPBase, enabling breeders to run powerful statistical analyses directly with SPBase instead of relying on additional software. An active working group focused on the many aspects needed to achieve success with Genomic Selection has been established and they meet on a monthly basis.

Acting on recent evidence that the ratio of clone mislabeling was significant in the MPD and other populations, which represents not only the loss of potential genetic gains, but also a less than ideal use of breeding resources, WP3 is developing several KASP[2] markers which, when available, will be used on a regular basis for QC purporses and to secure trueness-to-type from tissue culture plants through greenhouse multiplication and breeding trial establishment in the field.

Since higly efficient, cost effective and high throughput genotyping systems for complex polyploids such as sweetpotato are not as readily available as they are for diploid crops, steady progress has been made toward the development of anew genotyping platform, named OmeSeq/qRRS, coupled with an automated bioinformatic pipeline that streamlines the bioinformatic analysis component and makes it easier convert sequence information to genotypic information.

WP3 Main achievements

- A draft genome for the variety Beauregard has been generated and is currently being refined, whereas raw genome sequence of the variety Tanzania has been generated.
- Large training populations for Genomic Selection proof-of-concept studies have been developed by CIP, NaCRRI and NCSU.
- A utility patent was filed jointly by NCSU and UT for the OmeSeq/qRRS and OmeSeqArray genotyping platforms, developed under the GT4SP BMGF investment and carried forward under SweetGAINS.
- Progress with developing capabilities to conduct linkage analysis and haplotype identification work on multiple inter-connected families.
- A WP3 GS/SP working group consisting of key personnel from the CIP, NaCRRI, NCSU and UTK has been established and they meet monthly to drive program activities and lead discussions on GP/GP breeding needs (Output 3.5.1).
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Work Package 4

The primary outcome of Work Package 4 is establishing seed business models by early generation seed and commercial seed producers to deliver affordable, quality seed of market preferred varieties to farmers in specific geographies in Uganda and Tanzania by 2022, scalable in other contexts. It is led by Margaret McEwan from CIP. Rapid seed systems assessments were conducted in the proposed target areas in Tanzania and Uganda. These used a combination of key informant interviews with key seed system actors, sex disaggregated focus group discussions with rural and urban consumers of sweetpotato roots and household interviews of seed producers and seed users. Data collected will identify market preferred varieties, marketing efficiency of the existing seed distribution channels and seed value chain actors and inform implementation of field activities. Estimated seed requirements have been calculated for the target area in Tanzania, and will inform preparation of production plans, and strengthened delivery pathways. 12 different types of seed producer associations were interviewed in Uganda to better understand appropriate functions and structure of proposed self-financing seed producer associations. Draft SOPs were developed for seed production in open nurseries and screenhouses. These have drawn on best practices by North Carolina State University and Louisiana State University in addition to the experience of 11 NARIs involved in early generation seed production. The final rounds of planting and data collection for understanding seed degeneration and related management practices under different conditions studies in Lake Zone, Tanzania will be conducted in late 2020. In collaboration with IITA and the ISSD Africa project a new module, Sweetpotato Seed Tracker (SST) for registration and certification of sweetpotato seed has been developed and added to the (cassava) Seed Tracker (ST) platform. The online germplasm clean-up and distribution tracking system is being finalized. The online system allows the registration of germplasm being sent in for clean-up and tracking of the clean-up process. Customers sending in their germplasm will be able to follow the clean-up progress online. Similarly, customers will be able to place germplasm orders via the online system and track the order status till completion. In collaboration with IITA and ISSD Africa an inventory of decentralized quality seed quality experiences is being developed to (i) identify the best model(s) for enhancing seed quality assurance (QA), such as decentralization of certification services, implementation of QA by accredited seed inspectors, e-certification and accreditation-based systems.

WP4 Main achievements

- Rapid seed systems assessment field data collection completed in target areas of Tanzania and Uganda. Analysis will inform implementation activities.

[2] Kompetitive allele specific PCR

- Estimated seed requirement completed for target area in Tanzania to inform production plan and seed delivery pathway.
- SoPs for quality seed production in screenhouses and open nurseries drafted drawing on US industry and NARI best practices.
- The on line germplasm acquisition, clean-up, ordering and tracking system has been established at KEPHIS. This will be piloted and operational by the end of 2020.
- In collaboration with IITA and ISSD Africa the sweetpotato module has been added to Seed Tracker, for registration of seed producers, inspection and traceability of seed in the target areas in Tanzania.

Work Package 1- Demand-Driven Design of Improved Varieties, Governance and Operational Excellence

Intermediate Outcome 1.1 – Improved procedures to better characterize sweetpotato breeding TPEs by 2021.

Output 1.1.1 – Defined TPEs for each sub-region by 2021. PI: Bert De Boeck

In order to monitor and maximize genetic gains through optimized resource allocation for sweetpotato breeding in African sub-regions, new variety product profiles must target properly identified and characterized TPEs. TPEs are shaped by considering agroclimatic regions targeted by breeding programs, and are partitioned based on genetic correlations of germplasm among these regions (see https://doi.org/10.1002/csc2.20048).

The identification of TPEs will be carried out by analyzing patterns of genotype by environment interaction (GxE) in the targeted agroclimatic regions, as described in https://doi.org/10.1007/s00122-003-1541-4. For these analyses phenotypic datasets with genetic connectivity of multiple sites, covering targeted regions, are required. In order to gather such data, several specific TPE trials have been planned for the Mozambique, Uganda and Ghana breeding platforms. Due to the COVID-19 pandemic many of these trials have been delayed, but in Southern Africa a large multi-environmental trial to evaluate a common set of genotypes in 15 different locations has already been carried out. In addition, historical legacy datasets will be used for TPE analyses purposes. Though data gathered during SASHA I and II previous investments was digitally stored, it was not readily available for analyses nor properly curated. An extensive data curation process, which lasted several months, has been finalized for all three sub-regional CIP breeding platforms, comprising for Mozambique, Ghana and Uganda a total of 206, 235 and 140 fieldbooks, respectively. All fieldbooks were collected and correctly formatted for upload into SPBase. A final, centralized, curation of fieldbooks has been carried out in August and September to ensure data quality. The final curation process detected and resolved many issues, such as: mislabeling of traits; mislabeling of fieldbooks; incorrect column formatting; incorrect plot names; inconsistency of data and incorrect computation of derived traits; incorrect identification of treatments; incorrect identification and treatment of missing values; pedigree inconsistencies. Data collected during 2020 will be curated and added to the collection of historical phenotyping datasets available.

Intermediate Outcome 1.1 - Work planned for next period and COVID-19 implications

At the start of year 2 all curated data of the three sub-regional CIP breeding platforms, and the Peruvian breeding platform, will be uploaded to SPBase. BTI is already working on this upload, but the curation of accession names delays this process. TPE trials could be planted only at the SouthAfrican breeding hubs, so this intermediate outcome is behind schedule. To get back on track, TPE trials in the East African hub (Uganda) will be planted during the remaining of 2020.The upload to SPBase will facilitate analyses for TPE identification, and these analyses will start as soon as the upload is finalized. Linear mixed models, allowing for heterogeneity of genetic variances and genetic covariances across environments, will be used to estimate genetic correlations between environments to enable TPE characterization. The statistical software R, and in particular the asreml R-package (https://www.vsni.co.uk/software/asreml-r) and R programs provided by Excellence in breeding (EiB) (like https://data.cimmyt.org/dataset.xhtml?persistentId=hdl:11529/10201), will be applied. As already mentioned, the COVID-19 pandemic delayed the execution of some specific trials for TPE identification and has – to some extent – also had a negative impact on the dynamics of networking between CIP and NARIs for data gathering.

Intermediate Outcome 1.2 – Established and validated methods in at least 3 countries to develop gender and demand-responsive product profiles by 2022.

Output 1.2.1 –. Identified and evaluated reference varieties for preferred characteristics from the perspective of male and female end users in Mozambique, Uganda and Tanzania by 2020. PI: Justus Ochieng

Sweetpotato value chains are changing rapidly due to climate change, changing consumption patterns, increasing population and incomes, increased awareness and demand for quality products by end users. These changes have compelled producers to demand varieties that are more suitable to new market demands and processing scenarios. Thus, breeders need to respond to this demand by breeding new varieties that meet the preferences of the end users. In this output, qualitative research was conducted to understand the preferred and non-preferred characteristics of key reference varieties in these environments in Uganda and Tanzania. This aimed at pinpointing the key trait sets needed to replace existing reference varieties and the generated information will be included in gender responsive product profile revisions during Year 2.

In addition to gathering insight for product profiles and update purposes, data is needed to reduce the gap in understanding gender preferences and developing desirable new varieties. Two qualitative studies were conducted in targeted regions of Tanzania and Uganda during 2020 to identify and evaluate key reference varieties in the changing production and marketing environments. Study protocols and questionnaires are included in Annex 2. and Annex 3 respectively. The COVID-19 pandemic significantly affected the commencement of the research in the three countries and research has been done to date only in Tanzania and Uganda. However, the team is currently planning to conduct the pending study in Mozambique during months to come.

We conducted a targeted study in Bukombe and Butiama districts, which are major production and consumption hubs in Northern Tanzania. 14 Focus Group Discussions (FGDs) involving 95 producers (49 male; 46 female) and 51 consumers (23 male; 28 female) were conducted. Preliminary data from producers is shown in Table 1. Ukimwi, Ukg 16 and Kilihona were the the key reference varieties preferred by both male and female producers in Bukombe District, while in Butiama District Polista was preferred by female and Ukerewe preferred by men. Polista was preferred by women because it has high root yield, was good for making french fries (chips) with good taste, it had a long storage shelf life, and was liked by the children and elderly; thus, it had high demand in the local markets. A four-cell approach (FCA) was used to the assess the abundance and distribution of the preferred varieties in farming communities (number of farmers growing and the area under cultivation (large area/small area). Although, women ranked Polista as the most preferred, many of them grew it on small areas while many men grew it on large areas despite ranking it third after Ukerewe and Ramala. Such discrepancy can relate additional to individual choice, such as access to planting material or markets. A detailed report will be shared in the next reporting period, and will take into account the fact that oftentimes farmers grow a basket of varieties which correspond to different product profiles and market segments, and that white and orange flesh sweetpotato varieties should probably be considered as different market segments.

Table 1. Preferred sweetpotato varieties in proposed target areas in Tanzania

District	Sex of producers	Variety name	Participants growing (%)	Rank*	Abundance and distribution**
	Male	1.Ukimwi	83	1	MHHLA
	Male	**2.Ukg16 (Umeme)***	54	2	MHHLA
Bukombe	Male	3. Kilihona	42	3	MHHLA
	Female	1.Ukimwi	90	1	MHHLA
	Female	**2.Ukg16 (Umeme)**	80	2	MHHLA
	Female	3.Kilihona	60	3	MHHLA
	Male	**1.Ukerewe (Rwamkoma)**	100	1	MHHSA
	Male	2.Rumala	75	2	MHHSA
	Male	**3.Polista (Tunza Murume)**	50	3	MHHLA
Butiama	Female	**1 Polista (Tunza Murume)**	100	1	MHHSA
	Female	**2.Ukerewe (Rwamkoma)**	71	2	MHHLA
	Female	3.Rumala	67	3	MHHLA

*= Varieties highlighted in bold and larger font display large preference differences between male and female farmers

**MHHLA=variety is grown by many households in small area of land. MHHSA=variety is grown by many households in small area of land; FHHSA variety grown by few households and in small areas.

In Uganda, 24 FGDs involving 184 producers (93 males; 91 females) and 64 consumers (48 males; 46 females) were conducted in August/September 2020. Data on producers is shown in Table 2. What is reported is a preliminary analysis, which will be completed, and a more comprehensive once will be conducted once a full analysis is carried out. NASPOT 9 O was the most preferred sweetpotato variety, followed by NASPOT 8 and Kakamega in Kamuli District. About 67% and 100% of men and women grew NASPOT 9 O respectively, while 77% of female and 50% male grew NASPOT 8 (Table 2). Mwulu Aduduma and Budungua Omukaire and Namugwere were preferred in Iganga District. Similarly, the type of varieties preferred also varied between the two regions. NASPOT 9 O is early maturing making it a good crop for piece mealing. It is also resistant to pests, which reduces the cost on pesticides. Lastly, the variety is liked by children making many female farmers to grow it (Table 2). However, producers mentioned that its roots are very small, and its levels of beta-carotene should be increased. NASPOT 9 O is grown by many households and in large areas of land due to its unique traits (Table 2). Although NASPOT 8 has high levels of beta-carotene, its poor taste has made it less preferred among the producers and consumers. Secondly, it has a short shelf life, lacks drought tolerance like Kakamega, and it is susceptible to sweetpotato weevil. Data analysis have not been completed and a detailed report will be shared in the next reporting period. Regardless, in both regions clear differences are observed in the way male and female farmers pick sweetpotato varieties. This insight must be taken into account when Product Profiles targeting such TPEs are updated, and reflects the value of conducting this sort of field studies.

Table 2. Preferred sweetpotato varieties in proposed target areas in Uganda

District	Sex of producers	Variety name	Participants growing (%)	Rank	Abundance and distribution **
	Male	**Vita (NASPOT 9 O)**	67	1	MHHLA
	Male	Kakamega	58	2	MHHLA
	Male	**NASPOT 8***	50	3	MHHLA
Kamuli	Female	**Vita (NASPOT 9 O)**	100	1	MHHSA
	Female	**NASPOT 8**	77	2	MHHLA
	Female	Kakamega	75	3	MHHSA
	Male	Muwulu aduduma	75	1	FHHSA
	Male	Budunguza omukaire	70	2	MHHSA
	Male	**Namugwere**	33	3	MHHSA
Iganga	Female	Muwulu aduduma	60	2	MHHSA
	Female	Budunguza omukaire	60	2	MHHSA
	Female	**Namugwere**	67	1	MHHSA

*= Varieties highlighted in bold and larger font display large preference differences between male and female farmers

**MHHLA-variety is grown by many households in large areas; MHHSA=variety is grown by many households in small area of land; FHHSA variety grown by few households and in small areas.

Output 1.2.2 – Developed and validated tools for gender responsive, targeted consumer profiles and acceptance studies in Uganda and Mozambique for sweetpotato among different end users by 2021. PI: Justus Ochieng (left CIP on September 2020)

Tools to address breeding gender related aspects and preferred traits for men and/or women consumers have been developed by RTB Gender and Breeding Initiative.

These guidelines will be applied for two specific ways sweetpotato is prepared at household levels: boiled and fried sweetpotato. During the current reporting period the team has participated in several meetings with RTBFoods, Excellence in Breeding (EiB) and CGIAR gender platform colleagues to better understand how to apply G+tools for designing gender responsive consumer and acceptance studies to be carried out in 2021. For planning to achieve this milestone, several meetings were attended where previous work on gender responsive consumer profiles and acceptance studies are underway. This is in preparation to extend similar work in Southern Africa where such studies have never been conducted. In-depth work on boiled sweetpotato already done in Uganda (under RTBFoods) will be

extended to Mozambique. The work in Mozambique will focus on boiled and fried sweetpotato. Insight was also gathered from discussions with the gender responsive RTB Seed Systems Multi-Stakeholder Framework: a review of banana and sweetpotato seed systems in northern Uganda. Such document established the gender differentiated bottlenecks related to seed availability, access, knowledge and quality in the sweetpotato and banana seed systems in Uganda. These findings will be useful in planning upcoming research studies in Mozambique in Year 2.

Output 1.2.3 – Developed at least 2 initial gender responsive product profiles per country in Mozambique, Uganda, and core NARI partners by 2020, followed by a second round of more detailed product profiles in 2022. **PI: Justus Ochieng**

Product profile development relies on stakeholder consultations held at each sub-regional platform. This work draws upon outputs 1.2.1 and 1.2.2 described above, as well as on AbacusBIO evidence (refer to output 2.2.2). Though such evidence was delivered earlier than anticipated, it was not available at the time discussions on product profiles were held. Going forward, withn the Ugandan context, insights from the AbacusBIO will be used as input forproduct profiles a nd related matters. The work has however delayed due to COVID-19 and multi-stakeholder virtual meetings are still taking place to refine the product and customer profiles (refer to 1.2.2). We will rely on EiB's and RTB's guidelines (G+ tools) for developing product profiles to replace dominant existing varieties, instead of developing further tools. The structure of product profiles is still being developed and SweetGAINS scientists are actively participating in the consultative meetings. The SweetGAINS team will fill information from outputs 1.2.1 and 1.2.2 into the final structure generated and agreed upon by the stakeholders (OneCG Centers). The processes to be followed are: (1) overall framing of market segments, product concepts and product profiles; (2) product concept structure; and (3) market segment structure.

The refined tools will allow breeding programs across CGIAR to regularly update existing profiles and define new profiles in the most cost-efficient manner. Two product profiles for Uganda and Mozambique have been updated but are yet to be finalized, however the discussions to refine templates are still on-going and the structure will be updated to reflect the new changes. COVID-19 affected the commencement of the meetings to refine the product profile tools.

Intermediate Outcome 1.2 - Work planned for next period and COVID-19 implications

We will partner with the Mozambique Institute of Agricultural Research (IIAM) to conduct qualitative research to understand the preferred and non-preferred characteristics of key reference varieties in these environments. Based on current COVID-19 trends in the country, we do not expect serious disruption. For year 2, the following activities have been planned towards output 1.2.1: Complete writing a report on preferred and non-preferred characteristics of key reference varieties in Uganda and Tanzania; upload the data into SweetPotatoBase and Dataverse; collaborate with IIAM to replicate the Uganda and Tanzania studies in Mozambique; prepare a study protocol for Mozambique; and manuscript preparation and submission to a peer reviewed journal for publication. Since surveys and Focus Group Discussions (FGD) could only be held in Uganda and Tanzania this intermediate outcome is behind schedule. Pending FGDs will be held duting the remaining of 2020 to get back on track.

Also, during year 2 qualitative and quantitative research will be conducted, focusing on fried and boiled sweetpotato to identify the quality characteristics preferred by various stakeholders along the food chain (production, post-harvest and market). This work will also verify the multiple uses and trade-offs between uses of the products, which could reflect different interests of men and women. Severe COVID-19 disruptions are not expected. This activity is still on time and will be implemented as planned. For Year 2, the following activities have been planned towards output 1.2.2: gender develop responsive, targeted consumer profiles and acceptance studies in Uganda and Mozambique in 2021; upload the data into SPBase and Dataverse; and manuscript preparation.

Intermediate Outcome 1.3 – Implemented operational excellence and product advancement processes at CIP and breeding partners by 2022.

Output 1.3.1 – Developed quantitative metrics to assess breeding program quality and efficiency, including phenotyping and genotyping datasets, consumer sensory data and procedures to prevent varietal mixing by 2022. PIs: Hugo Campos, Bert De Boeck.

During year 1 of SweetGAINS, substantial attention has been given to operational excellence aspects of breeding data management. This output is linked to output 2.3.1 To harmonize and streamline efforts a breeding data management a Community of Practice (CoP) has been established. This CoP has developed several standard operating procedures (SOPs) for breeding data management. The CoP is having regular meetings to follow up data management practices and compliance with SOPs, and includes scientists from CIP, NCSU, BTI and all the NARIs partners involved in the project. A first version of the SOPs has already been published on CGSpace (https://cgspace.cgiar.org/handle/10568/109605), but the CoP framework allows addition or modification of procedures in the SOP document whenever it seems necessary after group discussion. SOPs ensure high quality data management practices and minimize unintended errors by addressing issues like barcode labelling, digital data recording, the use of standardized naming conventions and data curation, and are developed around data workflows with SPBase as a central data management system. Compliance with the SOPs

therefore automatically ensures that all breeding data will be uploaded to SPBase within a reasonable timeframe. More details about the SOPs can be found at Output 2.3.1, or in the link above provided.

Output 1.3.2 – Validated and built capacity for a product advancement process using Go/No Go and gender responsive criteria by 2021. PI: Hugo Campos

Planned activities to learn about operational excellence and product advancement process at Corteva facilities in Iowa were put on hold because of COVID-19. This output is behind schedule. Discussions are underway with Corteva to conduct such discussions and trainings during the remaining of 2020.

Intermediate Outcome 1.3 - Work planned for next period and COVID-19 implications

Implementation of the SOPs by all breeding programs, both NARIs and CIP, is crucial to obtain operational excellence. Extensive training to enable the implementation process has already started and is driven by the CoP, but will be a top priority in year 2. The CoP has therefore planned online training sessions to take place in October and November 2020. The foreseen training sessions are (see **Annex 4** for the complete agenda): Introduction to SPBase; Digital Tools for phenotyping experiments; Digital Tools for crossing experiments; R training for data management, data curation, and the creation of experimental designs for breeding trials (the need to learn more about R training was raised by NARs partners). COVID-19 implies that training has to be held online, which has advantages in terms of reachability, but can be challenging as well (e.g. when training the use of digital tools or label printing).

This intermediate outcome is behind schedule, as discussions with Corteva breeders about operational excellence and product advancement process could not be held. In order to get back on track, the current plan is to have them online during the reminding of 2020, in order to catch up and implement as originally planned.

Intermediate Outcome 1.4 – Modernized breeding efforts at CIP and at least 4 NARIs by 2022.

Output 1.4.1 – Established at least 4 agreements with NARIs on a novel model of partnership leading to increased adoption of new varieties by 2020. PI: Hugo Campos

Agreements have been already signed with all NARI partners (ZARI at Zambia, IIAM at Mozambique, RAB at Rwanda, NaCRRI at Uganda,DARS at Malawi, SARI at Ethiopia, INERA at Burkina Faso, NRCRI at Nigeria) but TARI (Tanzania), which is at an advanced stage of development. Such agreements are focused on activities leading to increased adoption of new varieties. For instance, they stipulate the use of product profiles to guide all breeding efforts. In addition, only modern experimental field designs and statistical analyses via linear mixed models will be deployed, and data must be uploaded onto SPBase in a reasonable period of time. Furthermore, NARIs will carry out surveys on variety dissemination, market segments and impact made by released varieties and traits most considered by farmers for adoption. SweetGAINS will providing training fro such activities as needed. As a whole such efforts should increase the likelihood of developing new sweetpotato varieties that replace older ones. The combination of such enhancements on the breeding side, plus those underway on seed delivery pathways, should lead to increased rates of adoption of new varieties as a consequence of SweetGAINS efforts, and result in increased varietal turnover. **Annex 5** shows the agreement established with DAR in Malawi, which embodies well agreements established with other NARI partners during 2020.

Intermediate Outcome 1.4 - Work planned for next period and COVID-19 implications

Because of COVID-19, discussions leading to signing agreements took much longer than desired. However, with the exception of Tanzania all agreements are signed already. This intermediate outcome is ahead of schedule as agreements have been discussed, agreed upon and signed with 7 NARIs. Planned work for the remaining of 2020 securing the agreement with TARI in Tanzania, and regularly provided the support needed by NARs so they are able to fulfill contractual agreements.

Intermediate Outcome 1.5 – Gathered evidence about breeding effectiveness, as well as documented, implemented and shared best practices by 2022.

Output 1.5.1 – Developed and validated statistical modelling to estimate long-term genetic gain and non-genetic trends, drawing on historic breeding datasets and farmer/NARIs field locations by 2021. PI: Bert De Boeck

As described in Output 1.1.1, an extensive list of properly curated phenotypic datasets from historical breeding trials is available and can be used to estimate genetic gain. A valuable subset of historically conducted trials are the so-called “Era trials”, which are trials conducted specifically to estimate genetic gain with material released during diverse decades under the same environment, increasing the connectivity with historical data. From 2016 onwards “Era” trials including varieties released in different decades have been conducted in Peru, Mozambique, Ghana and Uganda to evaluate the performance of released varieties in each breeding platform. An overview of the available Era trials is given in **Annex 6.**

Intermediate Outcome 1.5 - Work planned for next period and COVID-19 implications

All historical phenotypic data will be uploaded to SPBase (see Output 1.1.1) and genetic gains will be estimated using appropriate statistical models, taking advantage of the best practices provided by the EiB breeding scheme optimization manuals (https://excellenceinbreeding.org/sites/default/files/manual/EiB-M2_Breeding%20process%20assessment-Genetic%20Gain_04-05-20_0.pdf).

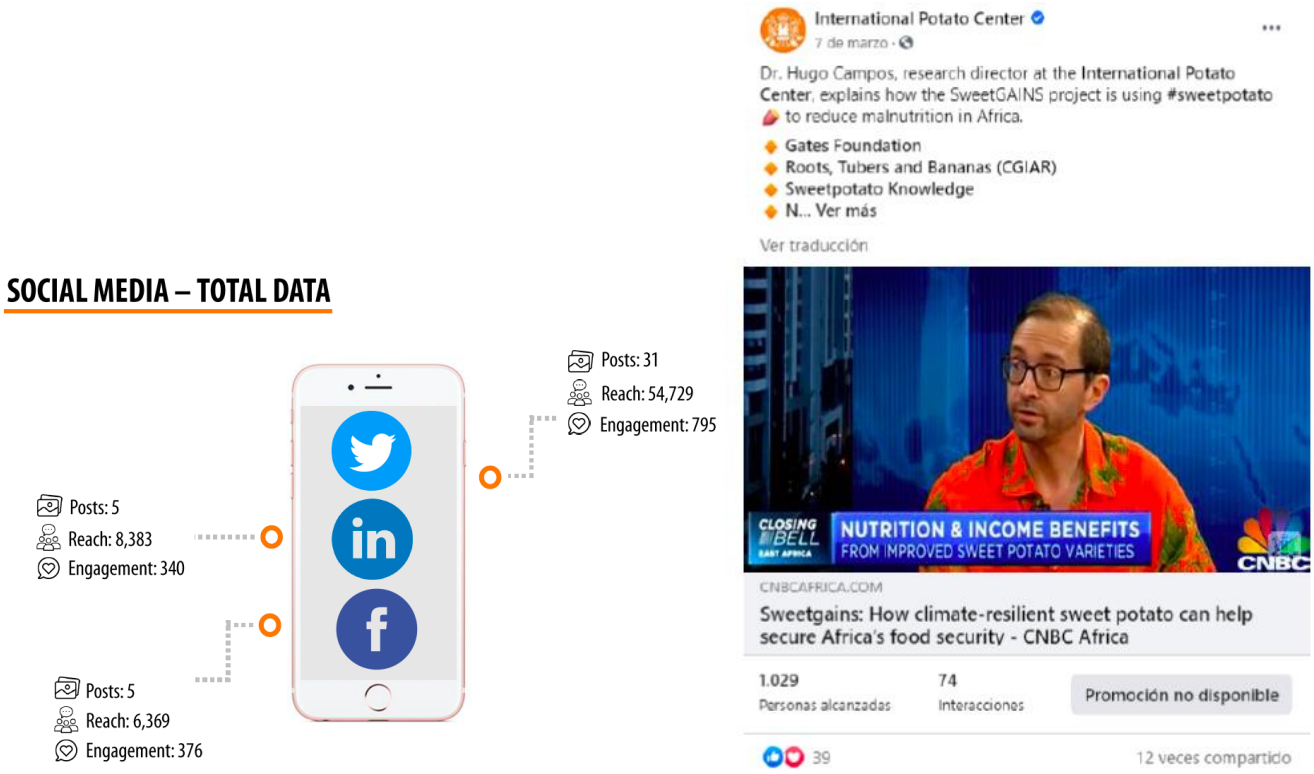
Intermediate Outcome 1.6 – Increased support to sweetpotato breeding and biofortification in at least 3 countries by 2022.

Output 1.6.1 – Documented evidence of targeted efforts in at least 3 countries to increase government investment and other investment sources for sweetpotato breeding and use. PI: Hugo Campos.

Nothing to report for this period.

Output 1.6.2 – Provided strategic communication outputs and monthly updates to Sweetpotato Knowledge Portal and social media, as well as a databases of major communication outputs. PI: Vivian Atakos.

The SweetGAINS Communication strategy was developed and shared with work package leaders and key staff for input then adopted for use in March 2020. Communication outputs as described in the communication strategy accomplished to date include a SweetGAINS project web site that enables dissemination of project successes to stakeholders and external audiences that was developed and launched. We continue to populate the site with project related information geared towards external audiences. For example a project profile providing background information, spelling out key partnerships and expected outcomes has been developed and is available online, open access project specific branding has been done, and a project logo is now in use by all partners. This site also includes some presentation templates for use during meetings and conferences. Also, eight blogs reporting about progress across work packages have also been published on the project page. In terms of social media engagement, SweetGAINs related posts (January - September) have spurred significant interest. Out of social media channels used, Twitter posts had the highest reach, of at least 54,000.



Three newsletters (also known as e-digests) have been sent out every three months with an average open rate of 57% between January and October. Although, we have initially planned to send monthly e-digests, we opted to have quarterly updates ensuring ample time to prepare communications products from a variety of partners. In September, we launched a podcast to further share information about the work being done by the project. By December 2020, three podcasts will be available for wider dissemination of project objectives and successes. Speakers include SweetGAINS colleagues from both CIP, NARs and advanced research institutions based in the US.
See communications outputs in the **Annex 7**.

Output 1.6.3 – Updated online sweetpotato varietal catalogue in 2020 and 2022. PI: Luka Wanjohi

Two sweetpotato landraces from Ivory Coast have been added to the collection on the online sweetpotato catalogue. This brings the total collection of varieties available on the catalogue to 82. The catalogue was designed with a form that allows breeders to self-upload new varieties to the catalogue, but so far only Ivory Coast has been able to successfully use this form. A data management intern will be coming onboard from mid-October to work with all sweetpotato breeding programs that have released varieties from October 2019 to date to get these uploaded on the catalogue before the end of the year. Additionally, an online germplasm ordering system is being developed and this platform will be linked to the online catalogue, to allow direct placement of orders from the catalogue.

Intermediate Outcome 1.6 - Work planned for next period and COVID-19 implications:

Activities related to increase national support for sweetpotato breeding and biofortification require in person discussions with several officers, scientists and senior public servants. Such will be activated as soon as COVID-19 related travel restrictions allow it.Some communication activities have been delayed, due to lockdowns aimed at curtailing COVID-19 infections. Therefore, digital story telling that would require talking to scientists and filming them at work so as to develop short video and photo stories will be undertaken in year 2 when it is safe to travel. Physical community of practice meetings would provide good ground to have these conversations and film progress. Moving these to the online space meant exploring having some virtual interviews. Subsequenlty, we have prepared written pieces based on virtual Q and A with these scientists and partners. An example is here: https://cipotato.org/africa-blog/modern-breeding-all-about-efficiency-sweetgains-uganda/

Through 2020 and 2021, we will continue sharing the project successes via a number of channels including newsletters, podcasts, blogs and social media outreach. As scientific papers are published, these will be shared widely through various channels. We experienced delays in terms of media outreach because of slow implementation. During the remaining of 2020, at least one media visit will be organized to ensure early gains from the project are shared widely. We will also prepare an op ed once early results are released.

A refresher catalog training session with breeders in SSA on how to add new varieties on the online catalogue will be conducted. Additionally, the offline version of the catalogue will be updated with new varieties from the period 2019 to 2021. The offline catalogue is avalable for download as a PDF file from the catalogue website. This intermediate outcome is on track and no adjustments are required at the moment.

Intermediate Outcome 1.7 – Enhanced governance and Monitoring, Evaluation and Learning systems by 2021.

Output 1.7.1 – Established an effective model of project management and governance by 2020. PI: Hugo Campos

Effective governance systems have been established at three levels: At a tactical level, one practice SweetGAINS has brought into CIP is the use of Microsoft Project (MSP) as a tool to support the monitoring tasks. MSP has proven to be an effective tool to merge the scientific and the financial aspects SweetGAINS. Although several trainings and advanced in-house support have been provided and several administrative team members have become very proficient with MSP, it is expected that the team will gain full familiarity with MSP only during 2021. A second level of governance has been implemented through SweetGAINS's Leadership Team (including all Work Package leaders, project management and financial specialist, plus NARI representation via Dr. Benard Yada (NaCRRI-Uganda)) has been set up, and mandated with the task of monitoring the execution of SweetGAINS and the discussion of issues and deviations arising in order to keep on track the implementation of SweetGAINS. During 2020, significant discussion time has been spent dealing with the aftermath of COVID-19, which included a comprehensive assessment, both at the science and financial levels, of this unforeseen pandemic. The SLT meets on a monthly basis, and ad-hoc discussions are set up on an as needed basis. Minutes are collected and used to monitor progress and follow up on the main issues arising. Moreover, at a more strategic level the SweetGAINS External Advisory Board was established (Sandra Milach – Corteva, USA, Robert Graveland – HZPC, The Netherlands, Steve Rounsley – Inari, USA, Nigel Motts – Private consultant, Botswana, Godfrey Asea – DG, NaCRRI, Uganda, Jeff Endelman – UW at Madison, USA, plus Work Package Leaders and Dr. Jim Lorenzen). The EAB meets on a quarterly basis to discuss strategic aspects of SweetGAINS and provide advice. In addition, as needed, ad-hoc discussions with specific EAB members have been held. For instance, Nigel Motts made multiple valuable contributions to the redesign of WP4 (seed research), working closely with Margaret McEwan and Hugo Campos. Also, several discussions were held among Sandra Milach, Craig Yencho and Hugo Campos, leading to a proposed collaboration where Corteva that would produce genome sequencing data for selected sweetptoato 6X genotypes. Finally, Robert Graveland met with Maria Andrade and Hugo Campos to discuss tactical aspects of sweetpotato operations in Mozambique.

Output 1.7.2 – Established Monitoring, Evaluation and Learning Methodology by 2021. PI: Haile Okuku, Jemimah Njenga-Kimata

The Monitoring, Evaluation and Learning (MEL) plan was developed, shared with key staff and adopted for use in March 2020 and covered the key planning tools and processes needed to set up and implement a MEL system. As demands for greater accountability and results grow, a useable results-based MEL systems to support project management is needed. A results-based MEL system represents a feedback system, a management tool to assess and evaluate outcomes, providing information for governance and decision making.

The MEL plan, which feeds directly into BMGF reporting requirements, describes the process of developing a MEL system in which data are systematically collected, reported and used to make project decisions. This will allow the project to work more effectively and efficiently towards achieving its goals and objectives through organizing plans for data collection, collation, analysis, dissemination, and learning. The plan aims to give comprehensive yet practical guidelines and in order to integrate it in the project management strategy and ensure progress throughout the life of the project, the MEL plan sets out to follow several key and overarching principles regarding how to conduct and manage monitoring activities, evaluations, and learning:

1-. The MEL process is an integrated part of project management and it informs programming, improve and ensure quality of interventions, and generate useful evidence of project's results and challenges.

2-. Monitoring information should be collected both on process and product/service, and monitoring activities should be aligned as much as possible and practical with project activities.

3-. Simple and clear indicators and targets are set for the project, with a focus on achieving results at intermediate- and outcome level.

4-. The learning agenda defined for the project is well-structured and planned out, with an increased emphasis on dissemination and sharing of lessons learned, as well as project's findings with a range of stakeholders.

This MEL plan serves as a tool to guide overall project performance and as such, it will be updated as necessary to reflect changes in SweetGAIN's strategy and ongoing tasks, and also to incorporate feedback from BMGF. The MEL plan will be reviewed and updated annually.

Intermediate Outcome 1.7 - Work planned for next period and COVID-19 implications

COVID-19 had not any impact on the interaction with EAB. Work planned for next period is to reinforce the work with EAB, mainly through more ad-hoc discussions as needed. This intermediate outcome is on track and no adjustments are required at the moment.
Regarding MEL and the COVID-19 crisis, SweetGAINS remains fully engaged and committed to meet the evidence and results oriented needs of BMGF. This could mean pausing non-critical MEL activities while maintaining essential or time-sensitive functions. Field missions will be restricted for the foreseeable future while lab and desk-based activities are largely unaffected. As governments issue lock-down, shelter-in-place, or work-from-home orders, in-person data collection methods will be unfeasible in the short term and may be impacted for quite some time. Data collection for SweetGAINS can still be facilitated using remote or virtual data collection strategies, both from a quantitative and qualitative perspective. Examples include mobile phone-based surveys, SMS surveys, videoconferencing, etc.. COVID-19 may require changes in how interviews are conducted, such as moving to outside venues where social distancing can be implemented and potentially coupled with fever checks and hand washing.

In addition to adjusting our MEL field methodologies, training has been provided to MEL staff on the use of personal protective equipment (PPE), particularly those conducting fieldwork. We make sure our teams understand the risk of exposing themselves and their communities to the virus and that they are empowered to make the appropriate decisions for their context.

WP2 -Redesigning the Core Breeding

Intermediate Outcome 2.1 – Optimized breeding pipelines to deliver sweetpotato varieties by 2022.

Output 2.1.1 Gender aware sensory descriptors inventory developed (main biophysical, sensorial and textural traits related to quality of product profiles established). PI: Sara Majanya, Godwill Makunde, Abdul Naico Maria Andrade and Mukani Moyo. MUKANI Moyo

A survey with the primary goal of developing gender responsive product profiles for boiled sweetpotato was conducted in three districts of Mozambique to understand the production, consumption and marketing of sweetpotato among individual farmers, traders/distributors and restaurant owners. For the survey, a total of 308 individual interviews (71 males; 237 females) were conducted. The respondents were drawn from **263** households. Further, 42 traders (9 males; 33 females) and 16 food vendors/restaurants (2 males; 14 females) were interviewed. At the farmer level, there were more male headed households (86%) than female (35%). Sweetpotato is mainly consumed as boiled roots according to 97% of the respondents, and women were the major decision makers with regards to selection of varieties suitable for preparing boiled sweetpotato. The preferred variety in the surveyed districts was Amelia (**Annex 8**). Taste and aroma were the two most important traits of boiled sweetpotato identified by both women and men respondents in both districts (**Annex 9**). The third most important traits were mealiness and firmness segregated by districts - Marracuene and Manhiça, respectively. Low dry matter (watery), tasteless and 'does not cook' were among the worst traits not to be associated with boiled sweetpotato (**Annex 10**). The

characteristic 'it takes longer to cook' was mentioned by women only; which aligned with the notion that women lead in food preparation at the household level. Most of sweetpotato traders were local retailers (Mozambiquans), the majority being women farmers. Both men and women traders were interested in 'not damaged and spotless roots' and medium sized roots (**Annex 11**). Restaurant owners preferred roots with good appearance, faster cooking, high dry matter (not watery) and firm when boiled and easy to cook, in descending order. Traits identified in the interviews with farmers, traders and restaurant will be translated into high throughput phenotyping platforms. This task was assigned to Food Science PhD students. Interviews for PhD students were earmarked to do the textural analysis and other cooking traits were completed for both Mozambique and Uganda. Suitable candidates were identified, and the process is now with HR to finalise the official recruitments. Texture analyser and cooking pots were bought for the kitchen in Mozambique.

Output 2.1.2 Established correlations for raw/boiled sweetpotato between product sensory and nutritional criteria. PIs: Maria Andrade, Godwill Makunde, Jolien Swanckaert and Mukani Moyo.

Contribution to this output was done at only two sweetpotato regional platforms, namely Uganda and Mozambique. Standard Operating Procedures (SOPs) for boiling time and textural analysis were developed in Uganda. SOP for boiling time was adapted and validated in Mozambique while SOPs for textural analysis shall be validated later due to delays with procurement of texture analyzer. In Mozambique, three advanced trials were established at Umbeluzi Research Station and two trials, one OFSP with 50 clones and a second non-OFSP with 30 clones were used for evaluation of cooking time and determination of dry matter (DM) of boiled samples. Cooking time widely varied, from 16 to 48 minutes in both trials (**Annex 12**)**.** Cooking caused a significant reduction in dry matter (DM) (%) in all genotypes in both trials. Heritabilities for DM in cooked samples were 0.67 and 0.60 in advanced trial (30 clones) non-OFSP and advanced trial OFSP (50 clones), respectively. The Mwanga Diversity Panel (MDP) trials provided roots for quality evaluation to fulfill Output 2.1.2 aligning also with the RTBFoods project. A subset of 220 clones was selected based on previous field data for quality evaluation (**Annex 13.)** The MDP genotypes were also used to compare family plots (5 siblings in a plot) with clonal plots (10 cuttings of 1 genotype in a plot) for the estimation of GCA **(Annex 14)**. In addition, eight advanced lines (all OFSP) are being evaluated for cooking and sensory traits in Uganda. This information will help inform the Uganda breeding program to select the final set of clones for on-farm trials and final release. In Southern Africa, monitoring of field trials was not possible and relied on partners where trials where established. Storage root samples for NIRS[3] analysis from outside Mozambique could not be received due to severe restrictions in movement of goods and people. Regional statistical training which was supposed to be held in Mozambique was not realized.

Output 2.1.3 Improved phenotyping tool enabling highthroughput cost-effective and quantitative SPVD resistance measurements developed and implemented in Uganda. PIs: Jolien Swanckaert, Robert Mwanga, Jan Kreuze.

Activities for this output were mainly done in Uganda and supported from Peru. This output is linked to output 3.4.1. A new pre-breeding population (PV19) for SPVD resistance was developed and in-vitro-germinated with 1,298 genotypes plus 10 parents, with medium to high resistance to sweetpotato chlorotic stunt virus **(Annex 15).** This partial diallel including selfings comprising 51 families will serve SPVD screening activities in Peru-Lima and Uganda-Namulonge. Shipment of the materials to Uganda was delayed due to the COVID-19 outbreak and is expected to be shipped mid of 2021. This pre-breeding population can also serve to identify the most suitable populations for bi-parental mapping and genomic selection purposes. Moreover, a highly precise phenotyping protocol has been developed on basis of serological tests **(Annex 16).**

Breeding and virology can assess larger breeding populations and develop tools applicable across regions. For laboratory work in Peru, the selected 1,298 genotypes plus 10 parents and virus inoculation sources were in the process of multiplication when the COVID-19 shutdown affected operations. One staff returned to work in September and started to recover virus inoculation sources, while the genebank also started to re-multiply genotypes required for the experiment. Field trials are expected to be conducted in San Ramon (Peru) in January-February 2021. In Uganda, an MSc (Makerere University) student phenotyped the BxT population (312 genotypes) for single and combined components of SPVD, and is awaiting reagents and equipment to do quantitative phenotyping.

Output 2.1.4 Improved population for sweetpotato weevil (SPW) resistance PIs: Benard Yada, Milton Otemo

Activities under this output were carried out by NaCRRI and its partners in Uganda. NaCRRI developed a product profile which included SPW tolerance as a value-added trait. With this background, seed was obtained from NaCRRI's population improvement crossing block. This output is linked with output 3.3.3.1. This crossing block consisted of elite clones, released varieties and some landraces that showed some level of field resistance towards SPW. At least 3,000 open pollinated seed harvested from the elite clones were scarified and

[3] Near Infrared Spectroscopy

germinated in seedling trays and only those that were vigorous were selected for evaluation as observation trial (OT). The OT was established at

NaSARRI on May 2020. A total of 1,353 genotypes were planted together with 12 parents and 2 checks (NASPOT 8 and NAROSPOT 1), and designed as an augmented row-column design with three planting positions per 1 m plot. Standard plot size was used. A total of 1,480 plots of the test genotypes and checks were planted. The trial is being managed and standard data is being collected till harvest anticipated to be done in October 2020. To further broaden the SPW resistance germplasm base, NaCRRI imported "Ruddy" a multiple insect resistant USA sweetpotato variety from NCSU in May. "Ruddy" is resistant to *Cylas formicarius*, the predominant *Cylas* species in the USA and is going to be included as a parent in NaCRRI's crossing blocks for generating more diverse SPW resistance populations for evaluation and selection against *Cylas brunneus* and *Cylas puncticollis*. NaCRRI had proposed to import "Murasaki", another C. *formicarius* resistant US cultivar for use in the breeding program. However, it was impossible since the variety is currently under patent protection from Louisiana State University.

Output 2.1.5 Integrated high Fe content alleles into sub-regional breeding platform in Mozambique PIs: Maria Andrade, Godwill Makunde, Wolfgang Gruneberg, and Mukani Moyo.

Activities under Output 2.1.5 were carried out in Mozambique, where hybrid breeding started in 2019, by hand crosses between two major gene-pools (geographical separation and origin differences). Gene pool A (Umbeluzi) represents a source of drought tolerance, and gene pool B (Gurue) rich sources of beta-carotene, iron, anthocyanins and other micronutrients. 50 parents were selected from each gene pool based on genetic distance to constitute the 2019 crossing block. The 100 parents were laid out and allowed to cross in a full diallel scheme. A total of 1,196 families from the inter-gene pool crosses (Umbeluzi x Gurue) with an average of 5 seeds germinated gave rise to 5,980 clones which are under field evaluation as observation trials at Umbeluzi Research Station (**Annex 17**), under two treatments water regimes – optimum irrigation and drought (planted on 01 August 2020). A total of four check clones, Irene, Alisha, Cemsa and Delvia together with the 98 parents which gave rise to the 5,980 clones are part of the OT evaluations, using augmented row-column designs. Harvesting of OTs will be done in January 2021 for quality analysis (Fe determination via NIRS). All released varieties, elite clones, seedling nurseries and other clones were maintained in greenhouses and tissue culture laboratory in Mozambique. Six greenhouses were rehabilitated in Mozambique and are full of breeding clones. The tissue culture laboratory cleaned planting materials. The training in next generation diagnostics and virus cleaning, which was supposed to be conducted in Kenya in April 2020, was postponed due to COVID-19. Participants for this training workshop were identified from Ghana, Peru, Mozambique, Kenya and Uganda. A SOP for tissue culture workflow is being revised and improved in KEPHIS, Kenya and Mozambique will adapt once finalized.

Intermediate Outcome 2.1 - Work planned for next period and COVID-19 implications

In year 2, the OT of hybrid clones established at Umbeluzi Research Station will be harvested and storage root samples analyzed for Fe and Zn content via NIRS in Maputo. All the agronomic and nutritional/NIRS data will be uploaded on SPBase in year 2. Clones with the highest Fe and Zn via NIRS will be identified and root samples (freeze dried raw and boiled samples) sent to FANEL-ILRI, Nairobi for further analysis of Fe using the ICP method. Part of the high Fe clones will be sent to Nottingham University in the UK for mre reliable Fe determination. The methodology to screen polyphenols and Vitamin C will be established. Though several field trials have been delayed, we do not anticipate COVID-19 to affect harvesting and determination of Fe& Zn in storage root samples. Trainings in next generation diagnostics and virus cleaning to technicians in sub Saharan Africa is behind schedule. Such training must be conducted in person, and a date is yet to be established.
A SOP for texture analysis for boiled sweetpotato will be validated in Mozambique in year 2. A texture analyzer, pots and water bath were purchased, and the texture analyzer has already arrived in Mozambique. A PhD student has been identified to work on this topic. Trials to support this work will be established in December 2020. Also during year 2, sensory panels for East and Southern Africa will be established and sensory lexicons for boiled sweetpotato developed. COVID-19 will limit travel of food scientists to Mozambique to give guidance and training of sensory panels. We shall rely on online discussions for the instructions. The breeding program in Uganda will continue to screen selected 40 parental lines for cooking quality. The eight advanced lines that are currently under on-station evaluation in Uganda will be tested on-farm in March 2021, and will be subjected to cooking quality analysis. We anticipate that the Uganda breeding program will meet the requirements of this output if travel is not restricted in the country due to COVID-19. Furthermore, in year 2, we are going to synthesis the information gathered from gender and market field studies to identify preferred sweetpotato traits and document the knowledge produced according to the gender roles. The data gathering process will involve consumer testing of boiled sweetpotato in Mozambique and workshop to validate sweetpotato profiles. The final product is multi-sectorial sweetpotato product profiles for Mozambique well documented. We do anticipate some activities to be pushed forward to March 2021 from the planned time, December 2020 due to COVID-19, which is also likely to delay the recruitment of a sensory panel and its training in Mozambique, until the first quarter of 2021. COVID-19 will also make it impossible for physical participation of expertise from outside Mozambique in a workshop to

validate sweetpotato profiles and conduct training of the sensory panel. The delays in these activities will influence the integration of gender responsive sensorial traits and processing traits into the crop ontology dictionary until September 2021. This output is still on time though and will rely more on online discussions for the implementation of activities.

Intermediate Outcome 2.2 – Established hybrid breeding pipelines across 2 sub-regional platforms by 2022.

Output 2.2.1 Defined traits and levels of genetic gains able to surpass checks PIs: Wolfgang Gruneberg, Jolien Swanckaert, Maria Andrade, Godwill Makunde, Bert De Boeck, Robert Mwanga, David Ramirez.

In Uganda, a crossing block to generate populations from intra-gene pool handcrosses (20A and 20B) was established and handcrosses are taking place (**Annex 18**)**.** The basis of selecting superior parents (**Annex 19**). and identifying testers (**Annex 20**) was discussed with help from EiB to guide development of a breeding pipeline. In Mozambique, the 2020 inter-gene pool crossing block (50 x 50) established at Umbeluzi in February 2020 (**Annex 21**) produced over 33,340 true seed from 5,944 families (hand crosses) and harvesting is still on-going. Twenty-two new parents (5 for Umbeluzi gene pool and 17 for Gurue gene pool) were introduced into the crossing block to replace poorly flowering clones. Selection of the new parents was based on agronomic performance (storage root yield, vine yield, DM%, Fe and Zn contents across environments, and flowering ability). With additional DFID support, two drought trials conducted at Umbeluzi under optimum and drought stressed treatments assisted in the selection of parents for crossing blocks. In these trials, a thermal and multispectral camera (Altum model, Micasense, USA) was assembled to an unmanned aerial vehicle (UAV - quadcopter, Inspire 2 model, DJI) which acquired images at 80 m height considering a flight plan with 80 % of images overlapping in shoot auto mode at 3 m s^{-1} of speed. Canopy temperature (CT), chlorophyll reflectance (Chl), and normalized difference vegetation (NDVI) indices were calculated after the mosaics were generated using Pix4D Mapper software. Productivity (PCI) and Resilience (RCI) indices were estimated based on total storage root yield following Thiry et al.'s (2016) procedure. A Principal Component Analysis in the scenarios with the highest effect of yield reduction (Early season drought treatments for trial A and late season drought for Trial B, respectively) was performed, including: Difference of Chl, NDVI, and CT in relation to control (Chl_{Amp}, $NDVI_{Amp}$, and CT_{Amp}), temporal variation of NDVI (ΔNDVI) and Chl (ΔChl), PCI, RCI, and percentage of reduction of vine weight in relation to control (PR_{VW}). Wards' method for the hierarchical clustering method was applied to determine genotypes groups. Under hot sweetpotato cropping season (Trial A), CT_{Amp} was the most critical trait to predict aboveground biomass production. In contrast, the temporal variation of Chl (ΔChl, a proxy of senescence) was mainly related to PCI and RCI. Xiadla xakau, Bela, MUSG15108-18, and Cecilia varieties showed higher productivity and resilience performance. In trial B, CT_{Amp} and Chl_{Amp} were negative and positively related to PR_{VW} under late season drought. Genotypes with highest resilience (RCI) were CN1448-49-37, MUSG15131-3, and MCKSGL13003-1294, whereas MUSG15108-12, MUSG09349-9, and MUSG14008-2 had the highest productivity. Genotypes with the highest aboveground biomass under water restriction were MUSG15100-3, MUSG16127-4, and MUSG16030-18. The drought scenario and cropping season are of essence for determining field high-throughput phenotyping in sweetpotato using UAV.

Since the Sweetpotato hub for West Africa was not one of the 2 sub-regional hubs selected for hybrid pipelines under SweetGAINS, there was need to consolidate achievements in breeding over the last 10 years at this platform during year 1 of the SweetGAINS project. One population adapted to the West African lowland tropical conditions was assembled, characterized and used to develop advanced clones of diverse culinary quality, including low sweet types preferred by West African consumers. This valuable population needed to be conserved as clean materials so that parental clones and advanced lines will be available to revive the breeding pipeline if future funding is secured. To date, 105 clones have been introduced *in vitro* including 65 parental lines and 40 advanced lines of the low sweet population adapted to West Africa (**Annex 22**). Four varieties SARI-Suyolo (PGA14008-9), SARI-Janlow (PGA14011-43), SARI-Tiemeh (PGA14372-3) and SARI-Nyoriberi-gu (PGA14398-4) from the breeding pipeline were released in Ghana by the CSIR-Savanah Agricultural Research Institute (SARI) in January 2020 **(**Annex 23). These varieties are among seventeen advanced genotypes shared with INERA in Burkina Faso and NRCRI in Nigeria to be evaluated in MET trials to help refine regional.

Two activities at Peru have led to the development of 953 elite, high Fe content, hybrid clones germinated *in vitro* tracing back to six elite crosses (target 1,200 genotypes) - **(**Annex 24**).** These clones were due for shipment to Mozambique by December 2020, but revised workplan due to COVID-19 crisis indicates shipment by CIP Lima genebank in June 2021. The field activity in Peru to evaluate these high Fe content hybrid clones across regions (Mozambique, Peru by SweetGAINS; Bangladesh by USAID) will start in December 2021.

Output 2.2.2 Prioritized traits and breeding approaches at Uganda sub-regional program PI: Julius Okello

The AbacusBIO-CIP 1000 minds study was carried out in Uganda on trait optimization and definitions, and Mpigi and Masaka districts were targeted for this trait preferences and trait valuation study, as they have a large cultivation of sweetpotato, and also significant amounts of sweet potato root value addition/processing and vine multiplication activities.In total, 1,000 root producers (48% women), 141 consumers (64% women, 147 traders (50% women), and 58 vine multipliers were interviewed, respectively. This activity was cofounded by SweetGAINS, DFID, Excellence in Breeding and the CGIAR Cooperative Research Program RTB (Roots, Tubers & Banana). Its final report was delivered by AbacusBIO in September 2020.

We identified groups of respondents with specific patterns of trait preference, based on the category of trait patterns and direction of preference ranks within each group, as follows: 1) Productive output, 2) Plant robustness, and 3) Root quality. Gender, years of formal education, main business activity, secondary business activity of root producers, production system, use of improved varieties, and preferred flesh colour of roots were tested for significant differences between cluster groups, across all respondents. Significant differences occur when assessing cluster groups by supply chain segment (main business activity), with consumers strongly represented in the 'root quality' cluster group. Traders and processors had an intermediate position between producers and consumers, with traders focusing on eating quality traits and on root shape. Thus, consumers, traders, and processors tended to prioritise root quality. These findings align with the analysis of trait preferences by supply chain segment. Within root producers, there were more women in the 'root quality' cluster group, a likely consequence of women being responsible for purchase and preparation of food within the household, and therefore these 'root eating quality' attributes are more important for women than men. Within consumers, there are more men in the 'productive output' cluster. Within traders, more men were in the 'plant robustness' and 'vine output' cluster groups. In general terms, within and across supply chain segments, women preferred quality traits (cluster into groups that have a preference pattern towards quality) while men preferred agronomic or production traits (cluster into groups that have a preference pattern towards production). Further, trait preferences for women were more diverse (they were spread more widely across the preferences space) in contrast to men. The implication of this is that a broad range of traits must be considered (rather than just addressing traits with high preference, on average) to capture the appropriate balance of traits for women and men.
The main findings from the study were that: 1) preference for production and agronomic traits outrank root quality traits and suggests their continued importance in national sweetpotato breeding program; 2) preference for yellow flesh colour is higher than orange flesh colour, with the latter currently more prominent only among vine multipliers; and 3) it is challenging to establish a consensus among smallholder farmers over desired traits, especially those relating to sensory/root-eating-quality traits. (**Annex 25**)**.** When all respondents were analysed together, the traits with the highest average preference rank (from 1 to 14, where 1 is most preferred and 14 is least preferred) were vine survival (3.5), followed by sweet potato weevil resistance (4.6) and sweet potato virus disease resistance (4.7), storage shelf life (5.7), and fresh root yield (6.5). The traits with the lowest average preference rank were vine yield (10.4), followed by flesh colour of roots (10.1) and hardness of roots after cooking (9.2).
In addition to the analysis described, AbacusBIO also provides selection indexes and economic weights, which are very valuable to drive discussions on product profiles and prioritized traits. Some issues remain though, as the difficulty of the current version of tools available at AbacusBIO to separate market segments for trait prioritization. During the months to come these findings will be further analysed and used to inform the development of product profiles in Uganda.

Output 2.2.3 Prioritized traits and breeding approaches at Mozambique sub-regional program PI: Maria Andrade, Godwill Makunde, David Ramirez, Bert De Boeck.

Protocols for evaluation of sweetpotato under drought stress were gathered and consolidation is on-going. All the selection indices were weighed, prioritized and traits described in line with the new SOPs for breeding which are under development. The phenotyping methods for drought tolerance are considered on the SOPs developed. Canopy temperature, Carbon and Nitrogen Isotopes were included in the sweetpotato ontology.

Output 2.2.4 Accelerated access to elite iron breeding material through in-vitro germination (ship *in vitro* germinated plantlets directly to Mozambique) PIs: Maria Andrade, Godwill Makunde, Wolfgang Gruneberg.

This output is under risk due to COVID-19, but the accelerated access to elite Fe breeding material (1,200 clones) by the concept of *in vitro* germination as well as the linked outputs to TPE in early breeding stages and phenotyping for genomic selection appears to be feasible within the project time frame provided that CIP Lima gene bank is able to ship the material mid- 2021. The target is to developed at least 1,200 genotypes from elite high Fe content hybrid genotypes available from Lima, peru. Owing to the COVID-19 crisis there are major delays compared to the original workplan: (i) stopping of crossings for elite HIFE from March to June 2020, but so far 953 new genotypes have been obtained; and (ii) severe restrictions at the CIP Lima gene bank where emphasis has been placed on keeping gene bank material over shipping breeding material during the COVID-19 crisis. The three Mozambique activities under output 2.2.4 have not started. This output is behind schedule.

Intermediate Outcome 2.2 - Work planned for next period and COVID-19 implications
Output 2.2.4 is behind schedule due to the COVID-19 pandemic. Handcrosses were affected due to the lockdown in Peru. The target is to have 1,200 clones from high Fe elite crosses and accelerate the process by in-vitro germination. Crossing program resumed only in August 2020. CIP Lima gene bank should start shipping genotypes only by mid- 2021. In year 2, the phenotyping methods will be described and published. We expect that there will be no interruption from COVID-19. Furhermore, in year 2, phenotyping methods for root storability will be developed in Mozambique. True seed harvested from 2020 crossings block will be processed and germinated to start a new nursery for 2021 OT at Umbeluzi Research Station. Data from AbacusBIo will be re run in order to gain more insight about what users and the market expect from sweetpotato varieites in Uganda, and findings will be shared and discussed with breeders, to reflect on the best use of the evidence gathered. Drought selection indices will be refined and we will start to validate them in at least two countries in southern Africa. In Uganda, new clones will be evaluated as field trials at 2 locations in year 2. After phenotyping for 1 season,

the number of clones will be reduced from 5,000 to 1,000. As the selected popularion will be the training population for GS, it will be QCed with SNPs to verify trueness to type from the screenhouse through to the field.

Intermediate Outcome 2.3 – Optimized selection stages at 2 sub-regional platforms and at least 4 NARIs by 2022. PI: Wolfgang Gruneberg, Jolien Swanckaert, Maria Andrade, Godwill Makunde, Bert De Boeck, Robert Mwanga, Fekadu Gurmu (Ethiopia), Jean Ndirigwe (Rwanda), Martin Chiona (Zambia) Kennedy Masamba (Malawi), Jose Ricardo (Mozambique).

Output 2.3.1 – Standardized data capture, digitalization and curation for agronomic and quality traits in all CIP sub-regional platforms and at least four NARIs, using SPBase. PIs: Lukas Mueller, Cristiano Costa Simoes Luka Wanjohi, Bert de Boeck.

This output is reported under three main activities, A1 to A3.

A1: Enabling the creation of experimental designs in SPBase and data collection using the Fieldbook APP in all CIP sub-regional platforms and all NARIs

New breeding data management SOPs were launched and adopted by all CIP and NARIs breeding programs (https://hdl.handle.net/10568/109605). The creation of experimental designs directly in SPBase is strongly recommended in these SOPs. A large set of experimental designs can already be generated in SPBase. However, we recommend the use of more modern experimental designs, such as resolvable row-column and augmented row-column designs. BTI (Boyce Thompson Institute) will work on the implementation of these experimental designs in SPBase with statistical support from CIP. The use of Fieldbook APP for digital data collection of phenotyping experiments is strongly recommended in the new SOPs. A data management CoP, that is holding monthly meetings, is supporting the compliance of all CIP sub-regional and NARIs breeding platforms with these SOPs. Recommendations have been issued to NARI partners to immediately upgrade their statistical designs, as CIP support will be available to create and analyze such datasets.

CIP's sub-regional program in Uganda and the NARIs program, NaCRRI, are now equipped with ruggedized Android data collection tablets. Field data collection is actively being done by using the FieldBook App in these two programs since February 2020. The improved ruggedized data collection tablets were only delivered in Maputo in August 2020. The delivery was delayed by international flight closures occasioned by COVID-19. Nonetheless, digital data collection for CIP's program in Mozambique using the FieldBook App has been ongoing since March 2020 using regular android tablets (Samsung 7" Tablets). Plans are underway to purchase digital data collection tablets for all the other NARIs programs in SweetGAINS. Additionally, each program will be equipped with Android compatible Bluetooth enabled digital handheld scales, barcode Zebra printers and handheld barcode scanners alongside data collection tablets, for both CIP and NARIs programs.

A2: Introducing proper data curation practices and uploading to SweetPotatoBase

Quality control for collected data has been implemented in the open source R package st4gi. SOPs provide detailed step by step guidelines for curating data using this R package. To make the data curation process more user-friendly it also has been implemented directly in the test version of SPBase, awaiting to be rolled out on the production SPBase website, and with the developed R code running in the background. Furthermore, SOPs also provide detailed guidelines on uploading all curated trial data to SPBase. After a trial is uploaded on SPBase, it is required to upload a copy of the trial's metadata on CIP's open access Dataverse repository, for that trial dataset to be deemed Open Access compliant.

A3: Providing trainings on creating experimental design in SPBase, digital data collection, data curation, and uploading to SPBase

Training on the use of the Fieldbook App and SPBase was delivered to CIP and NARIs breeding staff from Uganda, Tanzania, Ethiopia and Rwanda during breeding and seed system community of practice meetings held in Kigali in February 2020. A similar training scheduled for May 2020 for programs in Southern Africa was not conducted due to travel disruption by COVID-19, and it has been postponed until late November. Extensive online capacity building activities targeting all CIP breeding programs and NARIs programs under SweetGAINS have been scheduled for the months of October and November 2020. The activities will comprise of intensive virtual trainings on the use of SPBase for phenotyping activities, the use of the FieldBook App and data curation using R (st4gi). At the request of NARI partners, training on R will also be provided online.

Work planned for next period and COVID-19 implications.

BTI, with input of CIP, will work on updating experimental designs in SPBase. Modern experimental designs will be added, and some aspects of already integrated experimental designs will be revised when necessary. As mentioned in Output 1.3.1, training sessions are foreseen for all partners to support SOP implementation, including the creation of experimental design in SPBase, digital data collection for phenotyping and crossing experiments, data curation, and data uploading to SPBase. COVID-19 implies that training must held online, which has advantages in terms of reachability, but can be challenging as well (e.g. when training the use of digital tools or label printing).

Output 2.3.2 –Removed prior to final approval of SweetGAINS

Output 2.3.3 – Optimized resource allocation, breeding pipeline, and multistage/multi-trait selection PIs: Wolfgang Gruneberg, Bert De Boeck.

Research is focusing on optimizing later breeding stages across breeding programs (NARS and CIP) and multi-trait selection in early breeding stages with a clearly established population improvement (CIP breeding platforms). The output to be achieved in September 2021 and will be significant for the modernization of the sweetpotato breeding program especially in Africa.

The output has two activities.

Output 2.3.3.1 Optimized multi-stage selection

For the optimization of later and early breeding stages, responses to selection are determined by Cochran's approach. A small R script (**Annex 27**) as been developed which is easier to use than the SelectionGain procedure from the University of Hohenheim. Responses to selection have been optimized for one METs with respect to root yield (variance component ratios of σ^2_G:$\sigma^2_{G\times L}$:σ^2_{GxS}:$\sigma^2_{G\times L\times S}$:$\sigma^2_\varepsilon$ of 1:0.189:0.103:0.603:1.162). Differences between two- and three-stage selection scenarios appear to be small suggesting two stage selection in later breeding stages. So far one set of multi-environment trials (METs) with variance component ratios of σ^2_G:$\sigma^2_{G\times L}$:σ^2_{GxS}:$\sigma^2_{G\times L\times S}$:$\sigma^2_\varepsilon$ of 1:0.189:0.103:0.603:1.162 has been used for optimization later breeding stages (**Annex 28**). Currently, 5 METs are available to obtain such estimates, but results are expected to be similar since $\sigma^2_{GxS}$is in all 5 METs the smallest GxE interaction. For early breeding stages no optimization in stage selection has been conducted so far.

Output 2.3.3.2 Multi-trait selection in population improvement

Most breeding programs aim at the simultaneous improvement of several traits. For one cycle of selection, the classical Smith-Hazel index is maximising the response to selection. For long term selection other methods might be more efficient. Populations with 2x candidates and two negatively correlated traits were generated by the discrete simulation and were developed over several selection cycles. Methods compared were tandem selection, selection by independent culling, selection of extremes, the linear Smith-Hazel index, Pesek-Baker index and heritability index as well as the non-linear Elston index with concave truncation function and new selection indices with convex truncation functions. In populations where both traits have equal heritability the index for convex truncation is superior. In populations where heritability is unequal for traits and negative genetic correlations occur the selection methods differ considerably. In that case, the index for convex truncation and the Pesek-Baker index are clearly superior (**Annex 29**).

Output 2.3.4 – Elite clones developed surpassing current varieties by 10% in two key traits in their TPE PIs: Maria Andrade, Godwill Makunde, Reuben SSali, Jolien Swanckaert, Fekadu Gurmu (Ethiopia), Jean Ndirigwe (Rwanda), Martin Chiona (Zambia) Kennedy Masamba (Malawi), Jose Ricardo (Mozambique), Koussao Some (Burkina Faso).

East & Central Africa and Southern Africa sub-regions contributed to this output. All the activities for this output were completed for Southern Africa. Breeding trials were established in Mozambique, Zambia, Zimbabwe and Malawi. Management of trials in Zambia, Malawi, Zimbabwe and Mozambique were done in collaboration with NARI partners. Breeding trials evaluated in Southern Africa are presented below. Results from two locations in Zimbabwe, namely Makoholi Experiment Station and Dozmary Farm, clearly showed that sweetpotato is not affected by late season drought stress (**Annex 30**). These locations only had enough rain at establishment and root initiation stages. The process of identifying check clones for sweetpotato breeding in Uganda based on a GxE interaction approach using BLUPs from multi-environmental trials is shown in (Appendix A2, Tables 16 – 18, Figs 11 – 14). (**Annex 26**)

Table 3. Breeding trials evaluated in Southern Africa during the 2019/20 rainy season

Trial type	Description	Location	Comments

Advanced trial, 30 clones	Trial had 30 clones with flesh colours ranging from cream, white, yellow and purple (non-OFSP). Chingova was used as a check clone	Mozambique 1. Umbeluzi 2. Gurue	Trial was analysed for NIRS fresh for both locations and NIRS cooked for Umbeluzi only. Time to cook was also evaluated
Advanced trial, 50 clones	Trial had 50 OFSP clones. Irene was used as a check clone	Mozambique 1. Umbeluzi 2. Maniquinique	Trial was analysed for NIRS fresh for both locations and NIRS cooked for Umbeluzi only. Time to cook was also evaluated
Advanced trial, 84 clones	Trial had 84 OFSP clones. Irene was used as a check clone	Mozambique 1. Umbeluzi 2. Gurue	NIRS fresh determined for both trials
Multilocational trials, 20 clones (TPE)	Trial had 20 clones, mixed flesh colors- orange, purple and yellow. Purpose of trials is to define Sweetpotato TPEs for Southern Africa and introduction of new germplasm in the region	Mozambique 1. Umbeluzi 2. Gurue 3. Maniquinique 4. Nhacoongo Malawi 5. Bvumbwe 6. Chitala 7. Chitedze Zambia 8. Mansa 9. Kabwe Zimbabwe 10. Makoholi 11. Save Valley 12. Dozmary 13. Panmure 14. Gwebi 15. HRC-Marondera	Field data collected for all trials. NIRS fresh determined for all trials evaluated in Mozambique
Preliminary trials, 384 clones	Mixture of OFSP and PFSP clones	Mozambique 1. Gurue	NIRS fresh determined
Observation trials, 6,082 clones	Trial has 6,082 clones	Mozambique 1. Umbeluzi	Trial still in the field under two treatments
Observation trial, 126 clones	The trial had 116 clones and 10 parents, which included check clones as well.	Zambia 1. Mansa	Harvested and 60 clones were selected for advancement. Selection was based on root yield, cooking taste and tolerance to virus and diseases.
Observation trial, 3,963 clones Preliminary trials, 120 clones	The trial had 3,963 clones including two check clones	Malawi 1. Bvumbwe	-Harvested and 125 clones were selected from OT for advancement to PT. -57 clones were selected from PT for advancement
Crossing blocks	Block had 10 parents in Zambia, polycrosses. Block had 23 parents in Malawi, polycrosses	Zambia Malawi	Polycross seed collected in both countries. Seed cleaning and counting in progress in Zambia. Malawi recorded 14,612 true seed from polycrosses and 245 seeds from controlled crosses

Makoholi Experiment Station received 44 mm rainfall during establishment (1– 4 weeks after planting) and 100 mm at storage root formation (5 – 8 weeks after planting) for the whole crop cycle. Meanwhile, Dozemary Farm received most of the rainfall during

establishment and storage root formation stages and left exposed to terminal drought during the storage root bulking stage. The predicted harvest index (HI) was significantly higher at Makoholi Experiment Station in Zimbabwe than any other site. Environmental correlations based on storage root yield and harvest index indicated locations in Zambia were better correlated to locations in Zimbabwe. Locations in Malawi had better correlations to Mozambique (**Annex 31**). BLUPs for storage root yield (tons/ha) showed that locations in Zimbabwe had the highest means for this key trait compared to the other countries. Regional trials evaluated in Mozambique were also evaluated for quality traits and environmental correlations estimated based on dry matter (**Annex 32**).

A total of 24 clones had significantly higher storage root yield than Irene, the check clones across environments in OFSP[4] trials established in Mozambique (**Annex 33**). Four of these clones had significantly higher DM than Irene as well. Four clones had significantly higher storage root yield and DM than Chingova across environment in non-OFSP trials **Annex 33b**. Five varieties were given conditional release on 02 October 2020 in Mozambique. A few information and data concerning weather data, soil nutrition need to be included in the report. These five varieties had higher storage yield, dry matter (%) and taste than Irene, Alisha, Caelan, Bita and Chingova – the best clones in Mozambique.

In East & Central Africa, G x E interaction data obtained from previous multilocational trials in Uganda was used to select check clones for breeding program and the breeding trials presented below were conducted. BLUPs was used to estimate random effects (**Annex 34**). In this sub-region, breeding activities for elite clones surpassing current varieties by 10% was accomplished by dissemination of 4,000 true seed (polycrosses, 8 families) to each NARIs in Tanzania, Rwanda, and Ethiopia, and NaCRRI in Uganda obtained the first batch of H0 hybrids for advanced breeding stages (8 clones).RAB program maintained 17 accessions in tissue culture and established seedling nurseries with true seed from Mozambique and Uganda. Planting materials for OTs (from seedling nursery) and ATs are under multiplication. Uploading historical data into SPBase is one important task by RAB.

In Uganda, the following activities were postponed due to the COVID-19 pandemic: Harvesting 2019B trials in Serere and Kabale was delayed; Root samples were not taken from field trials, and no quality work done from March to August 2020; Quantitative phenotyping of SPDV in the BxT population was delayed; reagents and equipment procurement hampered by COVID-19 pandemic; PhD student to do quantitative phenotyping of the MDP population not recruited yet; a student accepted to do the work but changed to do another project on beans. Universities closed to date due to the COVID-19 pandemic.

In Tanzania, Rwanda and Ethiopia, establishment of OT (Observation Trials) and project activities were delayed due to delay signing of grant agreement and transfer of funds. The Ethiopia program lacks irrigation facilities to conserve vines during the off-season. Rwanda lacks ELISA kits for regular virus checks in tissue culture and screenhouses.

In West Africa, virus indexing and cleaning 105 sweetpotato lines from the low sweet population adapted to West Africa was delayed due to germination failure of *Ipomoea setosa* indicator plant seeds. A new stock of *Ipomoea setosa* seeds was obtained from Mozambique, and CSIR-CRI will continue with the process of virus indexing and cleaning of these clones. To ensure that the germplasm is conserved in the long run duplicate copies of the population have been sent to KEPHIS in Kenya for long term conservation and clean up there. In addition, establishing observational trials for the parent-offspring analysis for 434 families (5-16 progenies each) of the low sweet population adapted to West Africa at two sites (North & South) was not realized due to partial lockdown and restricted movement due to COVID-19. In Southern Africa, virtual trainings and meetings provided an opportunity for participation and learning by a larger audience. There is more and dynamic interaction with NARI partners. EiB training was very good.

Optimization plans of the breeding scheme for CIP-Uganda have been drafted with the guidance of the CGIAR Excellence in Breeding (EiB) Platform. Two simulation plans are being studied to i) optimize the number of parents, number of families, number of genotypes per family and ii) optimize the selection of new parents using testers for GCA estimation. Involvement with the Demand-driven sweetpotato trait prioritization project with AbacusBio is completed. Complementarity with the RTBfoods project – RTB sensory panel (based at Kawanda serving bananas, cassava, potato and sweetpotato), a kitchen was installed with a texturometer at NaCRRI. Complementarity with Development and Delivery of Biofortified Crops at Scale (DDBIO, funded by DFID) project for evaluation of promising OFSP in on-farm trials and national performance trials are in collaboration with NaCRRI; CIP-NARO agreement to conduct the trials is being finalized

Since breeding operations in Ghana were terminated on September 2020, CIP transferred breeding infrastructure to CSIR-CRI and CSIR-SARI, so these remain in use, preferably for sweetpotato breeding as presented below. Key advanced lines and parents from the Ghanaian program are kep at KEPHIS facilities in Nairobi.

Table 6. Breeding infrastructure transferred to NARS in Ghana.

Infrastructure	Institution donated to

[4] OFSP stands for Orange Flesh Sweetpotato, and are biofortified varieties enriched in beta-caroten, the precursor of Vitamin A.

Solar powered irrigation facilities for 10 acres	CRI and SARI
Storage barn	CRI
Cold room	CRI
Crossing block	CRI and SARI
Screenhouses	CRI(4) and SARI 1)
NIRS lab with food analytical equipment	CRI
Barcode printers	CRI and SARI
Polytanks	CRI and SARI

Table 4. Breeding trials conducted from 1st October 2019 to 30th September 2020 in East & Central Africa.

Trial type	Description	Location/AEZ*	Results/comments
Uganda			
Crossing blocks	Crossing block with 20 parents in population A and 20 parents in population B (selection of parents on basis of breeding values). Seeds were produced from crosses within the families, targeting 15 seeds per family.	Namulonge (warm, moist, tall grassland, high SPVD pressure zone)	Bi-parental and open-pollinated seed was colle from population A and B.
	15 isolated bi-parental crossing blocks: seed was produced from combinations of the pairs of eight elite parents to meet the requirements of NARS.	Namulonge (warm, moist, tall grassland, high SPVD pressure zone).	A total of 75,671 seeds were collected from the crossess. (Annex 35)
Observational Trials	Mwanga Diversity Panel (MDP): A set of 942 MDP clones + 16 parents were evaluated for agronomic traits and quality assessment. Experimental design: row/column with grid of 2 checks	Season 2019B - Namulonge (Planted 4th October 2019; harvested 2nd March 2020) - Serere (Planted 10th October 2019; 26th June 2020) - Kachwekano (Planted 15th November 2019; harvested 3rd August 2020) Season 2020A - Namulonge (Planted 24th March 2020; not yet harvested) - Serere (Planted 16th June 2020; not yet harvested) - Kachwekano (Planted 24th July 2020; not yet harvested)	Agronomic data was collected but harvesting del harvest date because due to COVID-19 lockdo Uganda. No root sampling and processing was c
	Mixed family plots. Same 942 MDP clones were planted. Data is collected on a family basis instead of individual basis. Experimental design: row/column with grid of 2 checks		
Preliminary trials	A selection of 52 clones was evaluated in three replicates (Annex 36)		
Tanzania			

Identify elite/advanced lines for MLT (high medium low altitudes)	A total of 81 advanced lines identified and multiplied in the screen house	-11 TARI Ukiriguru -10 TARI Tumbi -60 TARI Kibaha	All lines are still maintained in the screen house to have enough planting materials
Establish plants from True Seeds for Observation Trials	A total of 4900 sweet potato seeds were germinated in the lab and planted in the screen house	TARI Ukiriguru	A total of 1880 plants germinated and are maintained in the screen house for observation trial
Ethiopia			
National Variety Trials	A selection from 300 elite clones	Hawassa, Dilla, Halaba	Target is selection of superior clones which can be recommended for variety release
Preliminary Trials	A selection from 300 elite clones	Hawassa	Selection purposes for advancement
Maintenance of germplasm and characterization of clones at high altitude areas (2300-2500 m.a.s.l		Gedeo zone of Gedeb district	Conservation of planting material for future activities. Making selections for high altitude areas
Demonstration plots	Demonstration plots of newly released high dry matter OFSP varieties	Halaba	Popularizing new high yielding OFSP varieties
Rwanda			
Seedling nursery, 3,000 true seeds	Germination of true seed from Mozambique and Uganda	RAB	Germination percent recorded was 40% and program requires training by personnel in Mozambique.
Seed multiplication in tissue culture laboratory and greenhouses	Maintenance and multiplication of clean planting material, for advanced trials and preliminary trials.	RAB	Tissue culture has 17 clones under multiplication and conservation

Trials conducted in West Africa are presented below, mainly by NARIs.

Table 5. Breeding trials conducted by NARS in West Africa during year 1 of SweetGAINS project

Trial type	Description	Location/AEZ*	Results/comments
Burkina Faso			
Multilocational trials (TPE)	25 genotypes in total, with 17 genotypes coming from Ghana as advanced clones, and 5 advanced clones from INERA program and 3 local checks.	1. Kamboinse in central region 2. Wahabou lying between Central and Western regions 3. Farakoba in Western region.	Trials are currently under field evaluation. Agronomic management – weeding taking place.
Seed multiplication and conservation of breeding lines	The 25 genotypes in TPE trials are under multiplication for winter trials and	Winter trials will be planted at: 1. Bagre 2. Vallee du Kou 3. Loumbila	Winter trials to be planted

	conservation of planting material		
Nigeria	17 genotypes from Ghana	-	Planting materials received in August and are still under multiplication for planting in 4 locations.

Intermediate Outcome 2.3 - Work planned for next period and COVID-19 implications:

In year 2, the regional trials established in Mozambique, Malawi, Zambia and Zimbabwe will be repeated. In addition, each (national) program to continue with it breeding pipelines (OTs, PT sand AT) across different locations. We foresee difficulties in monitoring regional trials as travel can be restricted due to COVID-19. We anticipate official release of improved sweetpotato varieties in Zimbabwe in year 2, from regional trials. Support from Mozambique is required to support all NARs programs and we shall plan for this as soon as possible. In year 2, observational trials of 5000 new clones from the population improvement program at CIP-Uganda will be established at two locations. Selections from the PYT and MDP will be further evaluated in AYT at three locations. If travel in Uganda is not restricted by COVID-19, these trials should not face any delay.

Intermediate Outcome 2.4 – Enhanced statistical capabilities available at 2 sub-regional platforms and at least 4 NARIs by 2022

Output 2.4.1 – Correlated response patterns of Multi Environment Testing (MET) -TPE and novel approaches to early stage selection PIs: Bert De Boeck, Maria Andrade, Jolien Swanckaert.

For Southern Africa, 20 clones were evaluated at 16 locations in four countries, namely Mozambique, Zambia, Malawi and Zimbabwe. Agronomic data was processed and ready for curation. OTs under two treatments were established as an augmented row-column design on 01 August 2020 with the aim of estimating GCA and SCA. In West Africa, elite clones for MET trials were distributed to Burkina Faso, Nigeria and Ghana. Evaluations are ongoing. In East & Central Africa, the breeding programs are getting organized to establish METs in that region.

Output 2.4.2 – Modelled heritability landscapes for several locations and seasons of field testing. PI: Bert De Boeck

These activities are linked to the data gathering, and data curation, of historical data mentioned in WP1 (Output 1.1.1, deliverable 2). As data curation is just finished, the first activity for this output will start in Q4 of 2020.

Output 2.4.3 – Assessed the impact of statistical modelling on heritability, correlated response and ranking PI: Bert De Boeck

Activities has not been started yet.

Output 2.4.4 – Experimental design and biometric support to Genomic Selection efforts provided PI: Bert De Boeck

Two main activities were considered, namely designing experiments and perform analysis for Genomic Selection (GS) when requested and follow training to adequately support the biometrics for GS efforts.

A1: Design experiments and perform analysis for GS when requested

Resolvable row-column designs have been generated for phenotyping experiments executed by NaCRRI to evaluate the GS training population for weevil resistance. Through simulations and with the support of EiB, an optimization of the amount of families and progeny per family for the intra-pool crosses of the hybrid GS population for SPVD resistance has been made.

A2: Follow training to adequately support the biometrics for GS efforts

Due to COVID-19, training possibilities were strongly decreased. Training of the biometricians has therefore been mostly limited to self-study. In November 2020 staff will attend virtually ICQG6 (Sixth International Conference of Quantitative Genetics) to remain up to date with new developments in quantitative genetics and biometrics.

Output 2.4.5 – Biometrics school to train SweetGAINS teams on modern statistical methodologies for plant breeding launched.

Output 2.3.5 had two major activities, A1 and A2.

A1: Program, lecturers and participants for the biometrics school

In May 2020, a statistical training called "Phenotypic modelling across the target population of environments" was planned in collaboration with Wageningen University & Research. This one-week training was aiming to focus on modern design of experiments, single trial and multi-environment trial analysis through mixed models, understanding target population of environments, genetic gain calculations and the principles of genomic prediction. A preliminary program is shown below. Participants were selected, and all preparations were underway, but due to COVID-19 and the inability to travel this training was cancelled for 2020. As an alternative, an online edition of this training is being planned and should take place beginning in October for three months.

Preliminary program statistics training.

Time	Monday	Tuesday	Wednesday	Thursday	Friday
09.00-10.30	Introduction ANOVA, mixed models	Analysis of individual trials	TPE characterization and environment classification	Mixed models for GxE across TPE	Presentation of GxE analysis on CIP data
11.00-12.30	Computer exercises	Computer exercises	Computer exercises	Computer exercises	
12.30-13.30	Lunch				
13.30-15.00	Design of experiments (RCBD, row-col, p-rep)	Mixed models for Genotype x Management x Location x Year data	Field trial visit	GxE analysis of CIP data	Introduction to genomic prediction and concepts about the calculation of genetic gain in the context of predictive technologies
15.30-17.00	Computer exercises	Computer exercises			

A2: Execute training and ask feedback from participants to evaluate the need for future trainings and necessary adaptations

This activity could not yet take place due to the COVID-19 pandemic. The online biometrics school is scheduled to take place in Q4 of 2020.

Intermediate Outcome 2.4 - Work planned for next period and COVID-19 implications.

Several activities will start in year 2 as planned and there are no COVID-19 implications foreseen. Continuous biometrics support to the GS activities of WP3 will be given. As soon as the COVID-19 situation allows, more biometrics training activities will be undertaken, and whenever possible online training will be used as an alternative. The biometrics school will be organized online due to COVID-19. The aim is to have this take place still in Q4 of 2020, and otherwise in Q1 of 2021, depending on the availability of the WUR lecturers.

Box 1 RTBFoods-SweetGAINS interactions and main findings for SweetGAINS's First Year Report

The main findings from RTBFoods, a BMGF investment, feed into several SweetGAINS activities. The focus of RTBFoods is mainly on developing new assay methods for the traits in the product profile and screening of a wide range of clones to understand the cooking and sensory quality of sweetpotato. A sweetpotato study population (Mwanga Diversity Panel, MDP) with 1,800 diverse clones from an 8x8 cross (16 parents) is being used to build the knowledge in RTBFoods in Uganda. The focus of SweetGAINS is mainly on implementing the new techniques into the breeding program in Uganda and Mozambique by characterizing the parental lines and evaluating advanced clones.

In RTBFoods WP1, progress has been made in developing a product profile for boiled sweetpotato. The most preferred and least preferred traits were identified for the raw storage root, and for processing and boiled storage roots, with all information l segregated

for gender and region in Uganda. During the processing, appearance and easiness to peel are identified as preferred. After boiling, the smell, sweet taste, mealy and firm are preferred. A bad sweetpotato is watery, fibrous, tasteless, soft and bitter.

Several Standard Operating Procedures (SOPs) have been developed for the determination of cooking time, texture analysis and sensory profiling in WP2. A kitchen is being installed at NaCRRI in Namulonge to accommodate for cooking sweetpotato and other RTB crops. This is where the breeding activities are organized and screening of sweetpotato clones is mostly done. An RTB sensory panel was trained at NARL in Kawanda. A lexicon for boiled sweetpotato is now available and work is underway to enter it into the global crop ontology. Validation is in progress to link the sensory profiling with the texture SOP and cooking time. Other traits contributing to the texture are also being studies such as cell wall composition, pectin content, beta-amylase activity, gelatinization temperature in collaboration with the different partners in RTBFoods (CIRAD, CIAT and JHI).

A high-throughput method using Near-Infrared Spectroscopy (NIRs) is already in place for screening raw, freeze dried sweetpotato roots, and in RTBFoods WP3 we are extending the calibrations to bio-physical traits such as texture and cooking time. Having a NIRs scan of the fresh, raw root to predict the boiled quality traits would give the breeders the chance to screen thousands of clones in the early breeding stages. Once the roots need to be boiled to evaluate the boiled quality traits, the number of clones that can be screened will become limited. A proof of concept is underway with 60 diverse sweetpotato clones.

WP3 -Deployment of Genomic Selection (GS) and Genomic Prediction (GP) to Enhance Genetic Gains and Breeding Efficiency

Intermediate Outcome 3.1 – Increased range of genomic resources available for sweetpotato improvement in Africa by 2022.

Output 3.1.1 – Developed *I. batatas* reference genome and a core set of sweetpotato germplasm re-sequenced at intermediate depth. PI: Zhangjun Fei

3.1.1.1: Beauregard reference genome development

During the GT4SP project and leading into SweetGAINS, BTI began to assemble a phased genome for Beauregard, a major orange-fleshed genotype. The Beauregard genome was first sequenced using Illumina and 10x Chromium technologies, which generated total sequences of ~843 Gb, which is an ~ 281× coverage of the Beauregard genome (Annex 37). The resulting sequencing data were assembled using the NRGene DeNovoMAGIC platform. We then generated 91.4 Gb PacBio HiFi reads with a base accuracy >99% and an average length of ~11 kb (Annex 37), and the HiFi reads were assembled using hifiasm (https://arxiv.org/abs/2008.01237). The HiFi assembled contigs were integrated with the NRGene assembled scaffolds, which resulted in a final phased assembly with a total length of 3.02 Gb, and N50 scaffold and contig sizes of 2.17 Mb and 210.5 kb, respectively (Annex 38).

Dovetail Chicago and Hi-C reads were generated, which, combined with the Beauregard × Tanzania phased genetic map and syntenic information between genomes of Beauregard and I. trifida/I. triloba, are being used to construct phased pseudochromosomes of Beauregard from the assembled phased scaffolds.

The quality of the Beauregard assembled scaffolds was assessed via RNA-Seq read mapping and BUSCO analysis. Up to 97.6% of RNA-Seq reads from various root and seedling tissues could be mapped to the assembly, and ~99% of the core conserved plant genes were found complete in the Beauregard assembly (Annex 39), supporting the high completeness of the Beauregard assembly with regard to gene content. Furthermore, the duplicated BUSCOs (Annex 40) and the coverage of the assembly by Illumina reads (Annex 41) suggested that the phased Beauregard assembly contained most of the homeologous and heterozygous alleles in the hexaploid genome.

3.1.1.2: Tanzania reference genome development

Our second genome sequencing effort involved the east African landrace, Tanzania, which was crossed to Beauregard to form the BT population decribed above. A total of 128.8 Gb Tanzania PacBio HiFi reads were generated and assembled into 47,244 contigs with N50 length of 227.9 kb and total size of 3.1 Gb. The final Beauregard pseudomolecules will be used for anchoring the Tanzania contigs into pseudochromosomes.

In addition to the above progress, an opportunity for the creation of a sweetpotato pan-genome recently materialized due to our ties to Corteva. Dr. Sandra Milach, Research Director at Corteva and one of SweetGAINS' External Advisory Board members, has kindly offered Corteva's expert assistance with Bionano Optical mapping of the Beauregard line, and PacBio HiFi library construction and sequencing of an additional four sweetpotato accessions at preferential prices. Corteva will provide ca. 100Gb of unique molecular coverage per accession, while the SweetGAINS team will assemble and curate the additional genomes, if we can secure the needed bioinformatic and computational resources. This opportunity would enable the WP3 team develop the a pan-genome of this crop (a first). This development would certainly not have been possible for several more years without the assistance of Corteva. Though the previous success of the

GT4SP project and current work at SweetGAINS will provide reference genomes of the two highly heterozygous, hexaploid, cultivars Beauregard and Tanzania, the prospect of developing a hap map/pan-genome for sweetpotato would enhance our ability to quickly progress to initiate proof-of-concept haplotype-based, genomics assisted breeding as a prototype in Uganda, and subsequently in additional countries where sweetpotato represents a large and increasing crop. Thus, we have begun discussions with Dr. Lorenzen on how to achieve this goal through the reinvestment of Year 1 project savings, as the use of such nonimplemented funds is contingent on BMGF approval.

3.1.1.3: Core set of sweetpotato germplasm re-sequenced at intermediate depth

Nothing to report for this period. Activities scheduled for years 2 and 3.

3.1.1.4: Bioinformatic Analyses of 6x reference genomes and integration into genome browser and publication

Nothing to report for this period. Activities planned for year 2.

Output 3.1.2 – Annotated hexaploid I. batatas reference genome available on a user-friendly genome browser. PI: Robin Buell

3.1.2.1 Generate Oxford Nanopore Technologies and Illumina RNA-seq data to support gene model annotation

To support annotation of the Beauregard genome, we have isolated replicated RNA from fibrous and storage roots (30 DAP (Days After Planting) and 60 DAP) along with leaf tissue. We are constructing Oxford Nanopore cDNA libraries and generating full-length cDNA sequences from these tissues to support annotation of haplotype-specific gene models.

We have existing gene expression profiling data from heat and salt stress time course experiments with Beauregard. These data were generated in parallel with the PEG-treated samples that were analyzed previously (Lau et al. Plant Direct 2018). We have processed these through a bioinformatic pipeline using the I. trifida reference genome to identify differentially expressed genes. The on-going analyses with the heat and salt-treated samples will also serve to validate the datasets such that these, along with the PEG-treatment samples, can be overlaid on the Beauregard genome to support functional annotation of the genome. While we do have abiotic stress expression profiles for Beauregard, biotic stress gene expression profiles are lacking. We are in the progress of generating a methyl jasmonate (elicitor of biotic stress) time course gene expression profiling dataset that will be informative in the annotation of the Beauregard genome.

3.1.2.2 Develop gene models for hexaploid sweetpotato

Nothing to report for this period

3.1.2.3 Generate datasets and perform comparative analyses to support genome annotation

Nothing to report for this period

3.1.2.4 Release v1 Hexaploid sweetpotato genome browser and associated datasets

We have continued to support the Sweetpotato Genomics Resource that hosts the genome and annotation of the I. trifida and I. triloba genomes.

3.1.2.5 Update to v2, v3 hexaploid sweetpotato genome browser and associated datasets

Nothing to report for this period

Output 3.1.3 – Converted GBS SNP protocol to a cost-effective SNP-array format and Comparison and/or Implementation in an AmpSeq Format in the EiB Platform. PI: Bode Olukolu

3.1.3.1 Quantitative Reduced Representation Sequencing (qRRS using OmSeq) of panel representing global genetic diversity.

During the GT4SP project we initiated a project with the USDA-ARS Sweetpotato Germplasm program in Charleston, SC to develop an in-solution SNP array using a core panel of 96 sweetpotato accessions representating global genetic diversity obtained from the USDA-

ARS sweetpotato gene bank. Using GBSpoly (first iteration of OmeSeq/qRRS, using TseI/CviAII), an initial high-density genome-wide genotyping (~80,000 SNPs) of the USDA sweetpotato germplasm collection (767 accessions), was used to establish clusters of related individuals **Annex 42** and select the 96 accessions in the core set. Additionally, to ensure robust representation of diversity in SSA, a collection of 94 economically important African cultivars were genotyped with OmeSeq/qRRS (~75,000 SNPs; **Annex 42**. To derive sequence contexts compatible with OmeSeq-Array (NsiI/NlaIII), the USDA 96 core set will be re-sequenced with OmeSeq/qRRS and used for designing the in-solution array. The OmeSeq protocol, developed during year 5 of the GT4SP project and with the assistance of an Illumina Great Goods sequencing supplies grant, has provided significant improvements to the initial GBSpoly protocol, including generation of 20-50% more sequencing yield, improved quality scores for base calls, a ligation-free and PCR-free assay that ensures a quantitative assay required for dosage calling, and the inclusion of an optional DNA repair step that makes the protocol robust despite degradation of DNA samples (**Annex 43**).

3.1.3.2 Automate bioinformatic pipeline for designing omeSeq-array oligos and multiplexed oligo synthesis.

To streamline the analytical process following sequencing, we have developed modular, automated bioinformatic pipelines that complement the novel features of the genotyping platform (i.e. OmeSeq/qRRS and OmeSeq-Array). The software, ngsComposer and GBSapp, are also backward-/broadly- compatible with other library preparation methods. The ngsComposer pipeline (https://github.com/ryandkuster/ngsComposer) uses a combination of the traditional phred quality scores and an empirical based approach that allows for an unbiased filtering of NGS reads. The empirical approach was found to significantly improve read quality since phred quality scores are often inflated on NGS platforms (**Annex 44**). Other novel algorithms in the ngsComposer software revealed significant improvements for problematic issues such as barcode-swapping, a persistent problem for pooled libraries. Empirical analysis and comparison with mainstream software reveal the superior performance of ngsComposer for accurate demultiplexing (**Annex 45**). The SNP calling and filtering pipeline, GBSapp, provides multiple features, which include dosage calling at all ploidy levels, including allele-dosage in paleopolyploids, haplotype calling based on sequence reads, haplotype-based filtering, ploidy estimation, and various visualizations of data and QC.

3.1.3.3 Test array (approx. 48 SNPs) implementation for omeSeq-noSeq in various populations

Nothing to report for this period. This will be done in collaboration with CIP QC efforts.

3.1.3.3 Test array (a few thousands and tens of thousands) implementation for omeSeq-array in various populations (MDP, NCSU GS, NaCRRI GS populations).

Nothing to report for this period.

Intermediate Outcome 3.2 – Developed genomic prediction tools for sweetpotato.

Output 3.2.1 – Refined polyploid mapping and QTL analysis methods for bi-parental populations extended to GP algorithms using the MDP diallel population. PI: Zhao-Bang Zeng

Significant efforts have been made to extend our linkage analysis methods from a full-sib family to multiple inter-connected families like the MDP. The keys for this extension are: (1) improved marker dosage calling from bi-allelic markers to multi-allelic markers, which is essential for small families; and (2) efficient algorithms to merge linkage maps from multiple families to a joint map. For (1), we have tried using three local haplotyping algorithms developed for polyploids: PopPoly, dirHap, and WhatsHap. The preliminary results in our biparental Beauregard x Tanzania (BT) population dataset yielded a substantial improvement of the genotype calling compared to isolated SNP. This could be clearly observed when comparing the pairwise recombination fraction matrices in both cases. When combined with our linkage-based phasing algorithm, developed during GT4SP, dirHap provided consistent local haplotypes. We are currently using these multiallelic haplotypes to re-construct the BT map employing the updated version of our MAPpoly software, available at https://github.com/mmollina/MAPpoly. The multiallelic algorithm is available in functions "merge_maps" and "est_haplo_hmm". For (2), we applied our algorithms in current data of BT, TB, and NKB populations to come up with a joint map from the three families. Briefly, the joint map algorithm consists of exploring the full-sib and half-sib structures of the population coupled with SNP pairwise linkage analysis to reduce the linkage phase search space. For the remaining unresolved cases, we use an extension of our MAPpoly's hidden Markov model (HMM) based on the combination of gametes in parent-offspring trios to select the best linkage phase based on the multilocus-multipopulation likelihood (**Annex 46**).

Due to the disappointingly high frequency of poor-quality DNA obtained from the MDP materials in our initial DNA extractions of the MDP population, the genotyping of MDP has been delayed. This has significantly impacted the progress of this project as our analyses are dependent on the genotype information of the MDP progeny. Section 3.3.2.1 below describes what is being done to correct this mistake. Thus, we are using the available GT4SP biparental populations to test the algorithms.

3.2.1.1: Refined polyploid mapping and QTL analysis methods for bi-parental populations extended to GP algorithms using the MDP diallel population.

We have developed a general polyploid genetic model that is particularly suited for multiple families. Combined with a model selection procedure, such as LASSO (least absolute shrinkage and selection operator regression analysis), we believe this method will provide a more efficient method for QTL mapping analysis in multiple-connected families such as MDP. Particularly for MDP, QTL analysis may be able to provide specific QTL alleles that are responsible for General Combining Ability (GCA) and Special Combining Ability (SCA).

Output 3.2.2 – Developed computational framework for GS and GP in polyploids. PI: Zhao-Bang Zeng

3.2.2.1: Developed computational framework for GS and GP in polyploids.

We are working on a new GS and GP procedure for polyploid that is based on a joint linkage map construction and links parental haplotype inference in multiple families to specific genomic QTL through a general QTL genetic model and model selection procedure. This procedure can work in MDP and related populations, or pedigree populations. This model was applied in the BT and TB populations. Preliminary results showed that, for quality-related traits, our general model combined with LASSO selection performed as good as the random effect model approach (REMIM - Pereira et al., 2020), developed during the GT4SP, and was superior to dosage-based and diploidized GBLUB models. Nevertheless, when compared with REMIM, our model can be applied much more efficiently in multiple inter-connected families. For yield-related traits, our model performed at least as good as other genomic prediction methods. Even though the preliminary results are encouraging, testing the procedure in MDP will provide critical information on the prediction accuracy in a complex population.

Output 3.2.3 – Assessed database and digital data collection capacity at partner breeding programs through trainings and a broader Community of Practice. PIs: Lukas Mueller, Guilherme Da Silva Pereira

Sweetpotatobase (SPBase) runs on the Breedbase platform, which underpins Cassavabase, Yambase, and other sites. SPBase now encompasses over 436 field trials, 50,000 accessions, 136,702 plots, and ca. 1 million data points. The work described in WP2 Output 2.3.1 connects this effort with the WP2 team's efforts. SweetGAINS will increase researchers' ability to estimate BLUPs and Estimated Breeding Values (EBVs), as well as several other improvements, such as the ability to analyze both single location and multilocation datasets through LMMs. Ongoing database integration work includes analysis and data quality checks using CIP's HIDAP and the Breeding API (BrAPI). We have also been extensively involved with data curation and the updating of CIP data during the last year. Moving forward, we plan to also include GOBii backend genotyping integration and a BrAPI for the USDA ARS Breeding Insight Platform. CIP also plans to improve integration with the Field Book app from the PhenoApps team, implement interfaces with specific EiB genotyping data providers, and expand NIRS data management functionality.

3.2.3.1: Implement new experimental designs and enhanced data analysis features:

This is work in progress to be delivered by October 2020. Most recently, a quality control tool based on the R - st4gi was developed.

3.2.3.2: Mixed Models and BLUPs for sweetpotato

The analytic mixed model tools implemented in SPbase are working locally and just reaching the final phase of coding to allow implementation of the module in the database. A genomic selection tool developed for the cassava community is also available in SPBase (https://sweetpotatobase.org/solgs/search). However, we have some reservations on its utility for polyploid sweetpotato based on the experiences of our analytics group. Still, it is available for use by individuals interested in exploring their data and when enhancements become available we will work to implement them in SPBase.

3.2.3.3: Data base and functionalities (calibration and analysis pipeline) for NIRs.

The NIRS application is ready to merge and be available for both the SPBase main site and test site (**Annex 47**).

3.2.3.4: Integration with GOBii, BrAPI, and PhenoApps - Starting in September 2020.

3.2.3.5: Implement interfaces with specific EiB genotyping data providers - Starting in October 2020.

Intermediate Outcome 3.3 - Implemented Genomic Selection (GS) and Genomic Prediction (GP) in Uganda for SPVD and SPW by 2022.

Output 3.3.1 – Developed logistics and operational aspects of GS and GP in Africa breeding programs. Pls: Guilherme Da Silva Pereira, Bert De Boeck, Craig Yencho

This output links WP2 with WP3 outputs 3.2.3, 3.3.2 and 3.3.4. Learning from similar crop improvement efforts like NextGen Cassava, GOBii and working closely the EiB support platform we are developing Standard Operating Procedures (SOPs) for the SweetGAINS breeding programs. SOPs for GS and GP aspects will be coordinated with Output 3.1.3, WP3.2. This output will work with Output 2.5.4 to ensure good plot planting practices and plot ID tracking at all levels. Output accomplishments are as follows.

3.3.1.1: Purchases to support digitalized data collection

- Ruggedized android tablets, barcode printers, handgun barcode scanners and desktop barcode printers were purchased and delivered to CIP programs in Uganda and Mozambique, with a similar set of equipment purchased delivered to NaCRRI.
- Five barcode printers were purchased and they are awaiting delivery to national programs in Malawi, Zambia, Rwanda, Ethiopia and Tanzania.
- The Android tablets have yet to be purchased for national programs in Malawi, Zambia, Rwanda, Ethiopia and Tanzania.

3.3.1.2: Training and prioritization of QA/QC in breeding operations

Training re. the importance of QA/QC a breeding program has been conducted in the form of presentations in order to make people aware of the need for more accurate trials. These trainings were held during our Mozambique and East Africa sub-regional meetings as well as at our regular CoP meetings.

3.3.1.3: Establish a quality management team

At CIP, a quality management team has been established and they have been working on standard operating procedure (SOP) development. The CoP is having regular meetings to follow up data management practices and compliance with SOPs.

3.3.1.4: Map out the breeding operations with WP2 and SOPs

The breeding operations from WP2 have been mapped to five SOPs that have been established and discussed within the CoP.

3.3.1.5: Develop SOPs for DNA sample collection and tracking during genotyping

A DNA sample management and tracking SOP was drafted and presented in CoP meetings. It will be further edited to reflect (i) the provider (Intertek) which will be performing DNA extractions, and (ii) needs for NCSU/UTK genotyping protocols and the SPBase team.

3.3.1.6: Decide on genotyping platform/service providers and timelines

For QC markers, Intertek can deliver results for 30 SNP KASP markers within a 2-3 week window. The timeline for SNP genotyping for haplotype-based GS under 3.2 will be defined as testing by NCSU under 3.1.3 progresses.

3.3.1.6: Development of an end to end workflow of breeding operations with GS

The current status of SOPs and how they map to breeding operations (3.3.1.4) allows us to work with the SPBase team and the breeders to ensure that all phenomic data is being uploaded to SPBase as central repository. Linking the phenomic data to genomic data is ongoing as we define genotyping protocols under 3.3.1.5 and 3.3.1.6.

Output 3.3.2 – Deployed GS and GP in sweetpotato breeding at CIP-Uganda. Pls: Guilherme Da Silva Pereira, Hugo Campos

This output is closely linked to Output 2.3.2. CIP is beginning proof-of-concept GS in sweetpotato in Uganda for SPVD resistance, targeting parental selection and variety advancement, respectively. Training and prediction populations from the SPVD hybrid breeding population (described in Output 2.3.2) are be developed with the SOPs defined in Output 3.3.1.

3.3.2.1: DNA extraction and shipping of MDP to NCSU to support 3.2

DNA of ca. 2,000 MDP individuals (25, 96 well plates) was shipped Feb. 11 from CIP-Kenya and received at NCSU on Feb. 14 and placed in NCSU's -80C freezer immediately upon receipt. Prior to shipment Nanodrop 260/280 and 260/230 absorbance ratio purity checks were conducted on the samples, but no other quality checks were conducted. Within 2.5 weeks NCSU closed all labs due to the pandemic. NCSU's labs opened up again for approved projects under strict safety protocols in early June. Fortunately, the MDP genotyping project was approved as a high priority project and we received approval to proceed with genotyping. Unfortunately, our DNA quality checks of the MDP plates indicated that over 10% of the samples were either badly degraded or too low in concentration to accurately detect. The MDP samples were collected in July/Aug. 2019 at ILRI and held in the -80C unit at ILRI then shipped to NCSU and held at -80C for another ca. 2 months, we speculate that the samples had degraded during this time. This represented a major setback for the project as the MDP materials, which have already been phenotyped in 6 environments under the GT4SP project, are critical a critical resource for the polyploid mapping, QTL analysis and GS theory analytics team.

While the loss of the MDP samples was a clear set-back, we used this as an opportunity to move forward to start an earlier and deeper engagement with the EIB DNA extraction and genotyping collaboration with Intertek than originally planned. Instead of re-extracting DNA from the MDP materials in-house, we decided to use the Intertek service to do this work. Intertek had no prior experience with high molecular weight sweetpotato DNA extraction suitable for GBS, so we quickly arranged to conduct a small test DNA extraction experiment using two different DNA extraction protocols with MDP tissue samples that were dried prior to shipment to Intertek using two methods (freeze-dried and silica-gel dried). The samples were sent to Intertek July 24 and processed by Intertek by the end of Aug. We recently learned from Intertek that the DNA quantity and quality were sufficient to amplify QC KAPS markers and they were shipped and received at NCSU on Sep. 4 for further testing and OmeSeq genotyping under 3.1.3 will begin shortly.

3.3.2.2: Designing the training population linking to WP2

The training population was developed using two separate populations, each having 20 parents. Within-pool crosses were made resulting in a total of 500 families.

3.3.2.3: Vine multiplication of the training population

Seed germination in the screenhouse is already done for the 240 families with 16 or more seeds. Hand-crossing is continuing to fill the gaps. The remaining families will be germinated by the end of November.

3.3.2.4: Sampling of the training population for genotyping

This can be done by the end of this year when all families are established in the screenhouse.

3.3.2.5: Sampling the breeding population for haplotype validation under 3.2

To be defined once families are established under 3.3.2.4.

3.3.2.6: Establishing field experiments for the training population

We expect to have multiplied the material up to 6 cuttings to go to the field at two locations by season A in 2021 (March – April).

3.3.2.7: Data analyses

Output 3.3.3 – Developed and optimized SPW (Sweetpotato Weevil) phenotyping protocols. PI: Milton Otema

Similar to CIP above for SPVD, NaCRRI in Uganda will develop and optimize phenotyping protocols for SPW resistance in collaboration with NCSU. The program will use research outputs from the BMGF PEARL project, to determine priority parameters for evaluating SPW resistance. NaCRRI will conduct further experiments to validate and determine the exact timing for data collection, sample sizes and scales for scoring the key resistance screening parameters. Standard ontologies for phenotyping SPW resistance will be developed and

added to SPBase. Additional experiments will be designed to determine thresholds for bioassay parameters including, but not limited to, the number of weevils to be infested, number of feeding holes, oviposition sites, adult emergence, as well as duration of scoring.

Previous research has suggested that hydroxycinnamic acid (HCA) esters associated with the surface of storage roots in the NKB population were associated with resistance to SPW (field storage root infestation vs. total HCA r=0.603 p<0.01). Significant segregation for HCA concentration and SPW resistance was observed in the NKB population. However, when QTL analyses on these two traits were conducted, no co-segregating QTL were observed. However, CIP did observe significant transgressive segregation for resistance to SPW and HCA and these traits overlapped, suggesting that GS facilitated recurrent selection can be used to improve levels of resistance to SPW quickly, but only if NaCRRI is able to develop an improved bioassay platform. Therefore, SweetGAINS will focus attention on developing improved phenotypic bioassays for SPW evaluation. The focus on these studies will be SPW phenotyping.

3.3.3.1: Assembling of SPW resistant and susceptible clones

One of the major bottlenecks towards developing SPW resistance in Uganda has been inefficient phenotyping often leading to results with low heritability estimates. In order to advance on the SPW resistance screening optimization, we assembled a total of 48 sweetpotato genotypes for use in conducting phenotyping optimization studies. These genotypes possess varying levels of SPW resistance and have been identied in previous studies. The 48 genotypes consist of the landraces collected from farmers' fields in the sweetpotato weevil hotspot districts of Uganda that have been screened in earlier studies. In addition, some advanced clones from crosses between landraces, elite clones and released varieties were included. For this study, checks "New Kawogo" and "Ejumula" were used. The 48 genotypes and the checks are being maintained in the screen house and multiplication for the 2020B planting is already ongoing within the screen house and the swamp.

In May, we received "Ruddy", a multiple insect resistant sweetpotato cultivar released by the USDA-ARS, from NCSU. We are now maintaining the plantlets in vitro at NaCRRI. We also weaned some of the plantlets in the screen house for seed increase to obtain material for field trials and planting in the crossing block.

3.3.3.2: Establishment of field and screen house trials for SPW resistance evaluation

The field SPW phenotyping optimization trial was planted at NaSARRI on May 27, 2020 and AbiZARDI on June 19, 2020 using a resolvable row-column design. In each of the locations, the trial was replicated three times. In the planting, ridges were considered as the rows, and ther were nine and six columns per replicate. The plot size was 1.5 m and the spacing between plots was 1 m. On each ridge/plot five vines were planted 0.3 m apart. We are currently managing these trials using the standard practices including weeding and hilling up. We plan to harvest the trials at the beginning of October during which we will conduct SPW severity and incidence assessment. After harvest, we will obtain roots for setting up bioassay based SPW screening optimization experiments at NaCRRI. The screen house trials will be established after completion of the new screen house (currently under construction) as we currently lack screen house space.

3.3.3.3: Weevil rearing for bioassay

The sweetpotato weevil laboratory at NaCRRI has continued to maintain and multiply colonies of Cylas puncticollis and Cylas brunneus for routine use in SPW resistance screening. Presently, the team is on track in increasing the weevil colonies to be used for setting up the laboratory bioassay-based phenotyping optimization experiments.

3.3.3.4: Establishment of SPW bioassay optimization experiments

We plan on setting up these experiments at NaCRRI after harvesting the on-going field trials. These experiments will be set up in October and will run for four months in to the second year of the project.

Output 3.3.4 – Deployed GS and GP in NaCRRI breeding program for SPW resistance. PI: Benard Yada

3.3.4.1: Development of SPW training population (500 clones)

Based on the precept of a moderate training population size being sufficient to yield high predictive abilities, an all-encompassing and representative population of 500 genotypes was selected to constitute the NaCRRI sweetpotato training population. These genotypes included 1) progeny from crosses made between SPW tolerant varieties/ land races, 2) crosses of elite varieties and SPW tolerant varieties and 3) open pollinated seed/ progeny derived from the SPW improvement crossing block. The population has a composite of traits enlisted in the sweetpotato product profile for Uganda. The product profile guided traits including SPW resistance, SPVD resistance, beta-carotene content, and storage root shape and skin smoothness are segregating in the trainig population. In addition, we anticipate

a number of these genotypes being representative of the material at the program, as they possess the genetic background of the genotypes we have routinely used over the years. The focus is to use this population for developing predictive models for both genomic selection and genomic prediction for the lead traits. Similarly, this population possesses genotypes that have potential varieties for release, in particular, crosses from "New Kawogo" x "Covington" and "Tanzania" x "Covington" populations developed under the GT4SP and PEARL project. We are maintaining the population in the screen house for obtaining planting material for field trialing.

3.3.4.2: Preparation and shipment of leaf samples to NCSU for DNA extraction

Our current focus is to optimize the shipping protocols for sweetpotato leaf samples to service providers for routine DNA extraction. The recent tests of the MDP materials with CIP-Intertek-NCSU, which appear to be successful will be followed. Once the protocols and standard operating procedures for shipping sweetpotato leaf samples are finalized, we will first complete shipping of the MDP population. Then in the first quarter of second year of the project, we will ship the leaf samples for the training population Intertek for DNA extraction for downstream OmeSeq genotyping at NCSU.

3.3.4.3: Genotyping of SPW training population at NCSU

This activity has been deferred to the second year of the project, as the focus for our WP 3 team is to first get the MDP population genotyped.

3.3.4.4: SPW training population seed increase in the screen house

The 500 TP genotypes were multiplied in small buckets and continuously managed appropriately for conservation in the screen house. Prior to the cropping season, when additional planting material/ vines is required, the TP genotypes together with their parents are multiplied at the swamp. This is currently ongoing in the NaCRRI swamp.

3.3.4.5: SPW training population field trials

In the 2020A season, we established field trials for phenotyping the training population for SPW resistance and other agronomic traits at NaSARRI on May 28, 2020. With the support of. Bert De Boeck, SweetGAINS statistics lead the trial was designed as a resolvable row column design with two replications. The 500 test entries, 59 parents and 2 checks (NAROSPOT_1 and NASPOT_8, which are the varieties to be replaced in Uganda under the current product profile) were planted on 1.5 m ridges/ plots at a spacing of 1 m between plots. On each plot, 5 vines were planted 0.3 m apart. In this trial, the rows were considered as the ridges. The entire trial had 40 rows and 27 columns. We have weeded this trial and are in the process of collecting the first disease resistance data. The second training population phenotyping trial that was planned for NaCRRI was cut short by rains as we have not received stable rains at NaCRRI from June-August. We are in the process of planting this trial this September as this season's rains start.

Investments in human resources and physical infrastructure

The project hired and supports four Research Assistants, three Research Technicians and two Drivers in addition to support staff time for four scientists. To increase the screenhouse space that is badly needed NaCRRI has hired a contractor to construct a new screen house. The construction has started and it is anticipated that the screen house will be completed by October 30, 2020.

Output 3.3.5 – Deployed GS and GP in NCSU breeding program for variety development and nematode resistance. PI: Craig Yencho

Under the GT4SP project new genomic resources and analytical methods were developed to improve sweetpotato germplasm enhancement and variety development. SASHA I and II established excellent breeding support platforms in E, W and S SSA, enhanced SSA NARS breeding programs, and fostered improved seed systems. SweetGAINS will add new tools our breeder's toolbox and further enhance seed systems. The breeding programs at CIP, NaCRRI and NCSU are working to implement genomic selection (GS) and genomic prediction (GP) in our programs. Based on our experiences to date, there is no one, best way, to do this. The (**Annex 48**) provides an overview of the genomic selection studies conducted at NCSU and discusses some practical and operational breeding considerations toward GS and GP within the context of our program. Following is a brief summary of the NCSU activities.

3.3.5.1: Field evaluations of Year 1 vs. Year 2 GS populations.

Prior to the start of SweetGAINS project and with support of GT4SP, private industry and commodity projects, NCSU initiated two proof-of-concept projects to determine the most effective way to implement GS/GP in our program. The NCSU breeding program primarily uses OP polycross nurseries to generate diversity and true seed and it generally takes 3-5 years (dependent on goals) to cycle new parents into our polycross nurseries. Our initial efforts were focused on comparing the efficiency of deploying GS in YR1 vs. YR2 breeding materials. YR1 materials consist of selections derived from unlabeled single-plant plots planted in half-sib family rows with no previous selection and minimal phenotyping. YR2 materials consist of selections made in YR1 materials, which eliminate ~ 90+% of the YR1 materials, and they are evaluated in two unreplicated 25 plant plots that are planted at 2 sitest. Because YR2's are fewer in number and more storage roots are available for each clone, more extensive phenotyping can be conducted on these materials. YR1 vs YR2 experiments were started in 2017 and continued into 2018, and we suffered a major setback in 2018 due to hurricane Florence, when all of our GS trials were lost due to flooding. The two sets of trials were reestablished in 2019 from clonal materials, but the scientist managing the studies, Dr. Xiaofei Zhang left for a position as lead cassava breeder with CIAT in Aug. 2019, and the analyses are ongoing. Dr. Mohammed "Somo" Ibrahim was hired to replace Dr. Zhang in early Jan. 2020 but the coronavirus pandemic prevented his arrival into the program until June 2020 and he has begun to conduct the analyses of these trials in collaboration with the SweetGAINS analytical team. The current status of this research is described in more detail in the (**Annex 48**).

3.3.5.2: Development of GRKN mapping and GS population.

The Guava Root Knot Nematode (GRKN), Meloidogyne enterolobii, is a new pest recently detected in sweetpotato fields in NC, and it represents a significant threat to the US sweetpotato industry as it causes significant damage to the sweetpotato storage roots.There are no improved GRKN resistant varieties and the development of new varieties with resistance to GRKN has quickly become a high priority for sweetpotato farmers in NC. In SSA, it is widely speculated that nematodes are also associated with significant yield losses in sweetpotato that go undetected. Based on new GRKN and previous SRKN (Southern Root Knot Nematode, M. incognita) screening studies, it is thought that resistance to a wide range of nematode species has been passively selected for in SSA land races as several of the SSA land races screened for resistance to nematodes have proven to have high levels of resistance to multiple nematode species (e.g. Tanzania and Wagobolige, see Cervantes et al. 2002 and personal obs).

To develop improved GRKN resistant germplasm, the NCSU sweetpotato program developed a polycross breeding nursery focused on using GS and rapid recurrent selection that can be used for nematode resistance and variety development in the US and SSA. These studies were begun in 2019 with the establishment of a 16 parent polycross nursery for GRKN breeding and are describe in **Annex 48**. In 2019, 61,664 true seed were harvested from 16 parent polycross nursery. In 2020. 4,576 seeds were germinated from and 4,153 plants transferred into YR1 single plant plots on May 13, 2020 at the Caswell Research Station, Kinston, NC, and harvested on Aug. 28, 2020 (106 DAP). Our goal was to select 23 sibs from each family to establish foundational materials for training population development while keeping track of selection information. The YR1 average nursery selection rates in these materials were as follows: ~1.8% would have been kept using our typical variety development selection profile (this is slightly lower than normal), 4% were considered to be marginal selections and would not normally have been selected, while an additional 12.4% were selected to bring each half-sib family to the target number of 23 clones/half sib family, resulting in a TP=768. The storage roots from the single plant YR1 materials will be stored as storage roots in NCSU's storage facility over the winter, and then genotyped and planted into replicated trials in and evaluated for SRKN and GRKN resistance as well as yield during summer 2021 to obtain initial GEBV's for the first round of GS.

3.3.5.3: Genotyping and quality checks - all populations. - Planned for year 2.

3.3.5.4: Data analyses in collaboration with NCSU analytical team. - Planned for year 2.

3.3.5.5: Maintenance and propagation of training populations in NCSU greenhouse and storage facilities.

In progress with abovementioned populations.

Output 3.3.6 – Development of diagnostic markers for Quality Control. PI: Guilherme Da Silva Pereira

As hybrid breeding schemes are scaled up in WP2, this output will develop and deploy a low-density SNP set (≤30 SNPs) representative of the CIP and African breeding populations. The SNP set will be used for genotype fidelity tests and quality control (QC) [23]. This QC SNP set will be used within the joint genotyping platforms negotiated by EiB to better align with similar investments in other crops and to provide faster data turn-around for breeding decisions. This output is linked with output 2.2.1.

Thirty SNP KASP markers were tested on 94 samples (duplicates of the 16 MDP parents and 62 random progenies) replicated in four 96-well plates. Out of 30 SNPs testes, 16 were monomorphic, one failed, and 13 were polymorphic. The current results did not allow us to distinguish amongst the five heterozygous dosage classes as expected in a hexaploid species. Optimizations by Intertek are going to be discussed.

Intermediate Outcome 3.4 – Improved understanding of genetic resistance to SPVD and SPW in Uganda, and the genomic regions responsible for end user preferred quality traits defined in WP1 by 2022.

Output 3.4.1 – Dissected genetic basis of resistance to sweetpotato virus disease (SPVD). PIs: Jan Kreuze, Guilherme Da Silva Pereira, Robert Mwanga, Jolien Swanckaert

Program staff will conduct research to better understand the genetic basis of SPVD and its component viruses (SPCSV and SPFMV) to develop diagnostic markers for breeding. The team will use transcriptomic, genomic and quantitative phenotyping data linked with Outputs 2.2.3, 2.3.2 and 3.3.2. The combination of such datasets will also enhance the understanding of how symptomless viruses such as begomoviruses contribute to yield reductions, thereby compounding the effects of SPVD. Data generated from this activity will also be linked to Output 3.1.2. Based on previous experiences and challenges to dissect host resistance to SPVD, CIP will consult with other scientists from advanced breeding companies to map the best way towards achieving this output.

3.4.1.1: Quantitative phenotyping of BxT population for SPFMV, SPCSV and SPVD under controlled conditions in Uganda

Scoring data from SPFMV and SPVD was obtained as part of a master thesis. We are currently waiting for the antibodies (for quantitative assessment of SPFMV, SPCSV and SPVD). An ELISA reader was also ordered for the same work, but it has not been shipped to Uganda yet.

3.4.1.2: Quantitative evaluation of SPFMV, SPCSV and SPVD in selected MDP population families under controlled conditions in Uganda

Evaluation involving MDP families was delayed because the PhD student gave up the project, and recruiting another student with the universities closed has been difficult.

3.4.1.3: Genetic analysis for SPVD, SPCSV and SPFMV (Masters) in BxT population

Scoring data from 3.4.1.1 was analyzed using ASReml-R software and heritability values were estimated as 68.2% and 34.9% for SPVD and SPFMV, respectively. The adjusted means were used in QTLpoly software, and putative QTL were detected on LGs 3 and 10 (Annex 49.)

3.4.1.3: Analysis of datasets for genetic dissection of resistance in selected MDP families (SPVD, SPCSV and SPFMV (PhD)

Output 3.4.2 – Identified marker profiles associated with key textural and sensorial traits as defined from WP1 and RTBFoods and linked to WP2. PIs: Guilherme Da Silva Pereira, Jolien Swanckaert, Tawanda Muzhingi, Mukani Moyo

The food product profile for East and Central Africa targets good cooking quality with acceptable texture and sensory attributes after the sweetpotato has been boiled. This output will build on the experiences from the RTBFoods project and medium throughput phenotyping methods developed in WP2 to identify genetic markers associated with cooking ability behaviors, texture and sensory traits of sweetpotato. This will also generate new information to better incorporate GS and GP in routine selection for cooking quality, textural and sensorial characteristics in breeding programs.

3.4.2.1: Textural and sensorial traits in MDP linked to WP2 and RTBFoods

Data collection has been delayed due to the pandemic. Pending the status of the pandemic, it will start again by the end of August (next harvest in Namulonge) or in October (next harvest in Serere) this year.

3.4.2.2: Genetic analysis for marker profiles

Nothing to report for this period

Intermediate Outcome 3.5 – Implemented best practices and a CoP for the implementation of GS in Uganda by 2021.

Intermediate Outcome 3.5 is linked to WP2, EiB workflows, and WP1.

Output 3.5.1 – Developed best practice training on GS and GP as part of the modernization process of population hybrid breeding in WP2. PIs: Craig Yencho, Somo Ibrahim, Guilherme Da Silva Pereira, Hugo Campos

Lead scientists and support staff will be trained in quality management and operational excellence-related activities required for GS and GP. Assistance from EiB modules 3 and 5 will be sought for this training and the output will contribute to the success of Outputs 3.3.1-4. The training component will be linked to WP1.

Due to the loss of key personnel shortly before or after establishment of SweetGAINS, and complications arising from the pandemic, this aspect of the project has not progressed as quickly as anticipated. However, with the recruitment of Somo Ibrahim and Guilherme Da Silva, the project has begun to progress more. A WP3 GS/SP working group consisting of key personnel from the CIP, NaCRRI and NCSU has been established and they meet monthly to drive program activities and lead discussions on GP/GP breeding needs.

WP3 Project Adjustments

WP3 has the following outcome/output milestones: 3.1 - Increased range of genomic resources available for sweetpotato improvement in Africa by 2022; 3.2 - Developed Genomic Prediction tools for sweetpotato.; 3.3 - Implemented Genomic Selection (GS) and Genomic Prediction (GP) in Uganda for SPVD and SPW by 2022; 3.4 - Improved understanding of genetic resistance to SPVD and SPW in Uganda; and the genomic regions responsible for end-user preferred quality traits defined in WP1 by 2022; and 3.5 - Implemented best practices and a CoP for the implementation of GS in Uganda by 2021.

The WP3 team has made surprisingly good progress even during this pandemic, especially for milestones 3.1 and 3.5, where we have achieved out target goals toward the reference genome development of Beauregard and Tanzania (3.1) and hit our target progress on implementing best practices and a CoP for the implementation of GS in Uganda by 2021. We are however significantly behind in milestones 3.2, 3.3 and 3.4.

For milestone 3.2 our intermediate targets/milestones were: 1. Refined polyploid mapping and QTL analysis methods for bi-parental populations extended to GP algorithms using the MDP diallel population; 2. Developed computational framework for GP in polyploids based on the MDP data; and 3. Enhanced database and digital data collection capacity at partner breeding programs through trainings and a broader CoP. As mentioned above, while the loss of the MDP samples was a clear set-back for intermediate targets 1 and 2. However, we used this as an opportunity to move forward to start an earlier and deeper engagement with the EIB DNA extraction and genotyping collaboration with Intertek than originally planned. This work has gone well and we are currently testing the quality of the test samples, which were recently received by NCSU. If this next shipment passed QC testing then we will be sending the whole MDP set again and we expect to have OmeSeq genotyping completed by the end of the year are very early in the new year. Regarding intermediate target 3, we feel we are still on track and in the green zone for this project; however, it would be extremely helpful to do more in person training. Since this is not the case we have engaged in weekly Zoom training sessions with team members and these are working well.

For milestone 3.3, all of our intermediate targets: 1. Developed logistics and operational aspects of GP in Africa breeding programs; 2. Deployed GP in sweetpotato breeding programs at CIP-Uganda; 3. Developed and optimized SPW phenotyping protocols; 4. Deployed genomic prediction in NaCRRI breeding program for SPW resistance; and 5. Development of diagnostic markers for Quality Control purposes; have all suffered mostly as a result of the lock-downs experienced in each country. At this point we are in the yellow zone having achieved 25% of our expected progress toward these goals when we expected to be at 35% at the end of Year 1. Given the circumstances this is not poor progress and as of September most of WP3's field activites under these milestones have now been implemented. No major changes have been undertaken to modify these goals and we will re-evaluate our status in early 2021.

Milestone 3.4 intermediate targets include : 1. Dissected genetic basis of resistance to sweet potato virus disease (SPVD); and 2. Improved knowledge on the genetics of traits related to sweetpotato texture and cooking quality. We are in the red zone with these milestones. We are currently waiting for the antibodies (for quantitative assessment of SPFMV, SPCSV and SPVD) and an ELISA reader to be shipped to Uganda. This is expected to occur in November 2020. Also, quantitative evaluation of SPFMV, SPCSV and SPVD in selected MDP population families under controlled conditions in Uganda was delayed due to the loss of the PhD student assigned to the project. We have begun recruiting another student but with the universities closed this has been extremely difficult.

Work Package 4: Sustainable, Inclusive Seed Systems for the Accelerated Dissemination and Adoption of Market-Preferred Varieties

Intermediate outcome 4.1 Validated seed production and delivery plans implemented by commercial seed producers supply at least 80% of estimated effective demand for quality seed of market preferred varieties to male and female customers in target geographies by 2022

Output 4.1.1: Characterised existing sweetpotato seed system actors, identified efficient seed distribution channels and market preferred varieties. PIs: Srini Rajendran, Kwame Ogero, Sam Namanda, Margaret McEwan.

Rapid seed systems assessments were conducted in proposed target areas in Tanzania and Uganda. These used a combination of key informant interviews with key seed system actors, sex disaggregated focus group discussions with rural and urban consumers of sweetpotato roots and household interviews of seed producers and seed users. Detailed protocol and survey tools (i.e., questionnaires) are attached in **Annex 50**.

In **Tanzania** the assessment was implemented in Geita, Mara and Mwanza regions in the Lake Zone. In Mwanza, sweetpotato root traders source their roots at different times of the year from Geita, Butiama and Tarime districts. Preferred varieties are from Geita where Polista variety (cream-fleshed landrace with a purple skin) dominates. Bukombe and Butiama districts differ in seed acquisition systems, varietal preferences and target root markets.

Bukombe

There are two main channels for seed acquisition: (i) root producers conserve and multiply their own seed but can sell if they have surplus after planting their own fields. Their main business is roots but they also sell seed and have become known as key seed producers. They all have access to lowlands with permanent water supply. (ii) roots producers who are not able to conserve their own seed and have to buy every season. They understand that sweetpotato production is a business and are willing to buy seed. However, the cost of seed limits their area of production. To plant one acre for root production a farmer requires seed costing TZS. 150,000 (USD 65).

The main market for storage roots produced in Bukombe district is Dar es Salaam. Traders hire brokers who aggregate the roots and then take advantage of transit trucks returning empty from Rwanda. Preferred varieties are Ukimwi and Pisi Tatu (Three Piece). Ukimwi is orange-fleshed while Pisi Tatu is yellow-fleshed. Both have a purple skin and relatively long shelf life (can stay up to 7 days without getting rotten). They take about four months to mature. Other varieties grown in the area but not destined for Dar es Salaam include Sirari and Polista. Sirari has a short shelf life while Polista takes a long period to mature. The two are sold in the local markets.

Butiama

There are different types of seed acquisition channels in Butiama district: (i) free seed distribution by NGOs e.g. Project Concern International, who have established decentralized vine multipliers (DVMs), a financially unsustainable model since DVMs multiply to sell back to the NGO. (ii) Informal seed sharing among farmers. In Butiama, farmers plant varieties that take up to seven months to mature, which they then harvest at the start of the next season. This means that the vines from the previous crop can be used as planting material for the next one. Therefore farmers prefer varieties able to stay in the soil for many months without getting rotten or attacked by weevils. This is a big contrast with Bukombe district where farmers want fast maturing varieties (within two months).

The key commercial destination for roots from Butiama is Mwanza city. However, varieties from this district are least preferred in Mwanza. Traders go there because there is no alternative. This is usually between July and December when it is off season in other regions. The main variety grown in Butiama is Ukerewe. Other varieties include Berrita, Tunja Murume and Nyangubo. Ukerewe, Berrita (cream fleshed) and Tunja Murume have purple skins whereas Nyangubo is white-skinned. All varieties have white or cream flesh colour. Nyangubo is a favourite for local consumption and preferred for processing into '*Michembe'*- dried chips. However, traders in the market do not like it due to its short shelf life.

In **Uganda,** the study was carried out in in Kamuli and Iganga districts in Eastern region, where the highest per capita consumption of sweetpotato in Uganda is found. Sweetpotato is considered the number one food crop in Kamuli and Iganga districts, consumed as mashed in a mix of sweetpotato and beans (locally referred to as *Mugoyo*). The National Agricultural Research Organization (NARO) has a satellite station at Kiige. In each district, two sub-counties were selected (Bulamagi and Nambale sub counties in Iganga, and Nabwigulu and Bugulumbya sub-counties in Kamuli). In each sub-county, two parishes were selected. So, in total two districts, four sub-counties and eight parishes was selected.

In both districts, Bunduguza and Kipapali were noted as the major market preferred varieties. Bunduguza has two versions: Bunduguza new and Bunduguza old. Vine multipliers provided reasons for the name Bunduguza, which refers to the numerous roots it produces. Both Bunduguza versions produce more roots, and have white/cream flesh colour but the root skin colour is different, reddish purple and cream, respectively. Apart from the impressive numerous root formation, the variety has high dry matter, and contributes to the best

Mugoyo food. Its roots are tasty ("*Awoma*"), referring to sweetness. Regarding Kipapali, it means "The pawpaw" as it has a similar flesh colour, i.e. medium orange. Kipapali appears very similar to the released Tanzania variety (local name: *Soroti*); Bunduguza appears to have similar traits to Dimbuka Bukulula and NAROSPOT 1.

Samples of the market preferred varieties in Tanzania and Uganda have been taken for characterization, clean up, and conservation. Analysis of the survey data is ongoing for Tanzania and Uganda and more information on varietal preferences, seed distribution and marketing chains will be available by end of December 2020.

Output 4.1.2: Validated seed requirement estimates for national and target geographical areas Pls: Srini Rajendran, Margaret McEwan..

The effective demand is defined as the level of demand that *represents a real intention to purchase by people with the means to pay.* The seed requirement estimate tool is designed to determine effective demand based on a series of assumptions such as: adoption rate of improved varieties, area under improved varieties, seed replacement rate, proportion of purchased seed, seeding rate, multiplication rate, number of harvests, seasons and post-harvest losses. The tool provides estimates based on the recommended seed production method, i.e. rapid multiplication technologies using short cuttings and close spacing in seed beds.

The seed requirement has been estimated for the selected target areas in Tanzania (i.e., Bukombe district (Geita region) and Butiama district (Mara region)). For 2020, the requirement at the QDS production level is 1.1 million 30 cm cuttings; increasing to 3.7 million 30 cm cuttings by 2022. Working up the seed production chain this implies a requirement of only 114 tissue culture (TC) plantlets needed to multiply pre-basic and basic seeds. This limited use of TC plantlests should lead to a reduction in the cost of EGS materials, so that seed multipliers, and ultimately seed users can access improved planting materials at a lower price. (See **Annex 51**)

Each year the assumptions underlying the seed requirement estimate will be refined through expert elicitation from key informants, to reduce market surplus for individual seed enterprises and the whole distribution channel. Finally, the tool helps in validating the delivery pathway through tracing seed movement and understanding seed markets and segmentation of the market for preferred variety(s).

The seed requirement at national level has been estimated for Uganda, and the next step is to prepare the estimate for the target areas.

Output 4.1.3: Agreed production plans for each stage in seed value chain. Pls: Srini Rajendran, Margaret McEwan.

This output will be addressed in the first six months of year 2. Production plans will be developed on the basis of seed delivery plans, using data from rapid seed systems assessments. The *seed delivery plan* considers the pathway through the distribution channel whereby affordable quality seed of market preferred variety(s) can move smoothly from EGS producers to commercial seed producers to root producers on time. The seed delivery plan will be developed based on an understanding of: the sweetpotato seed market, the seed sourcing preferences and behaviour of different types of farmers, how seed flows from one actor to the next and the social-biophyscial and institutional challenges and conditions associated with the multiplication and delivery of planting materials in the target areas.

The production plan includes a seed multiplication calendar to schedule inputs and activities to meet production targets for the estimated effective demand of quality seed of market preferred seed variety(s). The production plan and multiplication calendar need to be defined for each linked seed enterprise, and communicated so that the quantities and timing are known to all actors in the distribution channel. The seed delivery and production plans will be validated each year by comparing the estimated seed requirements with actual seed sales.

Output 4.1.4: Assessed efficiency of business models to improve the performance of the sweetpotato seed system and to provide market preferred varieties to male and female root producers. Psl: Srini Rajendran, Margaret McEwan.

The first step towards this output has been completed with data collection on the marketing efficiency of the existing seed distribution channels in the target areas. Under output 4.3.1. candidate business models to improve the performance of the sweetpotato seed system will be identified based on a literature review of potential models and data from the rapid seed assessment. As the intervention is implemented the efficiency (financial viability) of the selected business models will be assessed. The study protocol is in **Annex 50**.

Intermediate Outcome 4.1 - Work planned for next period and COVID-19 implications

Reports on the two rapid seed assessments will be prepared and will provide inputs into refining field activities. Seed requirements will be estimated for the target areas and production plans for each stage in seed value chain will be developed with stakeholders.

Intermediate outcome 4.2: Established self-sustaining regional sweetpotato seed producer associations by capacitated commercial seed producers in target areas by 2022

Output 4.2.1: Commercial formal and informal seed producers capacitated with entrepreneurial skills to deliver seed of market preferred varieties to male and female root producers in target geographical areas by 2022 PIs: Srini Rajendran, Kwame Ogero, Margaret McEwan.

This output will be addressed based on the findings of the rapid seed system assessments. In the interim in order to better understand appropriate functions and structure of proposed seed producer associations, a study was designed and conducted to learn from experiences of seed associations for other commodities. A checklist was developed and Key Informant Interviews (KII) conducted by telephone with existing seed producer associations in Uganda to review their functions, structure, operations successes and challenges to inform future support for sweetpotato seed producer associations in the target areas of existing seed producers associations. The study questionnaire is in **Annex 52.**

12 different types of seed producer associations have been interviewed in Uganda to date[5]. These covered either multiple or single crops, including: sweetpotato, beans, groundnuts, cassava, soyabeans, green grams, cowpeas, potato, climbing beans, sugarcane, and banana. Initial analysis identified the following opportunities and challenges:

- Seed producers association are largely community based organisation (CBOs). Seed production and selling exist and members practice joint marketing of seed which enhances the bargaining power. Some, (in particular where women are a majority) start as "merry-go-round" savings schemes to enhance household incomes. The associations are registered as community based organisation in their respective areas of operation, and operate **savings accounts** to maintain their finances. Individual sweetpotato seed associations steered by HarvestPlus have amalgamated to form regional seed associations such as Eastern Sweetpotato Seed multipliers association (EUSEMO).
- There are linkages through which associations access starter material. Inspection and certification of seed is being piloted by MAAIF supplemented by internal association monitoring systems.
- The associations **do not decide on choice of varieties** to be commercialised. The choice is mainly driven by supporting NGOs and projects
- Seed production is a specialised business which requires sizeable access to land **– gender and youth implications**. Seed enterprises seems to be a viable business and hence men dominate the business
- Apart from sugarcane and potato seed associations, the majority are dealing in **more than one crop**. Whereas diversity may enhance incomes, there needs to be **wider range of skills** to ensure technical competency in seed production.
- Key buyers are institutions indirectly supporting by linking to markets or directly buying. Possibly because associations have limited decision on choice of varieties and what is being promoted **is less liked in the catchment community.**
- **Limited systematic record keeping** and having systematic customer database.

The study report is in preparation. Findings will help to identify self-financing business models to ensure sustainability of these associations.

The net profit of sweetpotato seed producer association member and non-members (registered and non-registered) will be estimated from the data collected through KII. We assume that those who are members of sweetpotato seed producers' association will have better access to market information, quality seed and extension support for good agricultural practice which will increase their net profit as compared to seed producers who are not member of the association.

One of the major activities for the association is to encourage members of the association to register with the seed regulatory body for timely inspections. The net profit will be estimated for seed producers who are members of the association and registered with regulatory body and will be compared with non-members and non-registered members. Quality seed producers should be able to attract larger markets with the support from seed producers' association and to sell at a more attractive price to end-users compared to seed producers who are not able to produce high quality seed and have lower market access.

In future, a self-financing business model will be identified and implemented for the associations.

[5] The initial analysis will determine whether further interviews are required.

Output 4.2.2: Association business plans and self-financing models developed by 2022; and Output 4.2.3: Validated technical and marketing innovations for seed production through challenge fund awards targeted to innovative entrepreneurs by 2022. PIs: Srini Rajendran, Kwame Ogero, Margaret McEwan.

Activities for the above outputs will start in year 2. The draft template to capture cost data for recurrent costs for the association is attached in **Annex 53**.

Output 4.2.4: Identified and assessed options for self-financing information communication technology (ICT) platform for improving communication and coordination of seed value chain actors by 2022. PIs: Srini Rajendran, Margaret McEwan.

One of the options to strengthen linkages within a seed producer association, and between an association and other seed claue chain actors is to use an information and communication technology platform value chain actors. In collaboration with HarvestPlus a systematic review to map out existing digital platforms for agriculture in Uganda, Tanzania and Kenya is underway. The study focuses on: how digital platforms strengthen food value chains and provide better income to various value chain actors who are connected with the platform; and the types of self-financing business models that support this. We have had initial inputs from Agri Experience Nairobi, Kenya. The report is expected early 2021.

Intermediate Outcome 4.2 - Work planned for next period and COVID-19 implications:

Findings of the study of existing seed producer associations will be used to identify areas for capacity strengthening and potential self-financing business models for the association. An agri-business consultant will work with identified commercial seed producers training in business skills, and mentoring existing (Uganda) or new (Tanzania) sweetpotato seed producer association. New modalities of training will be considered (e.g. use of e-learning platforms).

Intermediate outcome 4.3: Validated NARI-led sustainable Early Generation Seed (EGS) business models linked to seed producer associations by stakeholders in target geographies by 2022

Output 4.3.1: Strengthened NARI-led EGS business partnerships for consistent supply of quality seed of market-preferred varieties by 2022 PI: Srini Rajendran, Kwame Ogero, Sam Namanda, Margaret McEwan.

Business partnership models are required to contribute to overcoming the threats faced by the public sector running EGS businesses e.g. limited funding from external sources and marketing constraints. Potential partnership models will be identified and developed between NARIs, private sector seed companies (e.g. Tissue Culture Laboratories) and sweetpotato seed producers' associations. This will be done using a systematic process to better understand the common interest between public and private sectors in the target geographies. This will lead to the identification of revenue models that can generate benefits for all partners. The business models will be validated using a modified Sustainable Early Generation Seed Bussiness Tool (SEGSBAT) to measure the financial performance of the EGS partnership.

Methodology to be adopted for developing an business partnership models

- IFPRI's methodology for building public-private partnership (PPP) by Hartwich et al. 2008
- Seven Building Blocks of Mature Seed Systems developed by Context Global Development (https://www.agrilinks.org/post/introducing-seven-building-blocks-mature-seed-systems)

The detailed explanation is provided in **Annex 54**

Output 4.3.2: Best practice standard operating proecedures for seed production and quality management implemented by early generation seed producers PIs: Srini Rajendran, Kwame Ogero, Sam Namanda

Two draft standard operating procedures (SOPs) were developed for seed production in open nurseries and screenhouses. These have drawn on best practices by North Carolina State University and Louisiana State University in addition to the experience of 11 NARIs involved in early generation seed production.The SOPs have been reviewed internally within CIP. The next step is to share with NARI partners for further review and inputs. The SOPs for open nurseries will be used in establishing demo plots among farmers to demonstrate best agronomic practices for quality seed production. This is scheduled for October-November 2020.

Intermediate Outcome 4.3 - Work planned for next period and COVID-19 implications:

Potential EGS business models will be identified and step wise process followed to establish them.

Intermediate outcome 4.4: Adopted recommendations on management of seed degeneration by commercial seed producers, germplasm managers and regulatory bodies in Tanzania and Uganda by 2022

Output 4.4.1: Accelerated clean-up of pre-release varieties for NaCRRI and TARI, for timely multiplication by commercial seed producers by 2022. PIs: Margaret McEwan, Jan Kreuze.

Two Tanzania farmer-preferred varieties (Ukimwi and Pisi Tatu) and 8 recently released OFSP varieties were sent to KEPHIS for virus cleaning.These have been established in the greenhouse waiting to be introduced in the lab for virus cleaning procedure. The breeding programme in Mozambique has also sent materials for clean-up. Breeding accessions for conservation have been received from Mozambique, and are expected from Ghana for the West Africa breeding programme. NextGen virus Diagnostic course planned in March was canceled due to COVID-19 restrictions. Only one SweetGAINS staff has been able to return to work at CIP HQ since September and currently videos are being developed to perform remote training as in person training will unlikely take place until July 2021 earliest. SOPs were developed for sRSA and Data Management and Bioinformatics and are pending final review.

Output 4.4.2: Assessed seed-degeneration related productivity decline across the seed supply chain – by 2021. **PIs: Jan Kreuze, Margaret McEwan.**

To understand the rate at which clean planting material degenerates under different agroecologies, we are conducting a long-term study comparing performance of virus-tested and farmer-sourced planting material of two varieties in two agroecologies (unimodal and bimodal) in the Lake Zone, Tanzania. The study which is now in the fourth season will help inform variety replacement strategies. Preliminary results have shown differences in yield and rate of virus infection between the two sites and cultivars (Ejumula and Kabode). Ejumula variety sourced from farmers was 90% infected by the second season at the two sites. This increased to 100% by the third season. However, the effect on root yields was lower in Bunda district compared to Geita. The fifth and final season will be planted in October 2020. Data analysis on root yields for the first four seasons is ongoing and virus testing of leaf samples from the first two seasons was completed within the current reporting period.

Data analyses on the effectiveness of isolation distances in controlling sweetpotato virus disease was completed. There was a significant interaction between the sites of plots, SPVD incidence, and isolation distances on the total root yield ($F(3,148) = 3.8211.6$, $p = 0.030$). Total SPVD incidence at Iligamba was 13.3%, while at Kahunda it was 6.7%. SPVD incidence per plot varied across the sites with highest incidence being recorded at 10 m isolation distance in Iligamba and 5 m isolation distance in Kahunda. The findings re-affirm the importance of considering external sources of virus inoculum when implementing isolation distances in sweetpotato seed production. The strictness of SPVD management may vary depending on prevailing agroecological conditions.

Lastly, four generations of an experiment focusing on different aspects of crop physiology on planting material established in protected and open nurseries were completed. The experiment is in the final generation and focuses on other factors influencing seed quality other than viruses e.g. ratooning.

In collaboration with IITA and the ISSD Africa project a new module, Sweetpotato Seed Tracker (SST) for registration and certification of sweetpotato seed has been developed and added to the (cassava) Seed Tracker (ST) platform. It includes two forms: (i) a seed production registration form: This form is meant for seed producers to capture details of producer, location of seed production (with auto GPS information extraction, if device is enabled), source of seed, varieties grown, area of production and expected yield (**Annex 55**); and (ii) Seed inspection form (F-IV): this form is for seed certifiers captures basic information from F-II (**Annex 56**). This form is embedded with features to capture three stages of inspection: (i) pre-planting (site inspection and seed source), (ii) during crop stage (parameters for crop quality assessment during section seed certification, including diseases, off-types, isolation distance) and (iii) harvest (pest and disease, stem quality, stem quantity, certification tags and barcodes for easy tracking). All the seed tracking forms were developed to operate on-line (with live internet), off-line (data collection for auto uploading of information when device is contacted to internet) and enables auto e-mail and SMS messaging to next level user to stimulate follow-up action. Information collected is automatically collated in ST database and also generates raw data summary downloadable in MS Excel, CSV, Google Sheet, SAV, KML and ZIP folder format. GPS data enables preparation of maps indicating location of fields. User registration and log-in controls were incorporated for privacy and data security. Functional testing of the program for data collection and exchange of data between the data collection devices [smartphone (Android and IOS), tablet, laptop, and desktop) and central server is completed using internet enabled devices was completed and the program is ready for piloting in Tanzania. Discussions are ongoing with Tanzania Official Seed Certification Institute (TOSCI) for joint implementation of the SST with the Cassava Seed Tracker (CST). The SST app has been customized to meet existing sweetpotato seed certification standards for seed production. These features can be modified with changing circumstances to keep the program up to date and relevant.

Output 4.4.3: Regional germplasm management services provide access to preferred varieties by public, NGO and private sector customers by 2021. PIs: Jan Kreuze, Margaret McEwan.

The online germplasm cleanup and distribution tracking system is being finalized (Annex 57). The online system allows the registration of germplasm being sent in for cleanup and tracking of the cleanup process. Customers sending in their germplasm will be able to follow the cleanup progress online. Similarly, customers will be able to place germplasm orders via the online system and track the order status till completion. The system will be accessed via a computer with an internet connection at the germplasm station, and through a tablet connected to the internet using a GSM SIM card. The tablet will be useful in updating cleanup processes while inside tissue culture growth rooms or screenhouses. Additionally, the online system will be linked to the online sweetpotato catalogue to allow people to place orders of germplasm listed on the catalogue. Once completed, the system will automatically provide reports on the number of clones received for cleanup by country and breeder; number of germplasm cleaned up by country; number of germplasm orders received; number of germplasm orders fulfilled; germplasm cleanup turnaround time; germplasm order turnaround time; most popular germplasm ordered from the online sweetpotato catalogue; number of clones of land races received and conserved and the number of breeding accessions received for conservation. Automatic email alerts are generated by the system during the ordering system, including invoicing, and these are shared to both the person ordering germplasm and the team processing the germplasm orders.. The prototype has been demonstrated to the seed systems team and a section of the breeders, and comments incorporated into the database after each meeting.

Output 4.4.4: Improved recommendations for use of LAMP diagnostic tools in seed regulatory system in at least 1 country by 2021 by 2022. PI: Jan Kreuze

A LAMP Genie II machine was purchased for Tanzania. Field activities were delayed by COVID 19. However, several online meetings were held to discuss the protocols with partners from IITA and TOSCI. The next step is to finalize the protocols and start field validation. Multiplexing of SPFMV, SPCSV and begomoviruses LAMP assays was tested in laboratory an found to work, whereas a bulking rate of 5 samples was set as a maximum. However field testing of these modifications has not been possible due to COVID-19 restrictions. An SOP was developed for field LAMP and is pending final review.

Output 4.4.5: Developed recommendations for changes in seed regulations (QA) for VPCs and varietal release process by 2022. PI: Margaret McEwan.

In collaboration with IITA and ISSD Africa an inventory of decentralized quality seed quality experiences is being developed to (i) identify the best model(s) for enhancing seed quality assurance (QA), such as decentralization of certification services, implementation of QA by accredited seed inspectors, e-certification and accreditation-based systems. This study uses a two-step approach for getting user feedback using an on-line survey tool, followed by in-depth consultations and interviews with representatives for each group, data synthesis and preparation of technical report and a working paper. In addition to addressing seed quality issues, it will identify seed related aspects facilitating the uptake of novel varieties coming out of breeding pipelines. An electronic survey form was developed for feedback on seed certification by the regulators and seed producers and buyers on the value of seed certification and certified seed. These online survey forms will be used in October for preliminary data collection. The draft questionnaires are in **Annex 58 and 59**

Intermediate Outcome 4.4 - Work planned for next period and COVID-19 implications:
Under the seed degeneration trials planned activities include: completing data analysis on root yields from the first four seasons, virus testing of leaf samples from the third and fourth seasons, developing communication materials for different target audiences.

The current development version of the database will be completed by December 2020. To accelerate these efforts, a data management intern will come onboard from mid-October to support system testing and data migration activities. The intern will work under the direct supervision of the SweetGAINS senior knowledge management associate and will initially be based at KEPHIS. The system will initially be deployed for use at KEPHIS in Kenya and thereafter at the other germplasm stations in Mozambique, Ghana and Uganda.

The sweetpotato Seed Tracker will be piloted with seed producers and inspectors in Tanzania.

2. Project Adjustments

For each outcome or output that is behind schedule or under target, explain what adjustments you are making to get back on track.

Adjustments and countermeasures taking have been already provided as follows: As a short summary following every Outcome, and in the case of adjustments caused by COVID-19, through Annex 1

3. Geographic Areas to Be Served

Provide the most updated list of countries and sub-regions/states that have benefitted or will benefit from this work and associated dollar amounts. If areas to be served include the United States, indicate city and state. Reflect both spent and unspent funds. Add more rows as needed. More information about Geographic Areas to Be Served can be found here.

Location	Foundation Funding (U.S.$)

4. Geographic Location of Work

Provide the most updated list of countries and sub-regions/states where this work has been or will be performed and associated dollar amounts. If location of work includes the United States, indicate city and state. Reflect both spent and unspent funds. Add more rows as needed. More information about Geographic Location of Work can be found here.

Location	Foundation Funding (U.S.$)

5. Feedback for the Foundation

Provide one to three ways the foundation has successfully enabled your work so far. Provide one to three ways the foundation can improve.

6. Global Access and Intellectual Property

If your funding agreement is subject to Intellectual Property Reporting, please click the following link to complete an Intellectual Property (IP) Report.

If not, please acknowledge by typing "N/A": _____

To delegate permissions to another member of your project team or for any questions regarding the Intellectual Property Report, please contact GlobalAccess@gatesfoundation.org.

7. Regulated Activities

Do you represent that all Regulated Activities[1] related to your project are in compliance with all applicable safety, regulatory, ethical and legal requirements? Please mark with an "X":

_____ N/A (no Regulated Activities in project)

_____ Yes

_____ No (if no, please explain below)

Are any new Regulated Activities[1] planned which were not described in any documents previously submitted to the foundation? Please mark with an "X":

_____ No

_____ Yes (if yes, please explain below)

1 Regulated Activities include but are not limited to: clinical trials; research involving human subjects; provision of diagnostic, prophylactic, medical or health services; experimental medicine; the use of human tissue, animals, radioactive isotopes, pathogenic organisms, genetically modified organisms, recombinant nucleic acids, Select Agents or Toxins (www.selectagents.gov), Dual Use technology (http://export.gov/regulation/eg_main_018229.asp), or any substance, organism, or material that is toxic or hazardous; as well as the approvals, records, data, specimens, and materials related to any of the forgoing.

Financial Update

The purpose of this section is to help the foundation understand how programmatic performance affects actual and projected expenditures over the life of the investment.

Feel free to reach out to your foundation contact for support with these progress reporting requirements.

Note: Budget template and financial narrative instructions can be found here. If you are using an older version of the budget template, this information could be in a different location in your template.

1. Latest Period Variance:

"Latest period variance" compares expenditures that occurred in the reporting period against the most recent forecast. See "Financial Summary & Reporting" sheet in the foundation budget template for calculated variance (for example, column AD, starting on row 29 for period 1). Note that the allowable variance is defined in your grant agreement.

Latest Period Variance:

1. Did the project spend more-or-less than anticipated in comparison to the most recent forecast? Please explain the primary drivers and their causes of the overall variance for the latest period (for example – programmatic changes, delays in recruitment).

1. Please provide a detailed explanation for any expense category in which the variance was greater than 10%. This should include an explanation of programmatic decisions affecting expenditure amounts and/or how actual costs differed from prior assumptions.

1. Future Period Projections:

"Future period projections" includes forecast by expense category and any additional dimensions for the future remaining reporting periods.

When populating your projections, please provide realistic projections that take into account the latest plan of expected activities and up-to-date associated costs. For example, projections usually will not simply carry forward previously unspent budget amounts into the next period or exactly match the original period budget. However, in total, the projections should match the total budget amount.

Future Period Projections:

1. Explain how your future projections for the remaining periods compare to your previous forecast. Consider how the project's performance to date influences your forecast. In your response, please address the following:

    a. Any shifts (+/-10%) between expense categories, additional dimensions (if applicable), including the trade-offs and implications.
    a. Have these shifts to forecast been discussed with your BMGF Program Officer? Was there a decision/approval?
    b. Where your expected rate of spending has significantly increased/decreased, what is driving this difference?
    c. What are the key assumptions behind the forecast (e.g. scale of activities, hiring delays, timeline changes)?
    d. How have changes to your investment results framework affected your future period projections?

3. Sub-awards (if applicable)

This sub-award section provides visibility to an often critical component of the grant spending where the budget template provides limited insight. The total of actual disbursements for this reporting period should equal the actual sub-award expenses reported on the "Financial Summary & Reporting" sheet in the budget template for this reporting period.

Use the table below to provide the detail of all sub-grantee(s) or subcontractor(s).

Organization Name	Actual Disbursement for this Reporting Period (U.S.$)	Total Disbursed from Primary Awardee to Sub to Date (U.S.$)	Total Sub-Awardee Spent to Date (U.S.$)	Total Contracted Amount (U.S.$)
	$	$	$	$
	$	$	$	$
	$	$	$	$
Total (ties to budget file(s))	$	$	$	$

For sub-awards greater than $1M, please provide explanatory detail as requested in the latest and future period sections above.

Note: It is the foundation's discretion to ask for updated sub-award budget files as part of the traditional progress report review process.

4. Other Sources of Support (if applicable):

Other Sources of Support include interest earned, current foreign exchange impacts, and co-funding (in-kind and other contributions).

Other Sources of Support (if applicable): Explain any notable impacts from other sources of support.

5. Financial Progress Summary Assessment

This section will help the foundation determine whether changes are needed to the payment schedule.

Note: This assessment does not guarantee that the previously agreed to payment schedule will change.

Financial Progress Summary Assessment:

Based on the financial progress update provided, summarize your assessment of remaining financial payment needs and current payment requested to support your work. Please consider the following in your response:

- Cash on hand as of the end of the reporting period as compared to the future period projection(s).
- Financial and programmatic performance, and any potential changes proposed to the forecast through the remaining periods.

Checklist - As you review your answers to questions in the financial update section, ensure that your report provides the following:

1. Explanation of how project expenditures differed from plan and the implications on programmatic progress to date.
1. Realistic future period projections based on updated plans, results tracker and future cost expectations.
2. Explanation of how future period projections differ from the original budget and previous forecasts, and the implications.
3. Explanation of other sources of support (funds) from other funders, interest earned or converting to non-USD currencies.
4. Explanation of future financial payment needs based on the project's anticipated financial needs and cash on hand.

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For Foundation Staff to Complete

Analysis (required if contingent payment or PO assessment differs from grantee/vendor assessment)

Progress Analysis

Include analysis of significant project variances and key learnings that may inform portfolio discussions for progress against the strategic goals.

Budget and Financial Analysis

Include analysis of unexpended funds or over expenditures. Refer to the Unexpended Grant Funds Policy for options available when recommending how to handle unexpended grant funds, or reach out to your primary contact in GCM.

Scheduled Payment Amount	$
Carryover Amount	$
Recommended Payment Amount	$

Approver Comments (if applicable)

Name	Title	Date

Comments