BILL & MELINDA GATES foundation

Grant Proposal Narrative

We appreciate your interest in submitting a proposal to the Bill & Melinda Gates Foundation and we thank you for working with us throughout the proposal process. Your designated foundation contact will continue to work collaboratively with you as you prepare your proposal to help you understand the connection between the foundation's relevant program strategy and the proposed project, as well as to respond to any questions you might have over the course of this process. You are encouraged to communicate with your program officer to make sure that your efforts are aligned with the proposal requirements and that you are not expending unnecessary time or energy in this process.

Answer all of the questions in this Proposal Narrative template and submit it to your foundation program officer for review and collaborative discussion. Due to tax, legal, and reporting requirements, all proposals must be submitted in English. The proposal must be submitted in Word, as PDFs will not be accepted.

This is a proposal shaping document and not a commitment by the foundation to fund the work.

Proposal Details

The Foundation is prohibited from conducting or funding any lobbying or political campaign activities, as these terms are specifically defined under U.S. tax law. Unlike many of our grantees/vendors who may engage in limited lobbying, the Foundation cannot lobby or fund any lobbying activities carried out by its grantees/vendors. We request that you please review the information at the following link: Foundation Funds and Advocacy, to assess whether any of your proposed activities may constitute lobbying as defined by the IRS. If so, you should revise your proposal accordingly prior to submission.

1. Executive Summary

Provide a brief summary of the investment.

The Next Generation Cassava Breeding project (NextGen Cassava) seeks to modernize partner cassava breeding institutions in Africa and use cutting-edge tools for efficient delivery of improved varieties of cassava. An investment in NextGen Cassava will lead to a holistic optimization of cassava improvement programs among partners in Africa and sustainably accelerate the rates of genetic gain in cassava. The ultimate beneficiaries of this project are the cassava farmers of sub-Saharan Africa, who will receive improved varieties that increase fresh root yields, are more resilient to devastating virus diseases, and exhibit other traits preferred by smallholder farmers.

The NextGen Cassava project initially focused on improving cassava using genomic predictions. In Phase I, we were able to shorten breeding cycles, improve data collection and management, increase germplasm exchange, improve physical infrastructures of programs, and increase the number and capacity of cassava breeders in partner African breeding programs. Building on these successes, Phase II entails a shift toward implementation for the delivery of improved varieties to smallholder farmers. We will expand resources for applied breeding to obtain higher quality data and maximize our ability to improve varieties. We will initiate greater communication to multiple audiences, from smallholder farmers, to other African breeding programs, to other cassava research centers. We will consolidate research efforts to directly serve breeders and ensure quality control at all process steps. We will identify traits preferred by farmers and end-users, to ensure that breeding is demand-driven and inclusive. We believe these steps will accelerate not just genetic gain but *adopted* genetic gain, increase the yields and resilience of cassava production by smallholder farmers, and incrementally move African cassava breeding toward greater capacity. Building excellence in breeding programs contributes to the success of genomics-assisted cassava breeding and its importance cannot be overemphasized.

Our NextGen teams are composed of breeders, geneticists, data analysts, computer programmers, food technologists, social scientists and crop protectionists, who will work together in a coordinated and collaborative manner, leveraging germplasm, genotypic and phenotypic data from one another. We will also reach out to five other cassava breeding programs in Ghana, Rwanda, Mozambique, Sierra Leone and DR Congo for broader adoption of new breeding technologies and optimization of systems that will deliver better varieties for cassava farmers in sub-Saharan Africa.

This project will facilitate:

1. A model cassava breeding organization coordinating four programs to exemplify effective improvement through optimal breeding schemes, research integration, demand-led breeding goal identification, and sound organizational structure.

2. Successful outreach to national breeding programs throughout the sub-Saharan region enabling them to envision and take steps toward similar effective breeding organization.

3. The release of improved cassava varieties in each breeding program's region that meet criteria for quality acceptability and sustainably improve smallholder farmer livelihoods due to improved yield and disease resistance.

4. Sustainable means for the identification and quantification of cassava breeding goals based on survey and adoption evidence from smallholder farmers.

5. The improvement and diversification of cassava breeding program populations to ensure a solid foundation for future genetic gains, and greater understanding of the genetic architecture of traits to increase the efficiency of those gains.

Describe the charitable purpose of this work by completing the statement "This grant will be used [to …]." Please limit to one sentence, begin with "to" and do not include a period at the end. Example: "This grant will be used [to fund new schools and assist other organizations in the design of new schools]"

To develop a sustainable cassava breeding scheme with accelerated genetic gains, leading to the release of improved cassava cultivars that meet the agronomic and end-user needs of smallholder farmers in Africa

2. Problem Statement

Describe the problem, why it is a problem, and who is impacted by the problem. What specific elements of the problem is this investment trying to address?

Cassava is an important staple crop for about 500 million Africans who consume it daily. Cassava farmers in sub-Saharan Africa (SSA) produce about half of the global output and are faced with numerous problems including the impact of devastating virus diseases, low productivity, low nutritional value and poor access to improved seed. Additionally, cassava breeding is uniquely difficult in that it usually takes close to ten years before a new variety translates from a breeding nursery to farmers' fields. This limits the rate of variety improvement and breeders' ability to respond to new challenges. Cassava breeding in the past has primarily been driven by product development as defined by the breeder, and has been insufficiently inclusive of gender perspectives in the selection process.

In Phase I, we focused on obstacles to accelerated cassava breeding, testing prediction models to shorten the breeding cycle through genotype-based selection, improved flowering and seed set, enabling greater germplasm exchange, assessing gender roles in cassava breeding and improving information sharing. In Phase II, we will build on the successes of Phase I, going beyond testing the workings of genomic selection (GS). We will raise NextGen Cassava's impact levels by delivering improved cassava varieties to smallholder farmers for adoption. These varieties will have durable resistance to disease, higher productivity, higher nutritional value, and end-user preferred product-specific qualities. We will also effect a strategic and holistic optimization of partner breeding programs to accelerate the rate of delivery of these improved varieties to smallholders.

3. Scope and Approach

Describe the scope and approach of the proposed work. This should be a narrative description of the principal results the investment would achieve and how those results relate to the problem described above (rather than a list of outcomes and outputs.) Note: You will provide a list of outcomes and outputs in the Results Framework.

Overview

In its proposed Phase II, the NextGen Cassava project will continue its Phase I work of developing and using technologies to help accelerate genetic gains in cassava breeding programs in Africa**.** The application of these technologies in cassava breeding will improve agronomic performance, disease-resistance and nutritional value. In Phase II, NextGen Cassava will expand its reach to develop and contribute to the accelerated release of these improved cassava cultivars that will be adopted by smallholder farmers in partner countries.

NextGen Cassava received a set of valuable contributions from the mid-term review panel in February 2016. The reviewers found that our genomic-assisted breeding strategies adopted by the project partners were working well as part of an integrated cassava breeding program. However, they recommended that we go beyond testing the workings of GS and raise the impact levels by releasing best-bet cassava varieties to smallholder farmers. In Phase II, rather than organize NextGen Cassava into very typical discrete research-type objectives to be accomplished and declared done, we propose to restructure the project into three functional divisions as needed to deliver improved varieties continuously going forward. The three functions of Breeding, Survey, and Research map onto these three divisions. We will make deliberate efforts to ensure that these divisions cooperate and coordinate with each other, so as to best achieve the common goal of delivering genetic gains in cassava farmers' fields.

Breeding Division

The Breeding Division will serve as the fulcrum of the project, and bears a significant share of the work and resources. This division implements breeding pipelines at four breeding programs in Africa: the National Root Crops Research Institute (NRCRI), Umudike, Nigeria; the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria (with additional support from IITA/Uganda); the National Crops Resources Research Institute (NaCRRI), Namulonge, Uganda; and the Tanzanian Agricultural Research Institute (TARI),

Ukiriguru, Tanzania. These programs work on improving cassava populations and breeding pipelines and extensively test improved clones for variety release. Two other breeding programs in South America, the International Center for Tropical Agriculture (CIAT) and the Brazilian Agricultural Research Corporation (Embrapa), will carry out pre-breeding for traits relevant to Africa and aid in germplasm acquisition. Other centers such as the USDA-ARS Pacific West and the University of Hawaii at Hilo will play roles as centers for phytosanitary certification and as international nurseries for cassava germplasm transfer (disease-safe havens) for African breeding programs. Cornell University, the West African Center for Crop Improvement (WACCI) at the University of Ghana, and Makerere University, Uganda will all play roles in capacity building in plant breeding education (see Appendix 3 for more information).

Additionally, following the great successes we have recorded in the project in the pilot countries of Uganda, Nigeria and Tanzania, we seek to build a community of practice partnership (COPP) for the application of genomics-assisted cassava breeding across African cassava breeding programs. We have identified target breeding programs in Ghana, Rwanda, Malawi, Mozambique, Sierra Leone, Zambia and DR Congo. These cassava breeding teams will benefit from the genomic predictions that we have already developed for African cassava germplasm (varieties they also share), use of Cassavabase, and capacity for improved phenotyping, all of which will lead to better breeding decisions and improved livelihoods for African cassava farmers.

Survey Division

Cassava is widely grown and utilized in different agro-ecological zones across many African countries. Breeding targets for Nigeria, Uganda, Tanzania and the rest of Africa are influenced by general acceptability of varieties and by traits that have regional importance. To a large extent, many of these traits overlap across borders. In order to continue to breed for targeted preferences, breeders at IITA, NRCRI, NaCRRI, and TARI will continue to refine breeding targets guided by outcomes of scoping for product profiles and ideotypes. Attainment of these desired breeding targets will require that four fundamental issues are well understood and sorted: 1) target groups and their environment, 2) production systems, 3) cassava seed management, and 4) re-learn the drivers of men, women and youth cassava needs and/or preferences; of interest too will be how long varieties take before being absolute. The Survey Division is critical for understanding these issues. In this regard, the Survey Division is like the marketing arm of a private seed company. In Phase II, we will devote proportional resources to this key function. This division will translate RTBFOODS research, and conduct additional research to identify traits preferred by farmers for selected product quality to ensure that NextGen breeding is demand-driven and inclusive. Working with the Communications and Advocacy team, the Survey Division will ensure that smallholder farmers are aware of the opportunities created by NextGen Cassava. This is expected to build a two-way relationship among smallholders and the breeding programs and also be a conduit for data capture and dissemination.

Research Division

The Research and Breeding Divisions partner to improve NextGen's ability to deliver high-valued varieties rapidly and efficiently by developing and implementing technological advances. Breeders come to the Research Division with technology and research questions to be addressed. The Research Division also proposes new technologies breeders might not have considered. Thus, breeders are key members of the Research Division in addition to personnel at BTI, Cornell, USDA-ARS, Makerere University, CIAT, and Embrapa. The Research Division deliverables make their impact when they are deployed by the breeders. The scope of work outlined in the Research Division includes: flowering and seed set, breeding scheme optimization, Cassavabase development, genomic prediction and decision analysis support, and bioinformatics for improving prediction accuracies.

Communications & Advocacy

The Communications & Advocacy team's scope for Phase II will include internal and external communications, as well as technology outreach, and training and information sharing to ensure that farmers, researchers and other stakeholders will be able to derive all benefits from the progress made in the NextGen project. A central focus will be to help ensure that each of the divisions are integrated through regular, deliberate and continuous interactions, as each deliverable entails collaboration with other divisions; we will promote this through redesign of central project websites, and implementation and promotion of multimedia that will lead to mutual awareness and accountability by all team members. We hope to achieve better understanding and accelerated adoption of improved cassava varieties and associated technologies, promote a positive policy and donor environment to support adoption of improved cassava varieties in SSA, and support a collaborative COPP among project partners. Other activities will aim to increase awareness of the NextGen project, with messaging about the potential of genomics research in increasing genetic gains in cassava, the crop's role in ensuring food security in Africa, its climate resilience, and the need to secure ongoing funding for this important SSA food security crop. We will help the public understand the value and importance of public investment in cassava improvement, because we risk losing public investments in agriculture research in the current political environments in the UK and the US, especially if the public does not understand where the support comes from and why it is important.

Project Management

The project will continue to be administered and managed by the Project Management Unit (PMU) of the Office of International Programs in the College of Agriculture and Life Sciences (IP-CALS) at Cornell University. IP-CALS has the advantage of connecting the scientists at Cornell University and other global centers of excellence with developing country scientists. In addition, IP-CALS has been coordinating and managing large global projects such as the Delivering Genetic Gains in Wheat project (also funded by DFID and BMGF) and a few others. IP-CALS' long and successful donor-funded project experience includes timely execution of all subcontracts and satisfaction of all DFID and BMGF reporting requirements. The Director of IP-CALS, Ronnie Coffman, will serve as the Principal Investigator of the project and will supervise the coordinating staff based in IP-CALS. Chiedozie Egesi will continue with the

management of the project and will coordinate the various project teams. Chiedozie will provide oversight of the entire project implementation, while a project support specialist will serve as an administrator and intermediary between the project manager and designated in-house project quality-control task monitors for the field and laboratory, breeding program leads, and project division coordinators. At the request of the Foundation, in the event that a third phase of the project is approved by the Foundation, Cornell will work closely with IITA to plan for and implement a seamless transfer of management responsibility to IITA.

The project will also hire experienced plant breeders (from the private sector as recommended by the mid-term review team) as consultants annually to support the project manager in areas of plant breeding, verification of quality system, creation of process maps and focus on quality management. The consultant will coach the breeding teams with field-to-laboratory interaction partnerships and teamwork as implemented in the private sector for effective partnerships and troubleshooting in modern plant breeding programs. However, the engagement of the consultant will depend on the gaps that may be observed since the EPAC team includes David Meyer (Dow AgroScience's leader of plant breeding in North America) and Carlos Iglesia (former cassava breeder at CIAT and lead breeding team at Syngenta). David Meyer has further linked and enlisted the support of two leads for quality management in the laboratory and field at Dow, who will be providing training to NextGen Cassava project quality control task monitors beginning with a two-week scientific visit in August 2017 of three African scientists from the breeding programs.

As needed, describe why you believe the approach would lead to the desired results. Reference related work, existing evidence from evaluations or systematic reviews, and/or relevant experience, etc.

Please see Appendix 1.

4. Risk Mitigation

As needed, describe any significant risks to the success of this project and how you plan to address them.

Breeding Division: In Phase I, the issue of quality management was identified as a risk to this project. Accordingly, we have decided to emphasize it in Phase II, by continuing to enlist the support of breeders at the Dow AgroSciences humanitarian effort "Hunger Solutions" (David Meyer) and field breeders from Syngenta (Carlos Iglesia) to guide us in refining and progressively improving our breeding processes. Moving forward, we will work together toward the creation of an overall process map, the development of standard operating procedures that will work for all breeding teams, and discuss the use of technologies for sample-tracking, optimized experimental designs and analysis to control error and maximize information on locations/years, pedigree verification, and data sharing. We will also encourage the transition of breeders, from operating as individual champions to working as part of a team with other disciplines; we hope that the COPP will further help in addressing this.

Survey Division: Experience teaches us that some varieties (e.g TMS 30572) can last over 30 years in production, while others become obsolete within a few years after official release. We thus seek to avoid releasing new varieties that do not meet the needs of the end-users, thus limiting varietal adoption. Trait preferences are usually region-specific, making it difficult for one breeding program to address all consumer needs. Also, some of these traits do not have robust phenotyping protocols, which can at times discourage breeders from evaluating and using them in selections. In its goal of identifying the varietal preferences to be targeted by the Breeding Division, the Survey Division has recognized the need to work closely with multidisciplinary teams, public-private partnerships, and a diverse range of users and stakeholders to ensure the closest possible match between the developed varieties and demand. We will adopt an inclusive approach by conducting prototype development tests and informed participatory selection mindful of target groups and environments. We will also make efforts to avoid any potential distraction (e.g. amplifying a localized need to become a national priority) that the Survey Division work might cause to the Breeding Division's focus on target traits and critical goals (such as disease resistance and yield). Timely relay of accurate and representative information from Survey Division to Breeding and/or Research Division is critical; we admit this is relatively new to us and thus will quickly learn and adjust whenever deemed necessary.

Research Division: NextGen Cassava is a product development project; thus, we have deliberately chosen research topics that we believe have a high probability of success and a short time to application (five years or less). Our most significant research risk is centered around the genotyping system, which we are currently transitioning to a system which will involve whole genome sequencing of parents and low-density genotyping of progeny. Details of the research process involved are given in the Activities section, Research Division. Should our transition fail (a prospect we view as highly unlikely), our backup method would be to use genotyping-by-sequencing (GBS), as was done in Phase I, either by obtaining a license from KeyGene or having the genotyping work done in a country where the patent is not in force. Another potential challenge will be to ensure community adoption of all aspects of the Cassavabase "digital ecosystem." We will mitigate this risk through efforts such as the SolGS Task Force to get feedback from users including COPP members. We will also be rapid and transparent in error reporting so programs can quickly identify and correct problems, hopefully by energetically adopting standard operating procedures.

Communications & Advocacy: The main risk this group will address is the smooth exchange and flow of information among project partners in the various divisions, an essential element to the success of this project. Many of the Communications & Advocacy team's activities are centered around facilitating this internal communication to ensure we are making progress by clarifying objectives, identifying shared resources and developing training materials to reduce duplication of work and increase efficiencies. With many diverse project partners around the world, a conscious and deliberate effort must be made to ensure that necessary conversations are happening, and

that information is shared continuously. The group will also communicate with external stakeholders to share information about NextGen Cassava and increase buy-in and support for the Survey and Research divisions. If the public does not understand where the support comes from and why it is important, we risk losing public investments in agriculture research in the current political environments.

Project Management: To manage budgetary issues, the administrative team will continue to work to obtain timely technical and financial reports as well as invoices from each subcontractor, and to alert them to any potential over- or under-spending. In the past, the team has been able to effectively respond to any changes or amendments to subcontracts if and when they are needed, and we will continue to improve our operations and efficiency.

5. How We'll Work Together

This question is intended to begin the dialogue on how foundation staff would work with you to achieve the intended outcomes. Topics could include minimal staff support, any specific issues that would likely need on-going discussion, regular communications, or other information to help establish mutual expectations and assist with implementing the proposed work.

The NextGen Cassava team has more than 5 years of experience working very effectively with BMGF, going back even before the Phase I start date in 2012. Flexibility to move funds according to shifting needs or priorities and to fund special initiatives not initially in the proposal conception stage will remain vital. The foundation staff has previously demonstrated good will in accommodating such requests. We will maintain the harmonious working relationship we have experienced with our program officer at the foundation.

6. Global Access and Open Access

In order to establish that the projects we fund are charitable and will have a positive impact on the intended beneficiaries of our work, the foundation requires the projects it funds be conducted and managed in a manner that ensures Global Access and Open Access.

"Global Access" is a foundation policy requiring that: (a) the knowledge and information gained from the project will be promptly and broadly disseminated; and (b) the Funded Developments will be made available and accessible at an affordable price (i) to people most in need within developing countries, or (ii) in support of the U.S. educational system and public libraries, as applicable to the project.

"Funded Developments" means the products, services, processes, technologies, materials, software, data, other innovations, and intellectual property resulting from the project, including modifications, improvements, and further developments to Background Technology.

"Background Technology" means any and all products, services, processes, technologies, materials, software, data, or other innovations, and intellectual property created by You or a third party prior to or outside of the project used as part of the project.

Additional information about Global Access (including examples and case studies) can be found at http://globalaccess.gatesfoundation.org/.

"Open Access" is a foundation policy that sets the requirements, terms and conditions for publication of Funded Developments in a peer-reviewed journal. Additional Information on the foundation's Open Access Policy for peer-reviewed publications and underlying data can be found at www.gatesfoundation.org/How-We-Work/General-Information/Open-Access-Policy. Note: the foundation will pay directly for reasonable fees to effect publication on "open access" terms; such fees should not be included in the project budget (See the Open Access Policy FAQs for further detail).

a) Knowledge and Information

Describe how the knowledge and information gained from the project will be promptly and broadly disseminated (including how you will comply with the foundation's Open Access Policy, discussed above).

NextGen Cassava is committed to supporting the Global Open Access Policy. We disseminate data in near real-time through Cassavabase, an online and world-renowned open-source data repository, where anyone can freely search and download data. We will utilize the foundation's Chronos system to ensure we publish our peer-reviewed publications as Open Access and, where appropriate, encourage our researchers to utilize the Gates Open Research Portal (announced at time of writing this proposal) for additional rapid and open dissemination. These measures will ensure that data is made available continuously throughout the program's tenure.

b) Funded Developments (Indicate "not applicable," as appropriate)

i. **Describe any Funded Developments that may ultimately result from the project, including any Background Technology that will be used or incorporated in the proposed project. If applicable, briefly explain how the Funded Developments will be made available and accessible at an affordable price to the intended beneficiaries. The use of commonly-available, off-the-shelf products (such as Microsoft Excel, Adobe, etc.) need not be disclosed.**

The most important funded development from NextGen Cassava are new cassava varieties. We will seek to disseminate these varieties through seed systems available in partner countries and through on-farm participatory trials. We will not patent the varieties as intellectual property.

NextGen Cassava will continue to develop Cassavabase. Cassavabase is open source, with the code being available at https://github.com/solgenomics. Cassavabase is distributed under the MIT License which is permissive: third parties can use the code in whatever way they want as long as they provide attribution back to Cassavabase and they do not hold it liable.

NextGen Cassava will participate in the development of the plant breeding application program interface (BrAPI). The Breeding API specifies a standard interface for plant phenotype/genotype databases to serve their data to crop breeding applications. It is a shared, open API, to be used by all data providers and data consumers who wish to participate. The development of BrAPI has been driven by a community of researchers and computer scientists from various research institutions. While we do no not know if BrAPI is protected by some kind of license, because it is a standard, the more it is open, the more useful it becomes.

NextGen Cassava will continue to develop the Breeding Scheme Language (BSL) for simulation and optimization. The BSL constitutes an R package that is open source and available on github. It is made free by a GNU General Public License v3.0, which is a “copyleft” license that ensures that all modifications of the BSL must also be freely available.

NextGen Cassava will collaborate in the development of the mobile device phenotyping support tool, PhenoApps. PhenoApps is an existing Background Technology developed by Dr. Jesse Poland at Kansas State University. It is under ongoing development. Source code for PhenoApps is also available under the MIT license.

A number of cassava breeding methods will emerge from NextGen Cassava research. These methods will include breeding schemes, flower induction and seed abortion avoidance methods, as well as genomics-based methods for deleterious allele identification and prioritization in selection. We will not seek to protect any of these methods as intellectual property.

ii. **Please confirm that you will make the Funded Developments – including any Background Technology incorporated into or required to use the Funded Developments – available to achieve the proposed project’s goals and Global Access. If you foresee any obstacles to achieving Global Access (e.g., third party rights, broad access, time frame, affordability) please briefly summarize the obstacles and the specific steps that you will take to address them.**

We confirm that we will make all Funded Developments available in accordance with the Gates Global Access policy.

c) **If one or more of the following applies, please click the following link to complete an Intellectual Property (IP) Report:**

- Creation of Funded Developments will likely involve new IP rights (Note: copyrights in works intended to be published in accordance with the Open Access Policy need not be disclosed);
- Use of Background Technology requires access to existing IP rights; or
- For-Profit entities are engaged in the project.

Note: For login purposes, please use the email address to which this Proposal Narrative was sent. To delegate permissions to another member of your project team, or for any questions regarding the IP Report, please contact GlobalAccess@gatesfoundation.org.

7. Advocacy and Lobbying

US law prohibits foundation funds from being earmarked to support direct or grassroots lobbying communications. Describe how you will conduct this project in compliance with these rules, as summarized in the Advocacy Guidelines Handout, and any other relevant local, state, or non-US lobbying laws. If foundation grant funds will be earmarked to influence policies, budgets, innovations, frameworks, action plans, etc., that could require a legislative vote, please explain how such “legislative” activities will be conducted in accordance with the applicable rules and exceptions. Your explanation should address both direct and grassroots communications. If this does not apply, please indicate N/A.

The NextGen Cassava project’s Communications & Advocacy team is not engaged in supporting any direct or grassroots lobbying. We do not express views on any legislative proposals or issue calls to action on specific legislation proposals. We engage in advocacy around the issue of the potential of genomics research in cassava breeding, and of cassava in general, not specific bills or legislation, either in the U.S. or abroad.

The Biotechnology and Biosafety Education special initiative is implemented by the Uganda Biosciences Information Center (UBIC), an information sharing hub of NARO, Uganda. NARO is a non-profit agency of the government of Uganda mandated to undertake all aspects of agricultural research for the benefit of the public. NARO (and by extension UBIC) does not engage in any direct lobbying communication.

Any communications activities done for this project are in support of research activities and research institutions and distribution of new varieties of cassava to smallholder farmers. We define “advocacy” as proactive communication on behalf of the NextGen project and its objectives. We are public information officers for the project, and do not seek to influence any legislative proposals, either directly or indirectly. We will operate in compliance with all foundation restrictions and guidelines.

8. Conduct and Control of the Project [Complete if Global Health or Global Development Applicant]

1. **Please confirm that your organization:**

   a) **will maintain the expertise necessary to conduct, control, manage, and monitor all aspects of the Project in compliance with all applicable ethical, legal, regulatory, and safety requirements, including applicable international, national, local, and institutional standards and policies and is responsible for determining and complying with these requirements and standards;**
   b) **will not disclose any confidential or protected information to the Foundation without obtaining prior written approval from the foundation and all necessary consents to disclose such information;**
   c) **acknowledges that any activities by the Foundation in reviewing documents, providing input or funding does not modify your organization’s responsibility for determining and complying with all applicable ethical, legal, regulatory, and safety requirements for the Project in all places;**
   d) **will maintain insurance coverage sufficient to cover the activities, risks, and potential omissions of the Project in accordance with generally-accepted standards and as required by law (for instance, general, professional, clinical trial, product liability, medical malpractice, workers' compensation, or otherwise);**
   e) **will not transfer any biological materials, chemicals, reagents, hazardous materials or the like to the Foundation.**

   Confirmed ____

   Not confirmed ____ (please explain)

   Confirmed

2. **Does the Project involve any of the following: clinical trial, other trial involving human subjects, post-approval study, experimental medicine, genetically modified organism, or the provision of medical/health services?**

   No ____

   Yes ____ (If yes, please list all approvals and consents required for each site and describe the timeframe in which your organization will acquire the necessary approvals and consents.)

   No

3. **Please identify the name of the entity that will be the sponsor/responsible party of any clinical trials, studies involving human subjects, experimental medicine studies, post-approval studies, products, or regulatory filings contemplated by the Project. Note that the Foundation will not serve as the sponsor/responsible party nor accept delegation of any of these responsibilities. If the Project will not involve such activities, please indicate not applicable or N/A below.**

   Not applicable

9. Activities

Describe in further detail what activities are necessary to produce the principal results. Please ensure that these activities align with the results in the Results Framework.

BREEDING DIVISION

The Breeding Division will use technology and product profile information produced by the Research and Survey divisions to translate, develop, and release improved cassava varieties. The four African breeding programs — IITA, NRCRI, NaCRRI, TARI — are distinct, and are each at unique places in their transformation to genomics and information technology-assisted breeding programs. For the purpose of this proposal, however, we present a single prototype of the breeding pipelines to give a sense of the scale of breeding we are targeting for each program.

The Survey Division will provide the specifics of end-user-preferred varieties and traits, and market research to the four breeding programs while the Research Division will develop tools to measure target traits. The information and tools are expected to help in identification of clones that provide the best trait combinations. Each breeding program manages distinct pipelines that cassava clones traverse in the process of identifying and releasing new varieties to smallholder farmers:

● **Variety release:** Promising clones identified in modified Advanced, and Uniform yield trials (AYT, and UYT, respectively) are bulked and entered into National Performance and Variety Release trials. The varieties in the pre-release trials would be simultaneously entered into large-plot on-farm trials. Cassava clones selected from this pipeline leave NextGen, prepared for distribution in their areas of adaptation and for the specific food or end uses for which they were bred. Each of the programs is expected to generate enough clones for evaluations in readiness for release and distribution.

● **Breeding cycles:** All plant breeding programs generate improved populations of individuals in which future varieties will be identified and released. The strength of modern breeding is the speed at which it is able to increase average performance of these populations. The breeding cycle involves crossing and generating botanical seeds, germinating seeds and transplanting to a seedling nursery, genotyping and prediction, cloning seedlings to a Clonal Evaluation Trial (CET), and selecting the best to cycle back to the crossing nursery.

The breeding programs will continue to collect and upload phenotypic data to Cassavabase for the updating of genomic prediction models. Findings from participatory evaluation by the Survey Division will be used to fine-tune breeding targets and empirically determine product profiles for reproducible phenotyping. The number of location x year combinations in which clones have been tested are incrementally increased with each cycle, and refine our understanding of the agro-ecological zones for which we need to breed.

Breeding Sites and Environmental Characterization

Knowledge of test environments is a very important component of any breeding program. Testing cassava under diverse agro-ecological zones is needed to determine areas of highest adaptation and performance stability of genotypes. During Phase I, we relied on historically existing environments that were being used by breeding programs to test different trial types (CET, PYT, AYT, UYT and participatory variety selection [PVS]). In Phase II, we will continue to refine and/or rationalize the testing sites for purposes of increasing resource-use efficiency. We will also work on rationalization of plot sizes, replications or field plot capacity of each of the African breeding programs. Identification, characterization, and calibration of test environments will be done using a combination of GxE datasets and geographic information system (GIS) complemented with environmental variables (precipitation, temperature, elevation, soil texture, soil pH and water retention capacity). We will make investments in weather stations to accurately generate these weather data. The Breeding Division will also link up with the Research Division in implementing real time kinematic-global positioning system (RTK-GPS) from a complementary project (PhenoApps) and with Cassavabase, to ensure that tablets or phones used in phenotyping are equipped with software that makes them capable of identifying specific plots in real time. The aim will be to avoid errors in data collection.

In Nigeria, IITA and NRCRI's breeding programs together have a network of phenotyping sites that have been used over decades, ranging from the humid forests of the south to the Sahel savannah in the north. The sites include, Ibadan, Ubiaja, Umudike, Abuja, Mokwa, Otobi, Zaria, Kano, Ikenne, Onne, Warri, Igbariam, Uyo, Nsukka and, Ago-Owu. These sites will be part of environments used by the programs to evaluate new populations for target traits in Phase II. During Phase I, Uganda's breeding program identified five mega-environments and will continue to use these environments in Phase II. The environments are as follows: Namulonge (central region), Kasese (south western region), Serere (eastern region), Arua (northern region), and Tororo (eastern region). Tanzania has also traditionally used some testing sites for variety release regional evaluations but they have not been adequately characterized for different trial types. Working with the Tanzania Official Seed Certification Institute (TOSCI), the variety release partner, the program has identified the lowland warm coastal belt of Indian Ocean, mid-altitude humid areas, mid-altitude semi-arid areas and highland areas as the main testing environments.

Ubiaja in Nigeria, Namulonge in Uganda, and Ukiriguru in Tanzania will be used for crossing blocks because of associated flowering success rates in the sites. Namulonge, Serere and Kasese in Uganda, and Chambezi, Bunda, Ilonga, Suluti, Ifakara, Naliendele and Ukerewe in Tanzania have been used previously for the evaluation of clone responses to virus diseases. During Phase II, breeders will continue to use a select set of these sites for effective differentiation of clones for resistance to major diseases and pests.

Target Traits and Products Development

Cassava is widely grown and used in different agro-ecological zones across many African countries. Breeding targets for Nigeria, Uganda, Tanzania and the rest of Africa are influenced by the end-use acceptability of varieties as well as traits that are of regional importance. In order to continue to breed for targeted preferences, breeders at IITA Nigeria, NRCRI, NACRRI, and TARI will continue to refine breeding targets guided by outcomes of product profiles and ideotypes generated from the Survey Division. Breeding targets and product pipelines that will be targeted during Phase II are:

- **Gari and Fufu Products Target:** In Nigeria and West Africa, most communities consume cassava as gari and fufu. We will focus on developing cassava varieties with good processing qualities for making these key products. We will invest in rapid and inexpensive phenotyping strategies for assessing quality traits at early stage of breeding, especially at the CET and AYT when the number of segregating entries is fairly large. We will work with food scientists in the Survey Division to calibrate and

leverage processing and cooking characteristics, nutritional quality and cyanogenic potential of cassava varieties.

- **Starch and Flour Products Target:** Starch and flour are growing industrial markets for smallholder cassava farmers across Africa. Cassava is a competitive source of starch given that starch yield per unit area planted is very high. There are already on-going initiatives from indigenous and multinational investors to set up large starch processing facilities in Tanzania, Uganda and even much more in Nigeria. This provides a potential opportunity for smallholders (usually aggregated in clusters), which in turn will stimulate adoption of cassava varieties suitably improved for starch content. Current starch levels of commercially grown cassava varieties in Africa are mostly within the range of 15-22% (fresh weight basis), and this is usually unstable given the impact of precipitation on starch yields. Cassava varieties targeted to meet starch and flour market needs are expected to have high and stable yield in starch content of at least 25%, high dry matter of at least 35%, and low fiber content. We will identify cultivars to generate, improve, and advance high-starch genotypes for release across both East and West Africa. The use of genomic predictions and handheld near-infrared spectroscopy (NIRS) in rapidly assessing and predicting starch levels for new varieties will accelerate the enhanced-starch pipeline.

- **Cassava Biofortification Target:** A common problem in developing countries is the consumption of starchy staples such as cassava products with little or no additional micronutrients that are necessary for human health. Biofortified cassava for provitamin A micronutrient deficiency in women and children's diets will continue to be an important breeding objective in East and West Africa. Improved varieties with up to 10 µg/g of provitamin A were released to millions of farmers in Nigeria. These varieties were developed through phenotypic recurrent selection, which often takes longer compared to a genomic selection breeding scheme. During Phase I, we identified genomic segments that are associated with increased beta-carotene and dry matter in cassava. Preliminary cross-validation analysis from Phase I for provitamin A shows that it has high prediction accuracies and high rates of genetic gain. Our study further illustrated the negative relationship between the two traits, which has impeded progress in breeding for the trait. So far, the breeding pipeline for beta-carotene as implemented by the HarvestPlus project is through conventional breeding. In Phase II, we will work with the HarvestPlus project to integrate this essential trait into the genomic selection pipeline facilitated by NIRS predictions. In Uganda, we will move forward with the PEARL grant on biofortification to introgress CBSD tolerance into high provitamin A varieties, so as to provide this important nutrient to families faster.

- **Cooking Quality Target:** Cassava products with good cooking quality will be a catalyst for adoption by farmers and the fresh cassava market segment (particularly in East Africa). Consumers in the region mostly boil, make fries or roast the roots for their meals. One critical trait that is relevant for most fresh consumption is mealiness of the roots. Many of the cassava varieties introduced into East Africa for their resistance to virus diseases lack softness or mealy qualities after boiling. This significantly slows down the rate of adoption of these cassava varieties by communities who traditionally consume fresh cassava. Breeding will work together with the Survey and Research divisions to validate this rapid phenotyping tool and to determine how it can improve genomic prediction accuracy and thus selection efficiency.

Durable CBSD-Resistant Varieties and Pre-Emptive Breeding

Novel Sources of Resistance from Latin America: Resistance to CBSD (at screenhouse level) in ten accessions from the CIAT collection has been identified at a laboratory in Germany. These materials have been micro-propagated and the plan is to send clones to NaCRRI and IITA in Nigeria before the end of 2017. Field evaluation will be done in Uganda. We will make crosses in low disease pressure sites that should be relatively clean of virus, enabling crosses to be made before the CIAT clones die of disease. To get CIAT clones into a pre-breeding pipeline rapidly we will also pick a set of ~20 elite East African clones that combine high CMD resistance with high fresh root yields to cross to them. We will use selected 5CP clones as candidates for this purpose. The target will be to cross each CIAT clone to three or four elites. We will add IBA961089A from Nigeria, that is available in East Africa, to the list of CIAT clones as it has been found to be resistant to CBSD. At IITA Nigeria, a similar crossing scheme as for East Africa will be used, but with West African clones that have high CMD resistance.

Validation of Markers from Previous QTL Analysis: From previous QTL work on CBSD, we have about 500 progenies from crosses that should be segregating for identified QTL. These progenies have phenotypes for CBSD already and should enable QTL validation. DNA from the progeny will be sent to Cornell for rAmpSeq genotyping. Some parents of the prior CBSD QTL identification families have been whole-genome sequenced in the HapMap work of Ramu Punna. We will sequence the remaining parents.

Marker-assisted Selection: From association mapping for CBSD done in Uganda, we have SNP alleles we know to be in LD with causal alleles conferring increased resistance. We will start using the resistance-associated SNPs for MAS: in testing progeny from those MAS selections, we will discover how good the SNPs are as diagnostic of inheriting the causal resistance alleles. The following analyses will align GWAS with QTL studies:

a. Phase the QTL family parents using information from the progeny.

b. Given sequence on the parents, find out whether the resistance allele in the QTL parent is the same as the resistance-associated SNP from GWAS.

In East Africa, CBSD-resistant clones identified in Uganda and tested in Tanzania had lower yields compared to susceptible varieties. In Phase II we will continue to generate more crosses to improve our understanding of how to combine high yields and CBSD resistance.

***CBSV Titre*:** Disease resistance (manifested through the degree of symptom expression) was the major focus of studies conducted during Phase I. However, virus resistance (manifested through virus titre) was not considered due to lack of methods to quantify titre in breeding trials. We will explore ELISA and other quantitative virus diagnostics kits for quantifying virus loads in breeding trials. Validated protocols will be used in subsequent years during and beyond the scope of this project. Clones with reduced titre will reduce the spread of the virus and delay evolution of new virulence.

Pre-emptive breeding: While CBSD continues to devastate farmlands in East Africa, Nigeria (and more generally West Africa) has so far been spared. However, the continuous movement of germplasm and possibly the whitefly vector between the two regions make it likely that CBSD will come to West Africa. To prepare and reduce the impact of any future outbreak, West Africa needs to deploy resistant varieties pre-emptively. To implement pre-emptive breeding against CBSD for West Africa, sources of CBSD resistance from East Africa have already been identified and are being used in crosses with elite CMD-resistant lines in Nigeria. In Phase II, a progeny testing strategy will be adopted, whereby some of the progenies will be sent to East Africa for screening in disease hotspots, while the remainder will be evaluated in Nigeria for genomic prediction using models from NextGen East African populations. We will continuously validate this after each cycle, for at least the initial two seasons in order to estimate the prediction accuracies obtained.

Breeding Cycle and Pipelines

The genomics-assisted breeding cycles being implemented across the four breeding programs vary in terms of duration (one- or two-year cycle), and amount of resources dedicated to the number of plots, replication, number of locations, and number of years for evaluations. IITA/Nigeria operated on a one-year cycle while both NaCRRI and NRCRI operated on a two-year cycle and will continue this into Phase II. TARI, a late entrant to Phase I, is in the process of developing a two-year genomic selection cycle. To bring GS in TARI up to speed, the breeders will assemble a training population and initiate the several phases traversed by other breeding programs. Existing patterns of breeding cycle specific to countries will continue to be practiced with some alterations suitable to each program, as elaborated in specific country-level project activities and budget lines.

Varietal development will follow the stages of seedling evaluation, clonal evaluation trials, advanced yield trial, uniform yield trials and national performance trials. Across all breeding programs parental populations of 100-200 genotypes will be planted in crossing nurseries. Additional selection, based on new phenotypes from that year, will enable more accurate selection down to a set of 50 parents. From 5000 to 10,000 seedlings, preferably from controlled crosses, will be established annually (or semi-annually) from each program where DNA will be extracted and genotyped. Thereafter, we will clone between 600-1000 individuals to advance to CET for 1-2 years. We expect to advance the best 20-50% of CET to AYT and evaluate them in 2-3 locations depending on availability of planting materials and resources.

The selection intensity will be the prerogative of breeders in each program depending on available resources and optimization guidance from the Research division. We propose to adopt a strong selection intensity of 10% at AYT, advance the selected individuals to UYT, and test them between 3-5 locations preferably for two years. More rigorous yield evaluation, including genotype-by-environment stability analysis will be used to select top 5-10 clones for advancement to UYT. Clones that perform well after UYT will be bulked up and entered into National Performance and Variety Release trials as well as large-plot on-farm trials. Phenotyping data generated at the AYT and UYT stages will also be used to update the genomic selection predictions.

Marker-Assisted Selection

Genome-wide association studies (GWAS) carried out by NRCRI, NaCRRI and IITA in Phase I identified major genes that control resistance to CBSD, CMD, and cassava green mite (CGM), as well as enhanced provitamin A and dry matter content. GBS markers linked to these loci are currently being converted to allele-specific markers at ICRISAT. We will validate these markers with breeding populations to allow for deployment in the breeding programs for routine marker-assisted selection (MAS) assays. Genetic progress (in terms of combinations of desirable traits) is markedly different in white-fleshed versus beta-carotene cassava populations. For example, while reasonable progress has been made in white-fleshed populations for CBSD resistance and dry matter content, the yellow cassava populations remain deficient in these traits. Thus, MAS will be leveraged appropriately in this scenario. A two-step approach where cheap MAS is applied to screen tens of thousands of seedlings for must-have traits (for example, disease resistance) followed by genomic selection for quantitative traits is envisaged. Breeding will work with the Research Division to establish software tools to support the application of haplotype-based MAS.

Selection intensity Strategy

In Phase I, each breeding program genotyped about 2,500 clones per year for prediction. This throughput was under a GBS genotyping system where the cost, including DNA extraction, was close to $30 per sample. In Phase II, we project genotyping costs of $2 per sample for ten markers (set of 5-trait marker chip) for MAS, and $8 per sample for the rAmpSeq or very low-depth whole genome sequencing (WGS) methods for genomic prediction. These lowered costs justify genotyping higher numbers of clones per program per year. Two factors weigh against excessive increase in the genotyping throughput. First, we need to scale our genotyping to our ability to implement quality control. Repeated genotyping of clones in Phase I has revealed unacceptably high levels of mis-labeling errors. We propose a number of systems in this document to reduce such errors. We also need to follow through on systematic checking to ensure that those proposals are working. As we implement improved quality control and become confident that our efforts are leading to lower

error rates, we will ramp up genotyping. Second, from a breeding theory point of view, the marginal returns on increasing selection intensity diminish as selection intensity increases. For a normally distributed trait where we select the best 100 individuals, going from 2,500 to 10,000 increases selection intensity by 24%, whereas going from 10,000 to 40,000 only increases selection intensity by a further 16%. Thus, on balance given decreasing genotyping costs, quality control concerns, and benefit for selection gain, we propose to initially ramp up genotyping for MAS to 10,000 clones per program and for WGS to 5,000 clones per program. Over the course of Phase II, as we become confident in QC and possibly as genotyping costs drop further, we will revisit these numbers. The table below shows our planned genotyping per program and for each genotyping purpose. Initially, we plan to use Cornell Genomic Diversity Facility as the provider for sequencing given that they have invested in developing low cost WGS library preparation method. We will continue to seek lower cost providers.

Table 1. Genotyping assays planned per year per program

	Provider	*IITA*	*NaCRRI*	*NRCRI*	*TARI*
Low density MAS, 10 diagnostic SNPs for traits	Intertek	10,000	10,000	6,000	4,500
Low density QC, 20 high PIC SNPs for fingerprinting	Intertek	2,000	2,000	2,000	2,000
WGS low depth, 0.2x to 1x sequencing for prediction	Cornell GDF	5,000	5,000	2,000	1,500
WGS high depth, 10x sequencing of parental clones	Cornell GDF	50	50	40	40

Variety Release Pipelines

***NextGen Cassava Varieties*:** Breeding materials from Phase I and other breeding lines currently in the downstream cassava breeding pipeline will be candidates for official release during this project implementation time. Distinctive Uniform and Stability tests will be conducted by oversight agencies mandated for variety release processes in each country. NaCRRI, NRCRI and TARI with IITA have had a good working relationship with these agencies and their pipelines. The relationship has resulted in the release of several varieties in each of the project partner countries. Breeding will work together with the Survey division, using the metrics developed from product testing with end-users, to improve the process of selection for new varieties as this will enhance the likelihood of adoption.

***Multiplication and Distribution*:** The outcome-level success of the project will depend on scaling out of the technologies (i.e. improved varieties) developed by the Breeding Division. To achieve this goal, we will ensure that varieties being developed meet minimum acceptability criteria including resilience against biotic and abiotic stresses, good yield and dry matter content, and also possess acceptable processing and cooking qualities. One of pitfalls of the past that we seek to avoid is releasing new varieties, only to have them remain on the shelves. Due to the general lack of sufficient quantities of planting materials that can be produced and distributed, the Breeding Division will go a notch higher to multiply cassava plantings so as to increase adoption uptake. In East Africa, the lack of CBSD immunity among clones prioritizes the need to take any promising variety through thermotherapy, to generate virus-free breeder seed that will be taken through the formal seed multiplication schemes that are being optimized. We will collaborate with other BMGF-funded investments in the cassava value chains, such as the BASICS and ACAI. Both projects are being implemented in Nigeria and Tanzania and IITA, NRCRI and TARI cassava programs are implementing partners. To accelerate flow of varieties through the National Performance Trials, we will employ innovative high-throughput multiplication methods of planting materials such as the semi-autotrophic hydroponic (SAH) system of the BASICS project to overcome the multiplication ratio bottleneck. Once potential varieties have been released, the SAH system will also be used to mass produce disease-free planting materials for onward dissemination. We will also ensure that information on appropriate production technologies for the new varieties will be provided to farmers and interested seed producers, as developed by the ACAI project. In addition to traditional dissemination channels such as extension agencies, we will work with established community level seed entrepreneurs to roll-out winning varieties. These are called village seed entrepreneurs (VSEs) in the BASICS project. Head-to-head comparisons will be used to demonstrate superiority of the new varieties.

Breeding Backstopping Initiatives

We will work with breeders at IITA, Sendusu, Uganda to play a critical role in backstopping NextGen national breeding partners in East Africa, especially TARI. Historically, IITA has wide experience in germplasm exchange and in screening for resistance to CMD and CBSD in the region and can help in breeding against these devastating diseases. They will be involved in planting, routine data collection, harvesting of trials, and will participate in data management and developing publications. We will leverage from the 5CP project, which backstopped TARI and NaCRRI towards a targeted release of varieties resistant to both CMD and CBSD in Tanzania and Uganda, respectively, in 2019. These materials are currently deployed as parents for new population improvement in Phase I and even more so in Phase II. Lead breeders at IITA will also play a role in co-supervision of students at Makerere University. We propose to train three MSc students in plant breeding at the Makerere University Regional Centre for Crop Improvement, a World Bank African Center of Excellence.

Partnering to Harness the Breeding Experience and Expertise of CIAT and Embrapa

CIAT

Contribute to Strengthening Capacity of Breeding Programs: A selection of young cassava breeders or field technicians associated with NextGen Cassava will receive practical training at CIAT in an effort to re-tool them and enhance their capacity. In Phase II, CIAT

breeding personnel will be available for pre-breeding activities and periodic visits at strategic times (particularly during harvest) to collaborate during the fieldwork process in any of the breeding programs.

Germplasm Transfer to Africa through Pre-breeding for Special Traits: Germplasm provision by CIAT to the four African breeding programs will be a useful strategy to harness alleles found in Latin America. During Phase II, CIAT scientists will identify elite genotypes with desired traits (particularly high/stable DMC and starch content, high carotenoids content, new plant type architecture) and cross them with sources of resistance to CMD and other sources of resistance to pests and diseases found in the Americas (e.g. bacterial blight-CBB, thrips, mites, etc.). Previous introductions of germplasm from the Americas into East Africa allowed the identification of materials that showed interesting reaction to CBSD. These putative sources of resistance to CBSD will also be considered. Two approaches will be followed for introgressing these sources of genetic variability from South America into Africa: **a)** Sources of desirable traits will be crossed to those of CMD resistance available at CIAT to generate F_1 botanical seed that will be immediately shipped to breeding programs in Africa, and **b)** Few F_1genotypes will be grown in Colombia and crossed among themselves (unrelated origin) to generate "F_2 populations". Alternatively, the F_1genotypes will be self-pollinated to generate S_1 families. F_2 and S_1 seedling plants will be genotyped for marker-assisted selection for CMD resistance. F_2 or S_1 seedling plants will be selected based on number of alleles for resistance to CMD they carry and their phenotypic performance (e.g. plant architecture, reaction to thrips, specific traits such as carotenoids content, etc.). Selected F_2 or S_1 genotypes will then be grown in target environments on clonal evaluation trials (CET) and, at the same time, multiplied *in vitro* in preparation for shipments to Africa. CET evaluations will focus on the specific trait of interest (e.g. high and stable dry matter content, resistance to CBB, etc.). While CETs are conducted, plants growing *in vitro* will be indexed for diseases. Genotypes that show outstanding performance in the CET evaluation and complete the indexation process will be shipped, as *in vitro* plantlets, directly to Africa. If necessary selected genotypes may first be shipped to Stephan Winter´s DSMZ laboratory in Germany. If possible, they will also be shipped to Hawaii. A copy of these genotypes will be kept at CIAT, so they can be used as progenitors once they have been confirmed to express resistance to CMD. The above approach will be a valuable way to validate a system for the introgression of genetic variability from Latin America into African breeding populations and to expand the availability of genotypes confirmed to carry CMD resistance at CIAT.

Whitefly Resistance: Whitefly (*Bemisia tabaci*) transmits CBSD and CMD and its feeding reduces cassava vigor. Resistance to whitefly will reduce disease transmission rates, thus diminishing viral epidemics. Field phenotyping of whitefly is challenging. The African Cassava Whitefly Project (ACWP), of which CIAT is a prominent partner, is identifying sources, mechanisms, and genomic loci underlying resistance. In Year 1 of Phase II, we will work with ACWP to establish a mutually beneficial collaboration agreement. Through this agreement, CIAT will advise NextGen on priority crosses and experimental methods to enable CIAT-specified genotypes to be grown and crossed successfully in Africa. NextGen will benefit from CIAT expertise in whitefly phenotyping and help with incorporating that expertise into PhenoApp. Through regular meetings, we will collaborate with ACWP and leverage their knowledge to develop rational approaches to the introduction of whitefly resistance to smallholder desirable cassava varieties. These approaches will place value on the durability of the resistance, that is, the difficulty of overcoming it through whitefly evolution. This collaboration will ensure that the basic knowledge ACWP discover will be rapidly translated to improved cassava.

Other Traits: CIAT has significant expertise in other traits that could be of value in Africa, among which are physiological postharvest deterioration (PPD), fast cooking time, and mealiness. In some cases, that expertise is protected as intellectual property. We will engage with CIAT and the investors who hold IP on these traits to identify equitable ways in which alleles carried by clones showing valuable levels of a trait can undergo CMD2 conversion and be transferred to Africa.

Embrapa

Implementation of Genomic Selection in Breeding: Embrapa is the major national breeding program in Brazil and presents a huge potential for unique germplasm exchange with African breeding programs. In Phase I, we were committed to the implementation of genomic selection (GS) in cassava breeding programs in Latin America, and to studies of flowering induction. For GS, we focused on dry matter content of the roots, fresh root yield, and starch yield as traits of interest at Embrapa. Preliminary results of clones evaluated in over 23 environments indicated significant genetic gains, especially for reducing cassava breeding cycles and reducing the number of individuals to be phenotyped in evaluation trials. Once we adopted a two-year breeding cycle, we were able to carry out the whole first GS cycle and generate the seeds for the second GS cycle.

In Phase II, we intend to finish the second GS cycle, perform the whole third GS cycle and start the fourth cycle, to continue with validation of predictions for new cycles with diverse germplasm and under different environments. Moreover, phenotypic analysis of the clones selected by GS strategy will be evaluated in CET, AYT, and UYT, to re-calibrate the GS model aiming to increase the accuracy of predictions, and to develop new clones to be released as new cassava varieties. These results will be a great contribution to the application and better understanding of GS models under different environments in other partner African breeding programs. All of this information will be available for the cassava community, and this information and experience will benefit partner breeding programs in Africa who will receive botanic seeds and the best clones from the advanced cycles of the breeding populations in Brazil, for increasing the genetic variability through progeny testing and use of genomic predictions from Brazil. We will provide parents selected from NextGen trials, wild relatives, and other germplasm resources to NaCRRI, TARI, NRCRI and IITA as part of a germplasm exchange. Simultaneous to the GS activities, we will finalize the evaluation of our germplasm for root quality (carotenoid content, cooking time,

sensory taste, and friability) and for resistance to disease. Then, we will exchange germplasm with higher carotenoid content, high dry matter and starch contents, and resistance to important foliar diseases such as anthracnose and cassava bacterial blight.

Community of Practice Partnerships (COPP) for Cassava Breeding in Africa

Following the successes we have recorded in the project in the two pilot countries, Uganda and Nigeria (and now in Tanzania), we seek to build COPPs for the application of genomics-assisted cassava breeding across African cassava breeding programs. We have identified target cassava breeding programs in Ghana, Rwanda, Mozambique, Sierra Leone, Zambia, Malawi, and DR Congo; these breeding programs have been approached and have expressed interest in joining the initiative despite receiving only in-kind support. We believe that an expanded implementation of the gains of the project through the COPP will further broaden its impact in Africa, without losing focus on the target countries. These cassava breeding teams will benefit from the genomic predictions that we have already developed for African cassava germplasm (which they share), use of the Cassavabase, and capacity for improved phenotyping, which should all lead to better breeding decisions and improved livelihoods for African cassava farmers. We also realize that the new COPP members may all not be able to step up to fully implementing the new genomic tools and resources, we believe that this opportunity will set up the platform for introduction to modern breeding practices across different African breeding programs.

We will include these five national programs in our efforts without managing more subcontracts. The proposed support would include:

- Coordination by the Project Manager and mentoring by senior scientists. This will include visits by COPP members if they have other existing projects from which they can leverage support.
- Development of curriculum and organization of a central workshop bringing NextGen programs and COPP members together for training on breeding scheme optimization, networking and sharing and leveraging of new technologies.
- Visits by experienced cassava breeders to the national programs to understand their breeding schemes and germplasm, and to train national program staff on the use of the Fieldbook and PhenoApps. Contribution of electronic tablets as needed. Training on the uploading of data to Cassavabase and genomic selection.
- Development of a plan to collect leaf samples and genotype relevant clones from the program. Elite clones from NextGen programs could also be introduced to the national program as parent material and this will enable the leveraging of predictions from shared pedigrees and progeny testing.
- Bioinformatics support for COPP member breeding programs by NextGen scientists.
- Reciprocal exchange of breeding clones (cuttings or botanical seeds as determined by quarantine conditions) and reciprocal field trials to improve evaluation and understanding of GxE in elite materials.
- Evaluation of COPP clones by NextGen programs, who will provide additional data to partner countries regardless of their ability to reciprocate.

Upgrade of Breeding Infrastructure for Optimized Processes

Availability of functional research infrastructures can contribute significantly to the efficiency and optimal performance of any breeding program. Efficiency in land preparation will minimize errors and heterogeneity of trial field plots occurring as a result of soil physical structures. Lands, farm machinery, power supply, internet, laboratory, irrigation facilities, and data capture/storage tools are some of the basic needs required for success. Since these programs are at different stages of transformation, we intend to bring them to a level that will help operate an optimized process. During Phase I, IITA, NRCRI and NaCRRI benefitted from infrastructural improvements and this contributed to better data capture and data delivery. Recent review suggests that investment in irrigation systems in all four breeding programs is needed to ensure success in both crossing block and field trials. Another critical research tool needed is acquisition of farm machinery (tractors) and associated implements such as harrows, ploughs and ridgers in some programs. Furthermore, there is a need to minimally upgrade the laboratory at TARI with some basic equipment and upgrade IT infrastructure to improve communication and enhanced usage of the Cassavabase.

The three breeding programs will each acquire and have at least one of their stations (where seedlings are managed before cloning) installed with irrigation pumps, sprinkler pipes, and sprinklers or the drip system as needed, and where relevant, tractors with implements. The breeding programs will also need handheld NIRS to be able to use the predictions developed by NRCRI from Phase I activities for measuring dry matter, starch, beta carotene and cyanide contents. The project will invest in the acquisition of these resources to facilitate breeding.

SURVEY DIVISION

Overview:

The successful adoption of new cassava varieties generated in Phase II will depend on identifying and meeting the spectrum of different user preferences and acceptability criteria. The users of new cassava varieties include: producers, processors, vendors, and consumers. There is considerable diversity within these categories that are specific to each country. Each group can have multiple

interests: a local producer may process and sell a local cassava product, consume cassava in their household and sell it to industrial buyers. Each may require different sets of traits and have multiple purposes. This can result in tradeoffs when considering the needs of different user groups. As cassava is an important food security crop throughout SSA, this may have important consequences for household consumption. The trait preferences and acceptability of new cassava varieties will reflect the different roles (including gender), interests and environments of these different users, and thus, adoption.

The Survey division is designed to support Breeding in decision-making and trait prioritization, by generating information on consumer priorities and needs, to enhance adoption and impact. Concerns around tradeoffs and distraction away from target traits and critical goals (disease resistance and yield) will be carefully managed and tested. Each breeding program had very clear breeding targets for NextGen Phase I which underpinned selection indices, and which continue to guide breeding targets in Phase II. Further, during Phase 1, cassava gender-based studies were undertaken both in Uganda and Nigeria. One of the key findings from these studies was the documentation of trait preferences for cassava processing into selected products. Accordingly, phenotyping for these traits constitutes a major part of both Phase 2 and RTB-FOODs project. All this is testimony to the fact that the survey division findings (gender studies included) supplement, rather than supplant these breeding targets. Furthermore, specific trait targets for product (gari/fufu and boiled cassava) quality is currently a gap that Survey division will help fill through interaction with RTBFOODS results, and validation with 1000 minds and participatory testing. It also suffices to note that some varieties can be in production for > 30 years, while others are hardly in production beyond five years. Drivers of these trends and/or dynamics is information that is very relevant for the Breeding Division, and this can only be generated by the survey division through its multi-pronged approaches of stakeholder engagement.

The planned 1000 minds research, and field level prototype testing will help establish economic weights to all traits considered (including disease resistance and yield), this data will be presented to breeding programs for consideration in modifying selection indices later in the project lifecycle to guide subsequent crosses (Figure 1). If existing breeding targets (such as yield and disease resistance) remain heavily weighted by end users, we do not foresee significant changes to trait prioritization and indices for Breeding division. However for instances where “quality” traits (for gari/fufu and boiled cassava) emerge with equal or higher weights to existing breeding targets, Survey Division will only recommend these for consideration for breeding if traits are actionable, realistic and affordable. This implies that quality traits can only be acted on if at least two of the following criteria are met: 1) field testing with 1000 minds and prototype evaluation demonstrates equal or higher weights to current breeding targets (data generated in Section B and D below); 2) HTTPs have been developed by RTBFOODS to affordable and rapid measurement early in the breeding pipeline (Figure 2); and 3) the genetic architecture of traits has been determined (Figure 2 and Section C below).

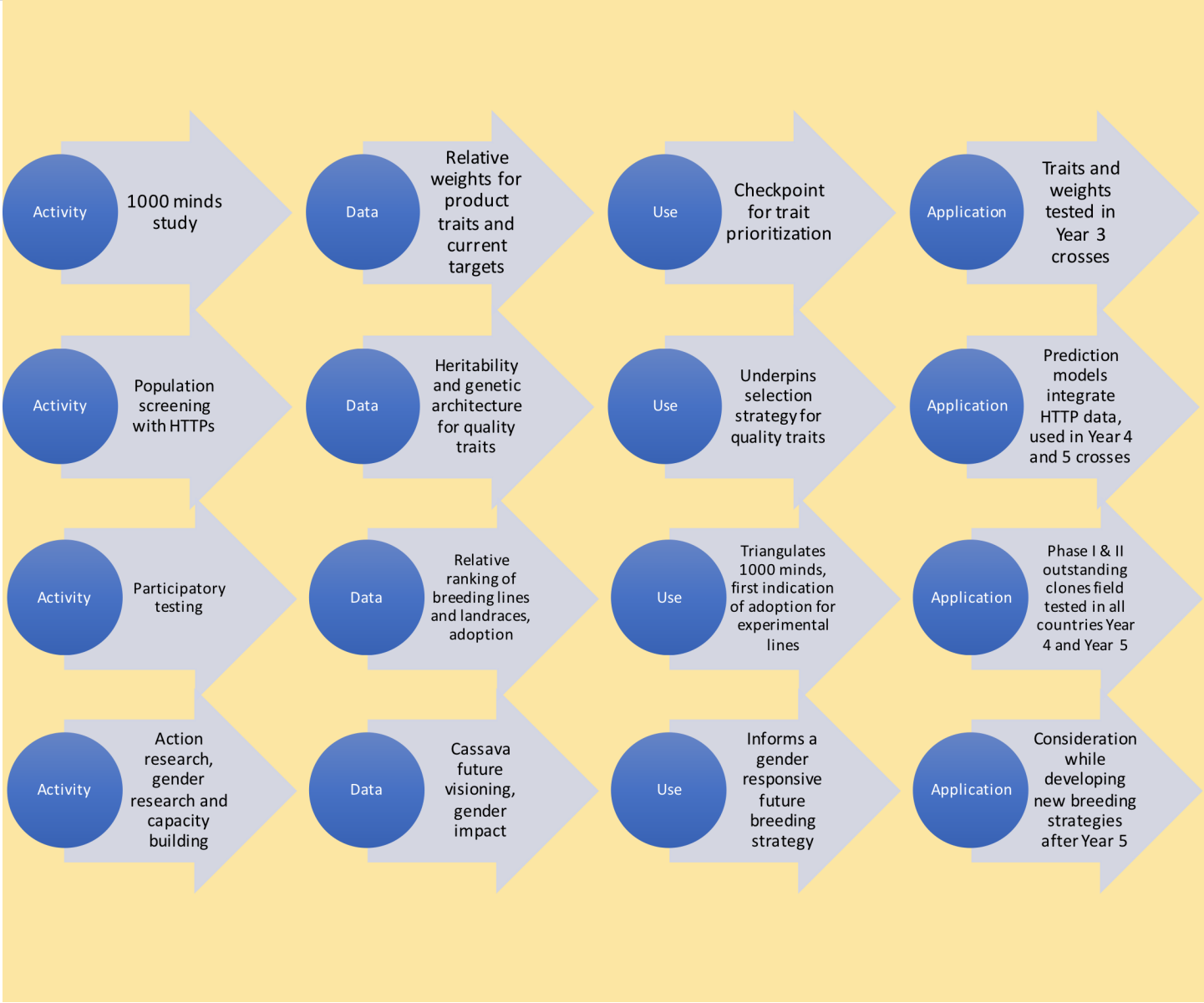

Figure 1: Survey Division- Breeding Division workflow. Note, this workflow will be largely informed by Section A activities to follow existing models in industry.

To understand preferences and acceptability of new cassava varieties, we will work closely with the RTBFOODS project and act on the outputs generated on identifying characteristics of the preferred varieties that match end-users, agro-ecologies and target market segments. This is intended to ensure the closest possible match between the developed varieties and demand. The Survey Division will model the Phase II approach to product profiling on industry standards and approaches. “Customer designed varieties” require market analysis and surveys with the intent of developing variety ideotypes for customer categories (covered under RTBFOOD WP1), prototype testing, and selection (covered under NextGen Survey Division) activities. NextGen Survey Division will act to communicate, triangulate and translate information for NextGen breeders on end user preferences and trait information, and high throughput phenotyping platforms developed under the RTBFOODS project. Essential to the success of the division in achieving its goals, is the involvement and participation of a diverse range of users and stakeholders in this process, and close links with the RTBFOODS project (Figure 2).

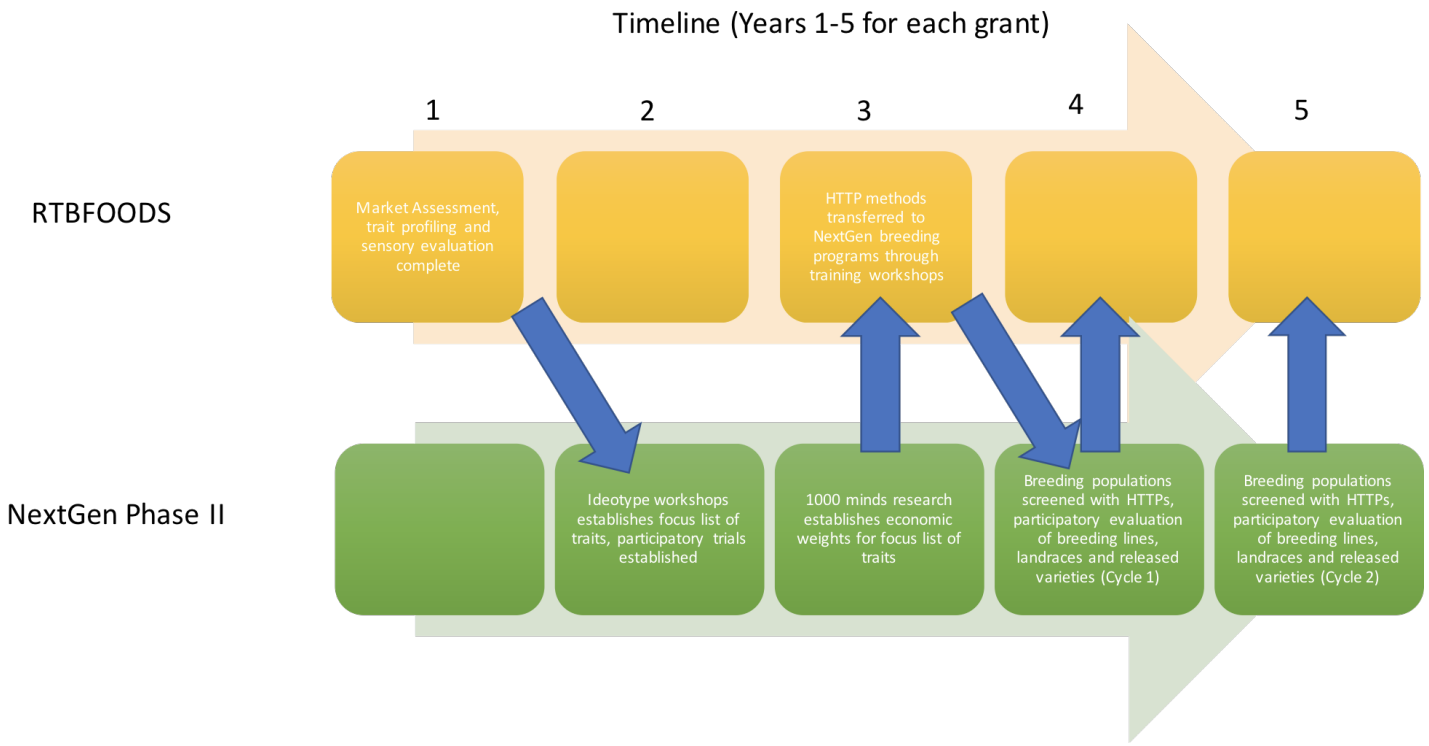

Figure 2: RTBFOODS-NextGen linkages. Note overlapping activities focus on gari, fufu and boiled cassava as products, in three countries (Uganda, Nigeria and Tanzania) working with four breeding programs (NaCRRI, IITA, NRCRI and TARI).

RTBFOODS and NextGen Phase II will work together as follows:

Year 1: RTBFOODS WP1 market assessment, surveys and sensory evaluation completed, generating product maps, trait lists and food product profiles (for gari/fufu and boiled cassava).

Year 2: RTBFOODS WP1 results on key traits and food product profiles presented and discussed with NextGen breeders in “ideotype development workshops” in each country (Uganda, Nigeria and Tanzania). Workshops result in agreement on key traits to focus on in each breeding program. NextGen supports 1000 minds MSc student recruitment, and NextGen participatory prototype evaluation work begins in each country.

Year 3: NextGen 1000 minds student conducts fieldwork with breeding programs in each country to develop relative weights for key traits that define ideotypes for gari/fufu and boiled cassava products (including existing breeding targets). First year of participatory evaluation data produced- results on relative ranking for selected products (gari-fufu and boiled) from landraces, improved varieties and breeding lines collected and shared with RTBFOODS. RTBFOODS delivers developed HTTP methods to NextGen breeding programs, and holds training workshops.

Year 4: NextGen populations screened with HTTPs. Heritability and genetic architecture data generated for quality traits using HTTPs, results fed back to RTBFOODS on ongoing basis and at annual meetings. Second year of NextGen participatory trials ongoing.

Year 5: NextGen population screening continues, results of second year of participatory evaluation collected and reported back to RTBFOODS

Activities:

Industry Scoping Study

We will begin the process of developing variety ideotypes by benchmarking our research design to industry approaches. This will involve online consultants/site visits with major plant breeding and food companies (for example Syngenta, DuPont Pioneer, and Nestle) at project inception. This consultative design strategy will ensure the planned research process for product profile development follows the highest possible standard and proven approaches. The industry scoping study will be carried out with the support of a postdoctoral fellow.

Building Variety Ideotypes

Here, we define an ideotype as a cassava variety that meets specific trait thresholds in a specific environment, as mutually understood by both its users and developers (or promoters). Information from the market research, value chain mapping, and end user profiling from the RTBFOODS (WP1) project will be synthesized into hypothetical variety ideotypes for gari/fufu and boiled cassava in Nigeria, and Uganda/Tanzania respectively. Variety ideotypes will be constructed collaboratively during a workshop bringing together market economists, end user profiling teams and breeders from NaCRRI, NRCRI, IITA and TARI. At these workshops, considering target

groups, and production environments (consultations with the breeding programs), we will review priority traits generated from product profiles for gari/fuf and boiled cassava in RTBFOODS, to develop “variety ideotypes” that would meet end user demands. We will triangulate this trait information and develop relative weights and prioritization through a student project using 1000minds software, tested on focus groups that participated in RTBFOODS end user profiling, formed of subsets of end user categories and value chain actors to verify trait sets identified. The 1000 minds approach will help the NextGen breeding programs act on trait packages for gari, fufu and boiled cassava products emerging from RTBFOODS through establish relative weights, ranges and prioritization of trait packages.

Screening Breeding Populations Using High Throughput Phenotyping Platforms for Quality

The Survey Division will act a node of communication and coordination between the RTBFOODS and NextGen projects. Indeed, Survey Division, will attend inception and all review and planning meeting of RTBFOODS to ensure timely relay of information. Planned end-user oriented breeding activities under RTBDFOODS (WP4) will include screening of ongoing NextGen breeding populations with high throughput phenotyping tools developed under this project. Survey Division will coordinate workshops in each NextGen target country working with breeding programs to showcase on RTBFOODS high throughput phenotyping (HTPP) technology developed (WP3) and provide training opportunities for the NextGen breeding programs. The HTPP platforms will then be used to screen selected (to be determined during the HTPP workshops) GS and GWAS populations generated under NextGen Phase II. Data generated from the population screening will in turn be fed back to RTBFOODS to inform WP4 activities on deciphering genetic architecture of quality traits in cassava.

Prototype Selection and Participatory Testing

The criteria used by smallholders and processor user-groups in selecting varieties is most readily understood by examining the varieties to which they are already accustomed, the multiple-uses and market-orientation for those varieties, and the plausible reasons for those preferences. This bottom-up approach will empirically test current breeding lines that theoretically match the varietal ideotypes on-farm, from production to processing and marketing. This prototype testing will establish if ideotypes that are conceptually developed actually meet market and consumer user group demands. By setting up a participatory trials and evaluation over several years (from cultivation to the preparation of the cassava product) of the varieties farmers already appreciate alongside elite and breeding material, we have a concrete base to identify end-users’ demands. The Breeding and Survey divisions will both have roles in these trials, with Survey division contacting and organizing farmers and developing survey instruments and Breeding supplying the clones and designing trials. The prototype testing will link all groundwork from RTBFOODS and NextGen leading up to this point: we will plant matching ideotypes on-farm using the tricot approach, track harvest and processing of the materials on-farm, trace how varieties are disseminated informally in nearby fields and if possible trace how the ideotypes perform on the market. This activity will bring together RTBFOODS Workpackages 1 and 2 and NextGen Breeding Division. We will evaluate: a) popular local landraces and officially released elite varieties that have been in production for >20 years; and b) best-bet elite clones resulting from NEXTGEN from each of the three breeding programmes, including those potentially matching prototypes identified. We will recruit 10 farmers in each of 10 groups for a total of 100 farmers in each country. Each farmer will receive 50 stakes of each of 3 clones, and each clone in the pipeline will be evaluated by six farmers. The farmers will simply rank and score genotypes for acceptability for focus products (gari, fufu or boiled cassava depending on country) the three clones they receive for preference traits determined by product profile discovery. The philosophy of the pipeline is to sample farmers broadly to get a representative sample but to give each farmer a very straightforward task so that there is little missing data. The partial rankings and acceptability scores of each farmer can be combined into an overall ranking across the clones and then correlated to researcher-managed trials. The varietal trials will be planned collaboratively between the Breeding Division and the Survey Division, with gender analysis from a consultant. An MSc student at University of Ibadan will examine the informal dissemination or “adoption” of introduced improved genotypes. Simultaneously, we will assemble a specific number of tested varieties from AYT, and UYT that have promising farmer- and market-preferred traits and then evaluate them in farmer participatory on-farm trials across different locations in different partner countries. This stage is generally one of the prerequisites for official variety release in these countries. The on-farm participatory trials will provide opportunity for the farmers and researchers to jointly identify valuable characteristics that promote variety adoption, as well as empowering farmers to becoming part of the breeding process. Due to success of Phase I, some of the outstanding clones (about 15 clones, including 2 controls) from C0 to C4 and other improved materials could also be fast-tracked for evaluation in PVS in Uganda and Nigeria while in Tanzania materials from the 5CP project will be candidates for testing and release. Up to 200 farmers in mega-environments relevant for cassava production and consumption will be randomly identified in each country. The trials will be implemented through a popular system known as the mother-baby design. We are in discussion with some NGOs like One Acre Fund, who have a large network of local farmers in our target countries in Africa, for conducting cost-effective participatory trials. If we are able to establish that using them will be better value for money, we will outsource this piece of work to them.

Building a Gender Responsive Sustainable Customer-Driven Innovation System

Cassava producers and processors in SSA are also consumers, in most cases, for the cassava that they produce and process, making the crop central to both food security and income generation. This creates a risk factor where preferred traits between user-groups differ and will most likely continue to do so, e.g. needs in communities the predominantly process into flour versus those that utilize fresh differ markedly. Ensuring our approaches and methods are gender-sensitive is crucial because women play a significant role in small-scale production, processing, marketing and household food preparation and management. We will consult multi-stakeholder representatives to capture anticipation of future traits that may be required in the context of technological advancement and market trends to ensure that different interests, such as food security and commercial interests, present and future, are taken into account. This action research will

take place during the prototype testing activities (described above) to leverage on going activities and engagement and ensure cost effectiveness by reducing additional fieldwork. Understanding gender differences in preferences and acceptability of new cassava varieties is vital in customer-driver approaches and an area that lacks rigorous research evidence. But the work will also elicit gender-specific views, opinions and perceptions of cassava traits and also of the research process itself. A postdoc will review how women's priorities and preferences, in all their diversity, are reflected at higher-level workshops and decision-making platforms throughout the course of the project. We will also organize NextGen-specific GREAT gender training events in each target country, to ensure project leadership, students and researchers design and implement gender responsive research. Lastly, we propose to take advantage of our prototype testing activities to examine the potential economic impact of gender inclusivity in setting breeding priorities and participatory research activities. A comparative study will examine two proximal intervention sites where prototype testing takes place, where experimental setup will intentionally be gender blind in one site, while gender responsive in another. The idea is to empirically test if gender responsiveness "matters" in cassava breeding research: do sites where women are intentionally targeted for a prototype cultivar yield richer trait information, more variety uptake, more equitable outcomes, and importantly greater potential economic impact through higher market potential for selected materials. Gender analysis and interdisciplinary action research will be led by a postdoc, working with the same country teams for trait profiling for fieldwork support. An MSc student will undertake the comparative study on gender responsiveness in cassava breeding research. Outcomes of all gender research carried out in conjunction with prototype testing under NextGen will be shared with RTBFOODS WP1 leadership to generate learning-loops for refinement of activities in spillover countries targeted by RTBFOODS.

RESEARCH DIVISION

The Research and Breeding Divisions partner to improve NextGen's ability to deliver high-valued varieties rapidly and efficiently by developing and implementing technological advances. Breeders come to the Research Division with technology and research questions to be addressed. The Research Division also proposes new technologies breeders might not have considered. Thus, breeders are key members of the Research Division in addition to personnel at BTI, Cornell, USDA-ARS, Makerere University, CIAT, and Embrapa. The Research Division deliverables make their impact when they are deployed by the breeders. The scope of work outlined in the Research Division includes: flowering and seed set, breeding scheme optimization, Cassavabase development, genomic prediction and decision analysis support, and bioinformatics for improving prediction accuracies.

Linking Research to Breeding: Research Steering Committee

In order to ensure the Research Division provides timely, useful tools and decision support that are adopted by the Breeding Division, strong and consistent communication and coordination between the two divisions is required. Thus, we propose a Research Steering Committee. The committee will consist of representatives from the Breeding and Research divisions, including members of each institute *and* the Cassavabase team. Meetings will be held regularly (every 2-3 months), with the exact structure and schedule of the meetings to be worked out early in Phase II. The committee facilitates a two-way process so that breeders and researchers are aware of each other's activities. Breeder tools coming from research are iterated through the committee: researchers demonstrate, breeders test and comment, features are revised or proposed and timeframes agreed upon, leading to new demonstrations. The approximate structure of the Steering Committee process will be to:

1. Update on ongoing work: Each group / representative can provide an update work already agreed upon and underway and provide an opportunity for feedback and questions from the rest of the group. This should include research projects, breeding activities and genomic evaluations (decisions support information).

2. Discussion of potential new work: Both groups have the opportunity to bring up and discuss new potential research projects and breeding needs.

3. Prioritization and planning: Each meeting must lead to an agreed upon plan of action. This will include prioritizing research work, identifying key people to do the work, setting timetables for the delivery of tools and analyses (e.g. genomic predictions) and the planning of integration of new methodology/strategy in the breeding programs (e.g. new trial designs).

It is crucial that meeting result in action items with responsibility identified. Participants then report back to their groups, advocate and ensure adoption and follow-through. Given the breadth of research, we may opt to nominate sub-committees tasked with more narrow objectives, which eventually would be reported and make recommendations to the wider group.

Cassavabase Development

The overall goal for database development is for all breeding activities to take place with digital breeding tools. We will migrate all breeding activities, including crossing, to a digital breeding information technology platform. Through an interactive process with breeders, driven by the Research Steering Committee, we will develop and fine-tune tools in Cassavabase that will ensure all such activities are made in it.

Cassavabase Communication, Accountability Tools and Standard Operating Procedures: NextGen Cassava involves distributed, collaborative and international teamwork. We therefore require increased communication, mutual awareness and accountability on the part of all team members in order to ensure consistent and optimal outcomes. Email and occasional Skype calls are *ad hoc* and insufficient communication between team members. In Phase II, we will develop and implement a centralized, cloud-based system for communication and tracking of breeding activities. The dashboard will be accessible by all teams facilitating accountability and

understanding of field, genotyping, and analysis activities. Part of this system will involve chain-of-custody (COC) accounting. The COC will track the timing and persons handling both phenotype and genotype data from the point of planting or DNA collection through quality control, bioinformatics and statistical analysis. Prior to the end of Phase I, we will collect user requirements for the system, to implement it within the first year of Phase II. The goal of this system is to serve breeders such that they receive decision support when needed. Breeders will be the focus of user requirement descriptions. We will develop the system iteratively, pushing prototypes out to breeders to obtain feedback and revision requests in an agile manner. The system will crucial to the Research Steering Committee to facilitate coordination and progress tracking in the interim between formal meetings. This system can be achieved using existing (often free) software tools such as Slack, Google Calendar/Drive, Trello, BaseCamp. We will explore the integration of these tools with Cassavabase and PhenoApps. The practices that are developed will be codified in the "standard operating procedures."

PhenoApps Integration: NextGen relied heavily on the Android Field Book, developed by Dr. Jesse Poland's lab, for data collection in Phase I. PhenoApps is Field Book's successor with new functions for user, geolocation, and image analysis. Integration of PhenoApps will be led by scientists at Makerere University to:

1. Use GPS-RTK global position to enable cell phone and tablets in identifying the plot being phenotyped

2. Add image analysis capability to Cassavabase

3. Use image analysis for CBSD and whitefly phenotyping

4. Track PhenoApps usage for real-time feedback to data collectors

SolGS Steering Committee: Current usage of Cassavabase shows it to be critical to the project's phenotype and genotype storage needs. Nevertheless, despite efforts to develop analysis tools to enable breeders to perform predictions and make selection decisions (Tecle et al., 2014), Cassavabase has not been used for this purpose. This SolGS committee will exemplify breeder oversight recommended above for all tools from research. It will consist of the scientific programmer(s) that are developing the tools and the researchers responsible for genomic prediction at each breeding program. The group will meet monthly to brainstorm, coordinate, set goals and benchmark progress. One of the group's initial goals will be to undertake a case study using a well-chosen example set of data to benchmark and compare SolGS against external tools being used for genomic selection.

Improved Experimental Designs: All experiments should be designed on Cassavabase, so that randomization is properly done and plots are assigned before stakes arrive at the field. Not all fields are rectangular so that spatial assignment of plots needs to be flexible. Cassavabase will implement RCBD, augmented, and partial replication design options, able to fit variable field configurations. The field maps will be able to sync up with PhenoApps so that the user has an overview of the trial available in the tablet in the field. The design will be tested by breeders and iterated based on feedback. From trial design, to transfer to PhenoApps, to data collection, to trial upload back to Cassavabase, no data or annotations will need to be collected outside of a digital tool. Given this process, Cassavabase will have fieldmap information on each trial and will be able to carry out a spatial analysis of the data as the trials are uploaded.

Crossing Nursery Design and Controlled Cross Tracking: We seek to minimize pedigree-recording errors. Using either a barcode reader device or the GPS-RTK, technicians will scan the plot in which they collect male flowers and the plot in which the cross is made to female flowers to record pedigree. We will explore equipment to print barcodes in the field that can be attached to the inflorescence. In all cases, pedigrees will be automatically uploaded to Cassavabase.

Selection and Advancement Decision Support: Contingent on Research Steering Committee approval, we propose the following extended analysis tools:

- **Crossing and population management**

It is important to ensure we maintain genetic diversity, given that GS can reduce it rapidly. We propose the following functions to support selection, crossing and maintenance of diversity: the selection of clones to maximize gain subject to a penalty for loss of diversity, and a genomic mating approach that suggests specific clone pairings to breeders.

- **Training population design**

To date, the NextGen Cassava genomic prediction strategy has been to use all phenotyped individuals from a program to train the prediction models. We will investigate several approaches to improve on this practice. We will test methods to combine data as a function of agro-ecological and genetic distances of the trials being considered. All data is available for training, regardless of breeding program of origin. When predictions for one program benefit from data from other programs, we will use that data.

- **Advancing clones to future evaluation trials**

After generating new seedlings, we select those with the highest genomic estimated breeding values (GEBVs) for crossing. Seedlings not selected for crossing can be planted in CETs, to identify clones with promising performance for variety release and to produce phenotypes for prediction model updating. Methods to best achieve both goals will be integrated into Cassavabase.

Genomic Prediction and Decision Analysis Support

We will continue to work in Phase II with data generators (both phenotype and genotype) to compute breeding value predictions for new clones and determine which clones should be advanced to clonal evaluation trials both as candidates for future varieties and for prediction model updating. In addition, the analysis group works as an intermediary between upstream genomics work performed by the Buckler lab and the breeding programs needing practical support. In this context, we will develop models that include discoveries from whole-genome sequencing and deploy them for applied breeding as they become ready.

Data Quality and Management

In the NextGen Phase I mid-term review, the need to achieve and maintain a high standard of data quality was highlighted. The chain-of-custody (COC) system outlined as part of Cassavabase Development will be one part of this, allowing traceback of all critical data steps and, hopefully, identification of potential problems that might occur. The Research Steering Committee will identify the key instances where metrics are needed. The SolGS Task Force will evaluate the efficacy of these metrics and make recommendations on what should be standard procedure.

In addition, we will develop a standardized set of analyses and metrics that will be associated with each dataset (or where relevant, each data point) and displayed on cassava base. This work will be done as part of the SolGS Task Force and in collaboration with breeders and other downstream data users. These metrics can then be used on a case-by-case basis to decide which data to use, for example, in genomic prediction.

Some of the quality metrics we are already considering include the following:

- Model summary statistics such as variance components, AIC and likelihood ratio tests to evaluate the important, identifiable sources of variability in each dataset.
- Estimates, of the heritability (broad- and narrow-sense) of each trial.
- Cross-validation accuracy (where possible), to assess internal predictive ability of each trial.
- The overall survival rate in a trial (difference between number of plants planted and the number harvested).
- The overall disease incidence/severity.

Data curation procedures, including checks of the range and distribution of variables to ensure the data match the expected units for each variable will also be evaluated and codified in Cassavabase, where possible.

Breeding Scheme Optimization

The goal for scheme optimization is to determine breeding resource allocations that maximize genetic gains and minimize the time from crossing until variety release given each program's capacity. Optimization objectives are:

1. Develop pipelines that maintain a consistent number of plots each year in each breeding program.

2. Ensure plots are allocated to maximize genomic prediction accuracy and the identification of promising varieties.

3. Integrate activity schedules to maximize new data used for each cycle of selection.

Optimization will depend greatly on communication between breeders, with their command of logistics, and researchers who identify possible efficiencies. As such, optimization will be an ongoing topic at Research Steering Committee meetings. We distinguish two components to the breeding scheme, population improvement and product development (Gaynor et al. 2017); both need optimization. Population improvement determines the slope of genetic gain over time: the value of a variety is tied to the mean value of the population from which the variety was derived. Optimizing population improvement maximizes that slope and ultimately drives the rate of gain of varieties per unit time over a longer time frame. Product development determines the efficiency of deriving the best varieties from a given population. Efficiency in this case means speed: if a variety of the same or perhaps slightly lower value can be brought to market a year sooner, that represents a win. Thus it may be efficient to skip a year or two of clonal evaluation if the accuracy of genotypic value assessment enables it.

We have developed a simulation environment (the Breeding Scheme language, Yabe et al., 2017) for optimization. We will estimate necessary parameters and simulate different breeding schemes to assess outcomes given resource levels specified by the breeding programs. A further optimization method, SelectionGain (Marulanda et al. 2016), uses maximization of a truncated multivariate normal distribution to search for the best allocation parameters. We will also test this method.

Research in Phase I indicated that cassava yield traits have a significant non-additive component and that modeling this component can improve prediction accuracy (Wolfe et al. 2016). In Phase II, we will further investigate non-additive prediction models and training population optimization algorithms to select clones for phenotyping that will include the best parents, the most promising variety candidates, and the most informative for prediction model updating. To test the accuracy of different prediction models, we will use data from the AYT and UYT that are replicated and planted at the most locations. Two problems with these trials for this purpose are 1. Selection will have reduced the variation among the clones making them insensitive estimators of accuracy, and 2. Selected clones benefited from favorable error deviations in past trials, making them a biased sample possibly generating artifacts (Ceballos et al. 2016; Barandica et al. 2016). To control for these problems we will include in the validation AYT and UYT trials up to a dozen randomly and negatively selected clones to increase variation and enable bias control. This practice should minimize the burden of additional trials while benefitting fully from ongoing breeding trials in the validation effort. In addition, we will use these data and simulations described above to explore alternatives to the conventional series of trials used for variety development in a cassava that leverage genomic prediction to shorten the time taken to evaluate and release varieties.

Genotype by Environment Interaction and Selection Index Optimization: We have observed high GxE for fresh root yield but not for dry matter or CMD in Nigeria. This observation suggests that we will need to identify separate clones for best yield performance

across locations. It also means that initial phenotyping for high heritability traits like CMD and dry matter could be conducted in one location and selections from this stage tested in multilocation yield trials. We will implement analysis pipelines using additive main effects and multiplicative interaction models for decision support in targeting clones to specific locations for further testing. This work will dovetail with analyses of genetic correlations between desired traits to optimize indices used by breeders to maximize gains in overall clone economic value.

***Ongoing Testing of Genetic Improvement*:** Dedicated evaluations of breeding progress that compare within a single trial clones from several cycles of selection are valuable retrospective tools. These evaluations, however, are costly and do not directly contribute to ongoing breeding efforts. Each year the breeding programs carry out trials to identify the best clones that are candidates for variety release (i.e., CET, PYT, AYT, and UYT trials). We will leverage these trials for annual assessments of genetic gain. In Phase I, we identified augmented experimental designs that include five to seven checks. These checks provide a good measure of the mean yield of a trial for comparative purposes across years and locations. We will further investigate trials that include clones from across two breeding cycles. For example, if in a coming planting cycle C2 clones move to a PYT and C3 clones move to a CET, we will include some C2 in the C3 CET experiment. That practice may present logistical challenges, but it would increase connectivity across cycles in the evaluation of genetic gain. Recently, Piepho and colleagues (Piepho et al. 2014; Laidig et al. 2017) have presented models to assess breeding progress across annual trials. The essence of the approach is to substitute the G_i term in the standard model:

$$y_{ijk} = \mu + G_i + L_j + Y_k + (LY)_{jk} + (GL)_{ij} + (GY)_{ik} + (GLY)_{ijk}$$

With

$$G_i = \beta r_i + H_i$$

Where r_i is the year of release of a clone (or in our case the year it was cloned out), β is a regression coefficient giving the annual gain from selection, and H_i is a genetic deviation from the annual gain. We will research such models to determine which give stable estimates of genetic gain generated by each program's efforts. We will run the models in December of each year prior to the project meeting of the following year to give each program a report on realized gains.

Transitioning to a new genotyping system

Whole genome genotyping using GBS served NextGen Cassava well in Phase I. It was inexpensive relative to other technologies and required little up-front development. Nevertheless, GBS required high-quality DNA and, sequencing costs have continued to decline. We are currently testing methods that involve whole-genome sequence (WGS) of parents and low density typing of progeny that leverage imputation. We are sequencing all parents of the current generation of seedlings from IITA, NRCRI, and NaCRRI (TARI, as of yet, has no progeny within the NextGen program), amounting to about 300 clones. Further, we are sequencing ten grand-parents that collectively have 30 sequenced progeny. We will type those progeny with three methods, rAmpSeq, very low depth WGS (0.1x to 0.2x depth), and a proprietary system from DArT that is expected to deliver 1,000 to 5,000 markers for $5. We expect all of these systems to cost less than $7 per progeny, a real savings relative to GBS. We will validate each method by using its markers to impute parental sequence down to the progeny and then comparing to the actual WGS of those progeny. We expect to conclude tests in October and November, in time to genotype current generation NextGen Cassava seedlings in December and January. That in turn will allow for predictions in time for crossing nursery planting, the first of which will take place in April in East Africa.

Genomics and Bioinformatics to Improve Prediction Accuracies

Whole genome sequencing (WGS) provides opportunities to incorporate biological information from outside of breeding into the models that drive cassava improvement. We will use the Cassava HapMap resource to test these opportunities. Furthermore, with the genotyping platform we will use for breeding, the project will continue to generate WGS sequence, enabling us to discover rare potentially deleterious alleles on an ongoing basis and to take account of them in our selection decisions. We will test directly whether sets of presumed deleterious amino acid changes help in prediction of phenotype by:

1. Developing a cassava pan-genome practical haplotype graph (PHG) for effective imputation and phasing of low density markers. The PHG identifies coordinates across the genome present in all reference sequences. Haplotypes between coordinates are exhaustively catalogued. The Buckler lab is inventing this system for maize and will adapt it for cassava.

2. Developing improved prediction of deleterious mutations in coding and non-coding regions by expression and chromatin profiling in cassava and surveying Euphorbiaceae sequence conservation. Three initiatives contribute to this objective. First, we will sequence a number of new species, the majority more closely related to cultivated cassava. This sequencing will enable multiple alignment of less-conserved, non-genic regions and allow us to determine levels of conservation in those regions. Second, we will identify open chromatin regions of the genome that are actively engaged in transcription and regulation of the phenotype. These regions will become priorities for the detection of conservation over evolution. Finally, we will assess gene expression across the genome, providing many new intermediate phenotypes that can guide model development of gene deleteriousness.

3. Measuring the efficiency of purging deleterious mutations by crossing and genomic selection against selfing of parents. We will sequence both parents and their selfed progeny. Loci never observed in the homozygous state and phenotypes on selfed progeny will further help estimate effects of putative deleterious loci.

4. Incorporating all annotations to calculate burden index and integrate into GS models. Throughout Phase II the Jannink Lab and the Buckler Lab will collaborate on introducing these measures of deleteriousness based on sequence data with measures from traditional genomic selection training populations to improve prediction accuracy.

Flowering and Seed Set

Work in Phase I identified photoperiod and temperature conditions that are favorable for flower induction, and plant growth regulators (PGRs) that are promising for the control of flower viability and longevity. Phase I also provided clues on regulatory systems in cassava for which there is the potential that further knowledge might improve ability to control the flowering process in the long term. Further development is needed to produce tools that breeders can use in practice. The overall goal is to develop and implement high-throughput, low-cost, easy methods to synchronize flowering and produce viable seed in cassava crossing nurseries. In Phase II, there will be increased emphasis on implementation in the breeding programs, and accordingly we will transition toward work that primarily takes place in our African breeding nurseries and with additional field trials at CIAT and Embrapa, and with Cornell serving to backstop, as needed, to troubleshoot, and provide informative diagnostic trials in controlled environments. Personnel at breeding programs will be part of the team performing crosses and will interact with the Cornell team to design and conduct beta-tests of methods, and to scale up implementation at crossing nurseries. We will implement this by manipulating photoperiod, temperature and plant growth regulators that we have identified in Phase I.

At CIAT, research will be conducted to combine extension of photoperiod and plant growth regulators to shorten the time to flowering and expand the number of genotypes in which the induction is feasible. A commercial scale system will be developed and used in the production of S_1 families to introgress genetic variability from Latin America into Africa as described above.

SPECIAL INITIATIVE: Biotechnology and Biosafety Education

In Phase I, the Biotechnology and Biosafety Education objective was a special of initiative to foster a positive policy environment for adoption of biotechnology products in Uganda. This objective was implemented by the Uganda Biosciences Information Center (UBIC), a knowledge and information-sharing hub for the National Agricultural Research Organization (NARO). UBIC will leverage its strengths in using the most effective approaches to carry out niche-focused communication and outreach activities in Phase II. The goal in Phase II will be to support the research and commercialization pathways for biotechnology products in Uganda and neighboring select countries. The specific objectives are to: accelerate demand and adoption of biotechnology products plus associated technologies; to support integration of biotechnology and biosafety training in the formal education system.

COMMUNICATIONS & ADVOCACY

The ultimate goal of the Communications and Advocacy team's activities is to improve and facilitate internal communication and integration between the Breeding, Research and Survey divisions. Our activities (in conjunction with those of the project management team) will support the sharing of vital information across the project, and connect project members so resources are leveraged appropriately. Additionally, what we have called "advocacy" activities for Phase II include communications to external audiences, including breeders and research partners in cassava, and more generally in roots, tubers, and banana farmers, end-users of the released cassava varieties, stakeholders (including donors), and media in SSA particularly. These activities will serve to promote acceptance and awareness of NextGen improved varieties (directly supporting Phase II's central efforts to place these varieties in the hands of the farmers), as well as to promote external awareness of the NextGen project and genomic selection's potential to improve genetic gains in cassava, expanding also into communicating cassava's role in ensuring food security in Africa. We also aim to help the public understand the value and importance of current and future public investment in cassava improvement. All of our proposed activities contribute to these guiding focuses, with improvements to methods and means of internal communication feeding directly into increased interaction and information exchange with wider audiences.

NextGen Website: We will upgrade the www.nextgencassava.org website by instituting a more dynamic management system that will encourage access and partner interaction to improve and contribute content. The website will be the gateway to updates, blogs, cassava resources, marketing and training videos, social media, research data, and articles. We will also engage with the Science Media Production Center at Cornell and partners on the ground in SSA to produce short videos about NextGen that will feature: interviews with project researchers, farmers, processors, and end users; videotaped lectures; and researcher-directed training videos that will serve as educational resources for the COPP.

Cassavabase Integration: During Phase II, we will seek to increase the visibility of our partner website (within and without the project), www.cassavabase.org. We will do so by linking prominently to Cassavabase on the Nextgencassava.org site, and by populating the NextGen site with research data as it becomes available. We will also feature Cassavabase in our quarterly newsletter, and include its developers and researchers among our profile features. We will coordinate with Cassavabase web managers to increase the exchanges and traffic between the two sites.

Multimedia Projects: In Phase I, NextGen benefitted from the expertise of IP-CALS's audiovisual media team in producing several YouTube videos that served as an introduction to cassava and the project. We will continue and expand upon these activities in Phase II, producing video interviews with a wide range of project stakeholders, from researchers and processors to farmers and end-users. We will also employ multimedia to widely disseminate project research progress, in the form of recorded lectures/talks; the production of training videos will allow us to easily and practically share methodology with project participants and others.

Social Media Presence**:** Very importantly, we will cultivate a more active presence on social media (Facebook, Twitter, Instagram, YouTube). This will help increase recognition of NextGen achievements and impacts, improve communications by and among project partners, raise the visibility of the project within the broader scientific and development communities, help NextGen scientists be seen as resources, thought leaders and champions within broader scientific communities.

Information and Communication Technology (ICT) Infrastructure**:** Scientific research and outreach at the SSA partner institutions critically need ICT. Activities to improve ICT infrastructure and performance at those institutions include improving and stabilizing Internet availability and bandwidth, reinforcing electrical backup to key ICT function points, providing robust firewalls and bandwidth control for efficient utilization of bandwidth, assisting with ICT equipment acquisition and installation, and training partners on use and maintenance of systems created and installed. In Phase I, NaCRRI and NRCRI were connected to modern microwave link to access national internet backbones to supply broadband to the researchers. Additionally, efforts were undertaken to provide reliable power to key infrastructure. In Phase II, we propose to increase the bandwidth to give researchers and support staff at least 1/10 of what typical US consumers have. Researchers will be able to connect reliably for important conference calls and the exchange of large data sets with partners in the developed world will become easier. Phase II will bring a new major partner in Tanzania up to the same standard. In Phase I, we successfully dealt with rampant power outages in Nigeria by putting in a small set of solar panels and associated control infrastructure. This dramatically improved researchers' ability to work consistently. Phase II will reinforce this approach in Nigeria and replicate it in Uganda and Tanzania where the problems also exist. Once institutions have reliable power and a base-level of internet bandwidth, smart routing will be installed to direct bandwidth to the appropriate scientists. Firewalls will protect them from external threats, like viruses, and from internal abuses of ICT resources.

PROJECT MANAGEMENT

Project management activities include the financial, administrative, legal, and IT services necessary to administer the project. In addition, the Project Management Unit (PMU) will handle all reporting to BMGF and DFID, and will work in conjunction with the Communications & Advocacy team to foster communication among the project partners. The PMU will host an annual meeting among all project participants, and create and disseminate a subsequent report documenting the outcomes of the meeting. The PMU will manage the project's global access and gender components. External guidance will be provided to the project through a reconstituted External Project Advisory Committee (EPAC). Members will be mutually acceptable to BMGF, DFID and Cornell and will serve for the duration of the project. The EPAC will convene semi-annually and will serve in an advisory capacity to BMGF, DFID and Cornell. The EPAC will convene in connection with annual project meetings that include all participating scientists, as well as independently with key project leaders. Meetings will be held quarterly (exploring both in-person and via teleconference opportunities).

In addition to the central administration already in place, we have added a full-time project support specialist position for Phase II (Canaan Boyer, already starting in Y5 of Phase I). This position should serve to add significant logistical and organizational support to the Project Manager, as the project support specialist works very closely with the Project Manager on all aspects of the project. They are responsible for (or deeply involved with): preparing reports and other materials for submission to the foundation, organizing and documenting project meetings (from conference calls with a few project members to the annual meeting), engaging with and providing logistical support to students and visiting scholars/researchers associated with the project, and any other project support tasks as they arise. They also act as part of the Communications & Advocacy team, focusing on coordinating effective internal communications between project partners (at Cornell and abroad) and other project stakeholders to promote an efficient workflow, and serve as a main point of contact within the project.

As part of quality control management of the breeding programs, the project will hire consultants who will be providing quality management at the field-to-laboratory interphases of the program level in order to drive a continuous improvement process. The project already has connections with the private industry by engaging two experienced private sector breeders as EPAC members. We have also devoted a token for a consultant who shall work with the Project Manager and division leads to implement a process mapping and stewardship scheme for all African breeding programs. The consultant, along with the Project Manager and division leads, will constitute the project technical management team.

10. Organizational Capacity

Describe any changes or improvements you plan to make to your organization's capacity to undertake or achieve the outcomes of the proposed investment.

Management costs will be decreased in part through reduced staff time and fewer physical training workshops than proposed in the first phase, instead using videos and appropriate social media for such knowledge or technology transfer. We will set up a system where the

project manager operates from IITA (Ibadan, Nigeria) for more efficient coordination of the project's breeding and management activities, while maintaining an adjunct position at Cornell University. Please see Appendix 2 for more information on project partner organizations.

11. Organizational Fit

What experience does your organization have to implement the proposed work?

Cornell University's committed, focused management of NextGen Cassava Phase I was effective in bringing to the fore the importance of genomics-assisted breeding for cassava, and in promoting a better understanding of the genetics underlying traits that farmers consider important. We propose to continue that efficient and objective effort with NextGen Cassava Phase II.

Cornell University's International Programs of the College of Agriculture and Life Sciences (IP-CALS) is a leader in cutting edge research and international outreach in food and energy systems, the life sciences, environmental sciences, and economic and community vitality. Directed by Ronnie Coffman, IP-CALS has over 50 years of history of developing leaders and improving lives in the world's emerging economies through teaching, research and outreach initiatives that prepare students at the undergraduate and graduate levels for careers in international agriculture and rural development.

Cornell recently combined five sections (formerly departments) related to plant science activities into one School of Integrative Plant Sciences. The NextGen Cassava Research division is comprised of faculty and researchers in the sections of Plant Breeding and Genetics, and Soil & Crop Sciences. The Plant Breeding and Genetics section is dedicated to the genetic improvement of crop plants for the benefit of society through the development of novel breeding methodologies, the discovery and deployment of economically important genes as genetic stocks, germplasm, and varieties, and the training of the next generation of plant breeders. The section has been consistently ranked as the premier program of its kind in the nation by the National Research Council. The Soil & Crop Sciences section is dedicated to the development of sustainable agricultural systems of food production for an increasing world population, and responding to the demands of climate change. In 2017, Cornell was ranked second highest in rankings of the best global university for plant and animal sciences by the US News & World Report, and continues to be a leader in these fields.

Please see Appendix 2 for more information on project partner organizations.

12. Beneficiaries

Who would benefit from this investment?

Cassava farmers and end-users in Africa's cassava-consuming areas (particularly in Nigeria, Uganda and Tanzania) will benefit from availability of high-yielding varieties that have traits appropriate to the preferences of their countries, and are resistant to major diseases. All cassava breeders will benefit from the use of tools that ensure greater genetic gain, including the implementation of the open-source Cassavabase with its decision support tools. NARS, IITA, CIAT and other partner scientists and administrators will gain from the institutional and human capacity building efforts. The Community of Practice Partnerships will be an initial platform for out-scaling the possibilities for increasing genetic gain that the project can offer to non-direct partners.

13. Critical Relationships

Describe any critical relationships with other partners or projects that may influence this work (or that this work may influence).

For Phase II, NextGen Cassava has increased the number of partners, most of whom have already been working together, either in Phase I or in other complementary cassava investments in Africa. This has raised the stakes for the importance of managing these critical relationships. Two of our best and most relevant examples of effective partnerships are the breeding pipelines and screening platforms for CBSD managed at NaCRRI in Uganda, and the breeding pipeline and synergy between Nigeria's NRCRI and IITA in using genomic tools to develop varieties that suit country target value chains of CMD resistance, gari, and high dry matter. Others include TARI, Tanzania, that joined the project mid-way and provides more screening platforms for CBSD. IITA in East Africa has capacity to provide germplasm, technical backstopping abilities, and mentorship for both Ugandan and Tanzanian NARS. In South America, Embrapa and CIAT provide additional experience and genetic resources that can help in enriching a cassava pan-genome sequence. Cornell has a team of genomics scientists and quantitative geneticists that play an important role in strengthening the new genomics-assisted breeding carried out by the African programs. Cassavabase, developed at BTI, is becoming the integral meeting point of all the breeding programs that would utilize the cassava-variety development models pioneered by the project. In the past, we have received technical guidance from an External Project Advisory Committee (EPAC). We expect this project to continue to draw on these critical partnerships while establishing new linkages as needed, especially as the African breeding programs emerge as stronger leaders in cassava breeding and project management. We will continue to rely on formal subcontracts to manage these critical relationships.

14. Sustainability

Describe the vision of the long-term sustainability of this project beyond the proposed time frame and funding with consideration to economic/financial, organizational, or behavioral factors.

NextGen Cassava will address sustainability issues with a multi-pronged approach to address financial challenges, organizational change and programmatic efficiency. Sustainability remains a cross-cutting theme across all the divisions.

A primary goal of NextGen Cassava is to simulate the setting of a seed company that can be referred to as Cassava Inc., with an aim of becoming less reliant on ever-reducing donor funding. The different national breeding programs participating in NextGen Cassava have historically been operating in a state of deprivation from public sources of funding. We hope this project will transform the mindset of the managers of these programs, and at a higher level, the mindset of local policy makers. The Communications & Advocacy team will produce messaging that will extend to the reach of policy makers and fiscal planning groups in the respective countries, with messaging on project impacts in Africa. The IITA is not immune from the issue of dwindling resources for cassava project execution due to competition from various initiatives from multiple sources. The approach of the NextGen Cassava project to link the CG centers in Africa and South America with African cassava breeding programs provides a sustainable platform for cross-fertilization of ideas, germplasm exchange, collaboration and incentives for the delivery of high-yielding cassava varieties that meet end-users' needs.

From a programmatic level, each division in the project framework is designed with sustainability in mind. Activities in the Breeding Division are aimed at ensuring that processes are optimized holistically in each of the breeding programs to sustainably deliver improved varieties of cassava needed by farmers. The integration of new tools, new germplasm and better processes in the system will endure as the community grows through the strengthening of the COPP partnerships. The Survey Division's entire purpose is to promote the sustainability of the project for the future, as the division's goal of identifying variety ideotypes that meet end-users' needs aims to ensure adoption and propagation of NextGen Cassava's improved varieties.

15. Measurement and Evaluation

Describe your plan for monitoring and evaluation of the outputs and outcomes you identify in the Results Framework & Tracker that accompanies your Proposal Narrative. Specifically address:

1. The learning/evaluation questions for this investment and how you plan to answer them through monitoring and/or evaluation;
2. The resources (financial, technical, human) you need to ensure high quality monitoring and/or evaluation data; and
3. If you are planning a formal evaluation, describe when it will be conducted during the grant, who will conduct it (external/third party or not), the methodology you will consider, and how the main evaluation audiences will use the findings.

See the foundation's evaluation policy for reference.

The project manager is responsible for ensuring that project implementation is achieved. Each division coordinator will work with the project manager to monitor and evaluate the proposed project outputs and outcomes of their division. Additionally, annual site visits will be made by the project manager or other relevant partners to monitor progress. In concordance with the BMGF and DFID reporting schedules, checks will be made against the proposed timeline for targets and outputs on a regular basis, and adjusted/reviewed as necessary. Facilitated regular communication among divisions and project partners, as well as the annual meeting of all project participants and the resulting report, will provide further avenues for monitoring and evaluation of project progress. In Phase I, we had the external mid-term review panel that greatly sharpened the future focus of the project. Together with our program officer, we will hold a similar mid-term review in Phase II to make sure we are on track to deliver our projections.