

WP4 Synthesis for Period 1

Activities Conducted, Key Research Findings & Perspectives

Main Author(s): CHAIR, Hana, CIRAD, France

Contributor(s):

- KOUAKOU, Michel Amani, CNRA, Côte d'Ivoire
- KAWUKI, Robert, NaCRRI, Nigeria
- EGESI, Chiedozi, NRCRI, Nigeria
- OBIDIEGWU, Jude, NRCRI, Nigeria
- MENDES, Thiago, CIP, Kenya
- UWIMANA, Brigitte, IITA, Uganda

This synthesis refers to the following teams

	Partner Institution(s)	Country	RTB crop(s) of interest for RTBfoods	Names of people involved in the team for this WP
Team 1	CIAT	Colombia	Cassava	Hernan Ceballos
Team 2	NaCRRI	Uganda	Cassava	Robert Kawuki; Esuma Williams; Michael Kanaabi; Emphraim Nuwamanya; Enock Wembabazi
Team 3	IITA	Nigeria	Cassava	Peter Kulakow ; Ismail Rabbi
Team 4	NRCRI	Nigeria	Cassava	Chiedozi Egese
Team 5	IITA	Nigeria	Yam	Asrat Amale
Team 6	NRCRI	Nigeria	Yam	Jude Obidiegwu
Team 7	CNRA	Côte d'Ivoire	Yam	Michel Amani Kouakou ; Ehounou Adou
Team 8	CIRAD/INRA	France	Yam	Fabien Cormier ; Gemma Arnau ; Hana Chair
Team 9	CIP-SSA	Uganda	Sweetpotato	Robert Mwanga ; Reuben Ssali
Team 10	CIP	Uganda	Potato	Thiago Mendes
Team 11	IITA	Uganda	Matooke	Brigitte Uwimana

Abstract

of the full document summarizing each section (NB: This section will be copied & pasted in the Annual Report delivered to BMGF). (2 pages)

The goals of WP4, as written in the proposal, are to assess the variability for quality traits that exist in current breeding populations, to support development of complementary populations when necessary, to apply high-throughput phenotyping protocols (HTPP) in order to determine the genetics of the trait and the possibilities for marker-assisted selection and to identify and rank the most promising accessions already available to be used as released varieties and/or progenitors. As described in the narrative, the inputs of WP1, 2 and 3 are strategic for breeders and geneticists to properly define the heritability of the quality traits and for the development of sensible breeding strategies to improve them. In fact, little knowledge is available regarding the heritability of roots, tubers and banana quality traits valued by processors and end-users.

This first year, the different teams involved in the WP4 worked on the identification of the populations to be used for the implementation of HTPP. These teams are already involved in different projects and have several populations (GS, biparental, GWAS, etc.). The challenge was to identify the most suitable for RTBfoods *ie* the one encompassing enough variability for the targeted product profile to be used for the implementation of the HTPP and the genetic architecture dissection. The teams have also already started working on the product quality, since it is part of most of on-going projects (exp. Africayam, NextGen, SASHA, etc.), using the common methods of phenotyping. Depending on the equipment available, the proximity of food quality laboratory and the knowledge, the progress of the teams is not the same.

Each team has written a state of the art on the breeding for quality for the crop it is working on. It was the opportunity to review what has been done so far. The fact that each team reported activities, which has not been published elsewhere before, was a way to inform each other in order to start sharing approaches and methods. In this document, gap analyses were identified for each crop. It was one of the objectives of the state of knowledge document. Some gaps are shared while others are not. RTBfoods should address this lack of knowledge and try as much as possible to fill up the gaps. We expect at the end of the project to increase our knowledge on the breeding for quality traits by identifying the key traits involved in quality, their heritability and the genomic regions underlying these traits.

We have also built a tracker to follow up our work progress. So, first we reported the context (institute, product profile, persons involved), then the origin of the population(s) which will be made available for RTBfoods activities (developed within the project or within on-going bilateral project) and the traits related to quality measured this year. This tracker will be complemented each year in order to summarize our activities, showing the synergies and the progress. It is a tool to monitor the activities and to keep all the partners and other WPs (1,2,3,5 and 6) informed on on-going breeding activities. It will also be a good tool for quickly identifying threats or weaknesses, so that we can deal with them early.

From a team coordination perspective, as WP leader, Hana Chair visited Uganda, Nigeria and Guadeloupe. It was the opportunity to meet all the collaborators working on cassava, sweetpotato and Matooke in Uganda and cassava and yam in Nigeria. The objective was to know more precisely the activities carried out by the different partners within the other projects they are already involved in. Hana took also time to visit the Food Technology Laboratories, in these countries, to get a better idea of the facilities available for the breeders. During these visits, the objectives of WP4 for each crop were discussed in each country. We have thus identified the populations that will be used in the RTBfoods project, while avoiding any duplication with the other on-going projects. To complement this work, Hana plans to visit Côte d'Ivoire and Colombia in 2019. Intra-WP4 coordination challenges are of two types. First, the limited of Availability of breeders involved in partner breeding programs had an impact on their reactivity and promptness. Besides, WP4 partners felt it difficult to identify populations to be used in the RTBfoods project without compromising previous commitments in partner breeding programs nor duplicating activities. Communication with other WPs could and should be reinforced especially because WP4 breeders are keen to get feedback on their strategy and their varieties as early as possible. To get back on good tracks, a more efficient communication strategy should be defined for Period 2 during the next RTBfoods annual meeting between WP4 breeders and other WP partners.

In terms of perspectives for Period 2 and to continue to contribute to the output 2.2.1 concerning the identification of the genetic architecture of users' preferred quality traits, field trials will be repeated in 2019 in the different identified environments for GxE studies. The traits will be adjusted, after the

annual meeting at Abuja, following the discussion with WP2, 3 and other colleagues from WP4 in order to measure the more relevant traits before the HTPP method is made available. Data storage and management will be in the agenda of the annual meeting in order to define the best practices.

WP4 Results-Tracker: Activities & Milestones achieved

Output 2.1.1: *Genetic architecture of users' preferred quality traits for VUE improvement in RTB breeding programs identified*

Activities conducted	Deliverables
State of Art on breeding populations and breeding for quality	M.1.1- State of Art on previous works on quality traits informing breeding (for each targeted RTB crop)
Unravelling genetic architecture of traits for VUE improvement in RTB breeding programs	M.2.1- Breeding population tracker in Period 1

Output 2.1.1 Indicators	Targets / Milestones		
	Planned for Period 1	Achieved	Variance & Brief Explanation
Nb of reports on correlation between traits, heritability and genetic gain per crop and product profile	1	1 document on State of Art with chapters per crop and per institute and a WP4 activities Tracker developed	Both documents were produced.

- *Key findings from the State of Art (Del. M.1.1), disaggregated by crops: gaps identified and lessons learnt from previous work on breeding for quality for the 5 RTB crops.*

In this document, for each crop in each country, the breeders described the knowledge acquired in terms of breeding for quality based on published papers, their published or unpublished works and finally the gap analysis. To summarize:

Four institutes work on **cassava**: CIAT (Colombia), NRCRI and IITA (Nigeria) and NaCRRI (Uganda). These institutes are involved in several projects including NextGen and HarvestPlus. Through their involvement in these projects, they have already started working on breeding for quality. Through the State of Knowledge document, we can retain that:

In Colombia, the target product profile is boiled cassava. At CIAT, a lot of work has been done to understand the traits important for consumers. Trials have been conducted to assess them and heritability studies have been conducted. So, the DMC is considered as a key trait for boiled cassava quality. When DMC is low, the uncooked root looks “watery” and, after boiling, it assumes a “glassy” appearance (tends to be translucent and its texture is hard to penetrate). A reduction in the level of DMC (and a parallel increase in sugar content) results in glassiness in the boiled root, which is highly undesirable. Harvesting at the end of the dry season increases heritability of DMC. Similarly, the reliability of phenotypic evaluations, after cassava reinitiates its growth with the arrival of the rains, decreases. HCN content is also an important target trait. The cassava-breeding program at CIAT has established a threshold of 200 ppm in the selection for genotypes suitable for the table consumption

markets. Perhaps the most relevant trait to identify cassava roots suitable for table consumption (in addition to low cyanogenic potential) is that they soften upon boiling. The biochemical basis for softening in response to boiling or fermentation have not yet been established. The degree of association between these two response variables has not been determined either. What is clear is that boiling results in a gradual and consistent reduction of starch and cyanogenic glucosides in the root. Cooking time and texture profiles can be linked to root physico-chemical and starch gelatinization properties

In Uganda, cassava marked its 158th anniversary since its introduction in 2018. For NaCRRI, boiled cassava is the main product profile targeted within RTBfoods project. As cassava virus incidences and severities decreased owing to breeding interventions, farmers reluctantly cultivated these improved varieties, and resorted back to their locally adapted varieties, for which, they have had a long historic association. This was partly attributed to the notion that many of the released varieties lacked desirable root quality attributes (taste, mealiness, texture and aroma) as compared to locally adapted varieties. At NaCRRI such as at CIAT, root dry matter (DMC) is recorded for all breeding trials at harvest (12 months) using two methods; specific gravity or the oven dry method. Total carotenoid content is analysed both on fresh and processed samples. Cyanide content is determined using the method of Howard et al., 1994. Finally, the softness of cooked roots is assessed routinely.

In Nigeria, current emphasis is on gari and fufu as the most widely consumed in Nigeria. Gari is most preferred because of its convenience, long shelf life and it is easy to eat either as a snack or a meal. The priority is genetic improvement of cassava varieties for identified quality traits based on diverse end-user preferences. These traits of preference include root dry matter content (relevant for root mealiness), product consistency (for gari and fufu) associated with cassava starch content, colour (especially with respect to beta-carotene content), aroma and taste. Biofortified cassava with enhanced levels of beta-carotene has been cultivated by Nigerian farmers since 2012 and it has become apparent that scaling out will be more successful if the biofortified varieties have higher dry matter and starch contents. Genomic dissection of the genes controlling both beta-carotene and dry matter indicated that they are co-located on at least chromosome 1. Genetic methods to manipulate this in a pleiotropic manner might be helpful.

Four institutes work on **yam**: IITA and NRCRI (Nigeria), CNRA (Côte d'Ivoire) and CIRAD (France). These institutes are also involved in several projects including Africayam. They are already working on breeding for quality. Unlike cassava, two main yam species are concerned. Through the State of Knowledge document, we can retain that:

In Nigeria at IITA, the yam quality phenotyping routinely used in yam breeding programs includes fresh tuber physical quality assessment, and physico-chemical and functional properties of fresh tuber for predicting boiled yam and pounded yam food quality. These included traits such as colour of tuber flesh, tuber oxidation, tuber shape, dry matter, peel loss, starch yield, pasting property of starch, flour yield, and other functional properties such as ash content, total protein, fat, amylose and sugar. In addition, tuber micronutrient density, specifically for iron, zinc, total carotenoids, ascorbic acid (vitamin C), phytate, and tannin content have been assessed in different yam germplasms. Many populations have been produced and varieties are at different stage of evaluation.

In Nigeria, the objective, at NRCRI, of the genetic improvement component has been to develop and disseminate improved yam genotypes with high and stable yield of tubers with good storage and food qualities suited to the relevant cropping systems. Yam breeding has resulted to 21 varietal releases and more recently official registration of five landraces. At the early stage of breeding cycles, NRCRI

breeders characterize and advance clones based on yield, response to diseases and pest. Food quality traits often considered alongside the agronomic traits include tuber flesh colour, physico-chemical factors in fresh yam tubers (granule morphology; starch granule size, histological structure of the cells), physico-chemical composition of yam starch (amylose/ amylopectin ratio, swelling, water binding capacity), pasting characteristics of fresh yam tubers, as well as calcium, phosphorus and cellulose contents of yam tubers that are indicators of textural quality in 'pounded yam. Starch accounts for 80% (on dry weight basis) of the yam tuber. Based on breeders experiences and literature, it has been reported that granule size, swelling power, amylose and water binding capacity of yam starch can be indicators of textural quality in "pounded yam". Investigating the physico chemical properties of yam flour, starch and also non-starchy polysaccharides (lignin, pectin, cellulose, hemicelluloses) in yam could also give insight to quality factors which can predict the quality of food products such as boiled yam, thus serving as screening tools to breed for these specific traits in order to produce tubers with qualities that will be acceptable by the end users (farmers, consumers, processors).

In Côte d'Ivoire, the main target product profiles at CNRA are boiled and pounded yam. Here again, a lot of work has been done to develop varieties and conduct participatory evaluation. Quality traits studied are DMC, yam tubers shapes, flesh color, flesh oxydation and the quality of the boiled and pounded yam assessed by consumers. Physico-chemical studies will link that traits with the quality of the boiled and pounded yam.

In France, populations developed by CIRAD breeders are under evaluation for quality. The main criteria linked to quality applied during the selection process are related to the tuber form, the flesh browning and colour and are visually assessed. Several "high-throughput" phenotyping methods are under development to measure other traits related to quality. These methods are mainly based on image analysis and will allow the phenotyping of large populations. For example, tuber flesh browning and colour are now automatically assessed using repeated images of sliced tubers.

Concerning the potato, CIP has adopted standard procedures for determining: i) specific gravity and dry matter content, ii) texture and flavour components of cooking quality, iii) storage behaviour, iv) chipping and French-frying performance, v) oil content, and vi) contents of undesirable secondary products such as glycoalkaloids. However, quality traits have not been a target on CIP's breeding population. It is expected that through the project there will be greater genetic gain combining new tools (HTTP, GWAS, GWS) accessing in earlier breeding stages, characteristics such as sugar profiles, texture profile (dry matter, cooking time, cell wall, cooking time), nutritional and antinutritional (glycoalkaloid) and sensorial (aroma, taste).

In Uganda, CIP has been involved for many years on different sweetpotato projects (SASHA, HarvestPlus, GT4SP, etc.). The traits in preferred sweetpotato are high yield, resistance to common pests and diseases, early or medium maturity with good in-ground storability, suitable for piecemeal harvest with no fibers, and of good marketability, medium sweetness, and powdery texture. Since, many varieties have been released. These populations are likely to have the diversity of user preference traits of interest for the targeted product profiles. NIRS is used for quality traits – beta-carotene, minerals and sugars at all the sweetpotato support platforms in SSA (Ghana, Mozambique and Uganda).

In Uganda, cooking banana cultivars are locally known as 'matooke' and serve as a staple food to a large part of the population. IITA has been working on this crop for many years. However, the "matookeness" is complex and little is known about the traits underlying this product profile. IITA in

collaboration with NARL is conducting sensory analysis. Genomic selection panel will be used to understand the traits linked to matookiness and to develop a HTPP method.

In this State of Knowledge document, breeders have identified the gap analysis. They are mainly related to the traits underlying the product profile and the need for high throughput phenotyping method.

- The populations which will be used within RTBfoods and the traits targeted are summarized below per crop and per institute:

Cassava Breeding program-Hernan Ceballos-CIAT-Colombia

Target Cassava Populations: One of the salient features of the trait CIAT focuses on (quality of boiled roots) is the large impact of environmental factors affecting the trait. It is only after many years of evaluation in different conditions that a given clone would be generally accepted to produce good quality boiled roots. CIAT, therefore, has screened a large data set in search of a group of clones that can reliably be used as source of good cooking quality as follows. Good cooking quality (white parenchyma): CM 2600-2; CM 2766-5; CM 5253-1; CM 7436-7; SM 1127-8; MCOL 1505M; MCOL 2066; MCOL 2246; MCR 138; MGUA 24; MMAL 3; MMEX 2; MPAN 70; MPAN 139; MPAR 57; MPAR 98; MPER 183; MPER 496; MVEN 77; MVEN 208; MVEN 218; MCUB 74. Good cooking quality (yellow parenchyma): GM 3674-41; GM 8373-46; GM 8391-4; GM 8413-1; SM 3759-36. CIAT also needed a set of clones known to have very poor cooking quality and selected the following genotypes: MBRA 318; MBRA 325; MBRA 512; MCOL 1722; MCOL 1910; MCUB 46; MVEN 25. There will be two main activities conducted with these genotypes: 1) Make crosses to generate biparental populations that will offer wide segregation for the trait of interest; and 2) Grow these materials in different locations to confirm that indeed they offer contrasting features.

Target Cassava Traits: The ultimate objective is to understand the factors affecting good quality traits when cassava roots are boiled. Some factors are already well known (e.g. cyanogenic potential should be lower than 100 ppm), but other have remained elusive for many decades. CIAT will select 2-3 biparental populations (100 to 200 genotypes per full-sib family) and evaluate them initially in one location but as soon as possible in 3-5 locations. Roots from each genotype, grown in different locations will be boiled to assess cooking quality, processed through NIRs to obtain spectra (hopefully a high throughput phenotyping protocol would be developed), while sections of these roots will be used for other traits (e.g. dry matter and sugar contents, proportion of amylose in the starch, different polysaccharides, etc.). The main purpose for these analyses is to gain a better understanding of the heritability of the main trait (cooking quality of boiled roots), develop high-throughput protocols for efficient selection for this trait and dissect the different factors affecting it.

Cassava Breeding program-Chiedozie Egesi-NRCRI-Nigeria

Target Cassava Populations: NRCRI has different cassava populations and/or clones at different evaluation stages. It is these populations and/or trials that we shall use to constitute the target populations for WP 4. First, for 2018, our target population was the NextGen mother trials and C1 population in advanced yield trials that comprised of ~200 clones. These trials will be harvested at different times corresponding to their planting schedules starting from June 2019. Roots will be sampled and taken to the laboratory for trait analyses.

Target Cassava Traits: The traits to be targeted includes “must-have-traits” and/or “value-added traits”. The “must-have-traits” are those that will entail optimal field agronomic performance and resilience to biotic and abiotic stresses. We will also pay attention to the “value-added traits” root quality and end-use characteristics. We will target dry matter content, starch content, gari and fufu yield, etc. and these would be done in a participatory manner.

Cassava Breeding program-Robert Kawuki-NaCRRI-Uganda

Target Cassava Populations: At NaCRRI, we have different cassava populations and/or clones at different evaluation stages. It is these populations and/or trials that we shall use to constitute the target populations for WP 4. First, for 2018, our target population was the NextGen C₁ population that comprised of ~730 clones established at Namulonge (NaCRRI). This trial was harvested in September 2018, roots sampled, waxed and shipped to the laboratory for trait analyses. Second, we specifically established a WP 4 trial comprising of 73 clones (52 elite and 21 local). This trial was established in August 2018 at two sites: Namulonge (central region) and Serere (eastern region), and will be due for harvesting in August 2019. Third, if resources permit, we shall also target a portion (~400 clones) of the NextGen C₂ cassava seedling population that was established at Namulonge in October 2018; this trial will be due for harvesting in October 2019.

Target Cassava Traits: Our desire is to have cassava varieties characterized by “*must-have-traits*” and/or “*value-added traits*”. The “*must-have-traits*” ensure that cassava optimally yields despite the prevailing pests, diseases and abiotic stresses in farmers’ fields. Of keen interest for WP 4 is to focus on the “*value-added traits*” most of which are within realms of root quality and use. Accordingly, our immediate target traits for 2018 are: 1) root dry matter content; 2) softness; and 3) cyanogenic potential. For 2019, our target traits will be: 1) root dry matter content; 2) beta-carotene content; 3) softness; 4) cyanogenic potential; and 5) starch content. Beyond 2019, we may add fibre content to these aforementioned root quality traits. Prioritization of this trait list will be informed by information collected from end-user surveys conducted under WP1.

Yam breeding program-Asrat Amal-IITA-Nigeria

Target Yam Populations: The yam breeding team at IITA has developed different populations for genetic studies and selection in two dominantly grown species of yams in West Africa: *D. rotundata* and *D. alata*. The populations are structured as bi-parental mapping population and diversity panels. The populations are genotyped with different genotyping platforms and currently under field phenotyping for agronomic and biotic stress traits. From these populations, two bi-parental mapping populations (one for white yam and one for water yam) and one diversity panel of water yam are nominated to constitute the target population for WP4. The bi-parental populations are TDr1401 constituting 151 white yam clones and TDa1402 constituting 207 water yam clones. The diversity panel includes 100 water yam accessions representing genebank collections and advanced breeding lines. In 2018, the bi-parental mapping populations were grown at one site in Nigeria while the diversity panels were planted at three locations. The trials will be harvested in January 2019 and will be replanted in April 2019 for more detail phenotyping for quality traits under WP4.

Target Yam Traits: The phenotyping efforts with these populations include agronomic, biotic stress and quality traits. Traits to phenotype within WP4 include physicochemical and functional properties for predicting major food quality of fresh yams. The immediate targets for 2018 are tuber dry matter content, starch content, and tuber oxidation. For 2019 and beyond, our focus will be on tuber flesh color, NIRS scan for tuber quality traits, boiled tuber quality (texture, taste, color, after cooking

hardening and darkening), pounded tuber quality (color, texture, stretchability, aroma, consistency), and yam flour quality (% dry matter, color, peel loss %).

Yam breeding program- Jude Obidiegwu -NRCRI-Nigeria

Target yam populations: NRCRI is nominating one (1) breeding population (TDr 1620). This bi-parental population comprises of 128 individuals of *D. rotundata*. This population in the last two years has undergone some sort of multiplication so as to regenerate sizeable tubers for phenotyping of our numerous routine post-harvest quality traits within our breeding pipeline. These materials will be planted out in 2019 farming season. The diversity panel for WP2 will be nominated from advanced and early breeding lines consisting of 10 individuals. Three (3) Nominations will be made from advanced breeding materials to actualise the target of WP5.

Target yam traits: Harvesting of 2018 yam field trials was just recently concluded. The dry matter and tuber flesh colour of this population is ongoing. In 2019 we envisage phenotyping tuber flesh oxidation potential of this population. Most critical is the post boiling qualities for boiled yam including texture, aroma, colour, cooking time and rate of hardening after cooking. Target for pounded yams alongside others earlier mentioned will include stickiness, mouldability and stretchability.

Yam breeding program-Michel Amani Kouakou-CNRA-Côte d'Ivoire

Target yam populations: CNRA has two kinds of populations for yam: 1- Panel of diversity consisting of more than 419 accessions of *D. alata* and *D. rotundata*; 214 accessions of *D. alata* and 205 accessions of *D. rotundata*. All these accessions are characterized for dry pounded yam and boiled yam quality. 2- Breeding populations deriving from crosses within each species. There are 4 generations of populations. For *D. alata*: 177 hybrids at clonal evaluation, 183 hybrids at preliminary yield evaluation, and 6 hybrids are tested for release. For *D. rotundata* 568 hybrids at clonal evaluation and 762 hybrids at preliminary yield evaluation stages.

Target yam traits: Boiled and pounded yam are measured by the lumpiness, the springiness, the looseness, the sweetness, the stickiness, the smoothness, the brown spot, firmness, elasticity. Other traits on the yam tuber are: yam tubers shapes, flesh color, fresh flesh oxidation, brown spot in the flesh, cooking time, aroma, acceptability, flavor and dry matter content of the tuber.

Yam breeding program-Fabien Cormier-CIRAD-France

Target yam populations: CIRAD is working on two types of populations genotyped by GBS: a diversity panel developed for the project and two biparental populations already developed within AfricaYam project. The diversity panel is replicated in three different environments to allow research on GxE interactions. In each environment, each accession is replicated 20 times. In 2018, this panel of 43 accessions has been developed to maintain statistical power while a sample of CIRAD and INRA collection is studied (independent and complementary accession). During the project, this panel will increase to a final one of around 70 accessions. The biparental populations are composed of 130 progenies for population A (74F × Kabusa) and 200 from population B (74F × 14M). They are actually in field (two complete block of 9 replicates).

Target yam traits: For the diversity panel the targeted traits are: tuber weight, tuber shape, browning and flesh colour, dry matter, starch and protein content, starch grain size, amylose/amylopectine ratio and pounded ability. For the biparental populations, within the AfricaYam project, the targeted traits

are tuber weight, shape and size and physico-chemical parameters estimated through NIRS. Within the RTBfoods project, they are: tuber flesh browning (started) and other physico-chemical parameters (e.g. amylose/amylopectine ratio).

Sweetpotato breeding program-Robert Mwanga and Reuben Ssali-CIP-Uganda

Target Sweetpotato Populations: The sweetpotato food product profile selected for the study under WP4 includes: a) boiled sweetpotato – which is the commonest form in which sweetpotato is consumed in most countries in SSA b) puree (mashed sweetpotato) – for producing bakery and other products is increasing in importance. c) and fried sweetpotato. Overall, CIP-Uganda has the following sweetpotato specific breeding objectives: (1) continue to improve sweetpotato population development in sub-Saharan Africa (SSA), linked with participatory varietal selection at the national level; (2) breed for key biotic constraints in Africa; in East Africa the focus is on sweetpotato virus disease (SPVD) resistance and weevil resistance; and (3) breed quality types of sweetpotato for urban markets. The populations used for the three specific objectives at the East and Central Africa Sweetpotato Support Platform are: 1) 80 Population Uganda B x 50 Population Uganda A (130 genotypes/parents); 2) 80 x 50 diallel population for SPVD resistance (diallel progeny, over 6,000 genotypes); 3) 8 SPVD resistant x 6 SPVD resistant population (diallel progeny, over 2,000 genotypes); 4) Beauregard x Tanzania (BxT) population (317 genotypes) and 5) Mwanga diversity panel (MDP) of 1886 genotypes (from 8 x 8 population Uganda B x population Uganda A parents). Under WP4, the BxT and the MDP populations will be used [i.e. 4) and 5) above].

Target Sweetpotato traits: Within RTBfoods, the targeted traits are dry matter content, quality traits related to boiled and mashed sweetpotato, beta-carotene, minerals and sugars. However, SPVD resistance, Alternaria blight and weevil damage are major traits in sweetpotato breeding. The traits related to yield are also of importance (storage root yield, foliage yield, biomass yield, commercial root yield, percentage of marketable roots, harvest index, number of roots per plant, yield per plant, establishment index, and number of commercial roots per plant).

Potato breeding program-Thiago Mendes-CIP-Uganda

Target Potato Populations: The genetic population is comprised of most groups of CIP's advanced tetraploid populations B3, B1 and LTVR and is a dynamic collection of bred clones previously subject to analysis of structure and successfully used for GWAS. Population B is under improvement for high levels of horizontal resistance to late blight along with economically important traits such as tuber yield, quality for table and industry, adaptation to wide environments and tolerances to other biotic/abiotic stresses. The LTVR population is characterized mainly for its resistance to the most important virus diseases (PVY, PVX and PLRV) of potato, early tuberization in short days, mid-maturity under long days and adaptation to warm, arid environments. A group CIP's advanced tetraploid clones was introduced in Uganda (Oct/2018) as potato minituber and multiplication for further testing in the field has started. All the activities have been planned and executed in collaboration of our local partners on potato - National Agricultural Research Organisation (NARO). The most popular varieties for farms, industry and consumers (Kabele red, Wanale, Singo, Cruza, Victoria, Rwangume, Bumbamagara) have also be considered for further field evaluation. In 2019 a trial will be established in the highland area of South Western Uganda.

Target Potato traits: Fried and boiled are the target product profiles on potato. It's been agreed with colleagues that the traits to start working with will be: sugar profiles, texture profile (dry after, cooking time, cell wall, cooking time), nutritional and antinutritional (glycoalkaloid) and sensory analysis. A group of 20 clones have been already delivered to WP2 for the first round of quality assessment in the laboratory and second round of materials will be delivered in Feb/19 for a second wave of assessment. Agronomical evaluation will be done in field, as yield and the level of resistance to the main diseases (Late blight and Virus). It's expected that the results from WP1 in 2019, will help to better define the traits that have to be considered.

Matooke breeding program- Brigitte Uwimana- IITA-Uganda

Target banana “matooke” populations: A number of mapping populations have been developed by IITA together with BBB project partners. However, these populations are from diploid parents, with no “matooke” background. Moreover, their progenies are full of seeds and have no pulp. Consequently, they are not qualified to be used to the quality of “matooke”. One population in particular is better suited for RTBfoods WP4. This is the Training Population (TP), used to develop predictive models for yield and other agronomic traits in “matooke” breeding. The population comprises almost all the breeding material used by IITA and NARO for “matooke” improvement. It is made of 3x, 4x and 2x parents and their hybrids, making up 320 genotypes. However, some of the hybrids have bunches without pulp (something common in banana breeding). Therefore, only genotypes with bunch containing pulp will be used under WP4. These are about 260 lines. The population is planted in Sendusu, IITA breeding station and in Mbarara, Western Uganda. It has been phenotyped for agronomic traits, and genotyped using the GBS platform, resulting in about 11,000 SNPs scored bi-allelically, and 5,300 SNPs scored by allelic dosage (taking into account the ploidy of each line).

Target “matooke” traits: At this phase of the project, it is not clear yet which traits will be targeted for “matooke” quality. In the breeding programme, “matooke” quality of the hybrids is evaluated in acceptability evaluation, looking at pulp colour, aroma, taste, mouthfeel and general acceptability. The process is tedious, involving a lot of logistics, people, and it is not accurate. We are waiting for the results of WP1 to fine-tune the traits linked to “matooke” quality. Meanwhile, WP2 to convert the qualitative traits into quantitatively lab-based measurable traits. We hope that WP3 will come up with a high throughput phenotyping method, which can be used in remote areas, given that banana trials are conducted far from the laboratory, and bananas are harvested around the year, few times at a time, making it difficult to transport the bunches to the laboratory for analysis.

Team coordination

- *Challenges faced in coordination of WP4 teams & Strategies to be reinforced/developed by WP4 coordination team for Risk mitigation?*

This first year, the major challenge was to know more precisely the activities carried out by the different partners within the different projects they are already involved in. In WP4, the breeding programs on the five crops targeted by the project are carried out by 11 different teams. To get informed, skype meetings were organized. In addition, as WP4 coordinator, Hana Chair visited Uganda, Nigeria and Guadeloupe. It was the opportunity to meet all the collaborators working on cassava, sweetpotato and matooke in Uganda and cassava and yam in Nigeria. Hana also visited the Food Technology Laboratories, in these countries, to get better idea of the facilities available for the breeders. To complement this, she plans to visit Côte d'Ivoire and Colombia in 2019.

The second challenge is the fact that most of the partners are already engaged in bilateral projects and have included breeding for quality as a deliverable of their projects. It took time for the partners to identify the populations to be used in the RTBfoods project without compromising their commitments in their current projects or duplicating their activities. Through visits to partners and discussions, populations have been identified. The traits that will be measured in the bilateral projects and those to be developed in the RTBfoods project have been separated but are no less complementary. We must remain vigilant so that no confusion will come later.

Finally, since the breeders are the next users of deliverables and it is their responsibility to produce varieties that meet the users' needs, they want to be more informed and as much as possible involved in the other WPs in progress. They are one of the users to be considered in WP1. They are ready to provide varieties to be used in WP2 and WP3 and are keen to get feedback on their strategy and their varieties. At the next annual meeting, we plan to organise a workshop with the different WP leaders, so that the breeders can discuss with them and define an efficient communication strategy.

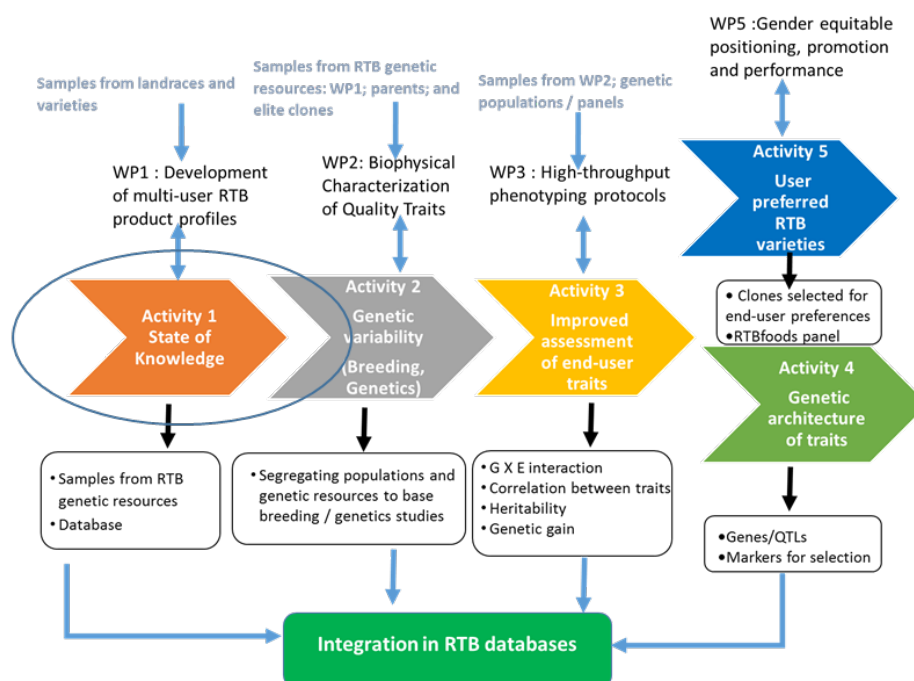
Cross-WP Coordination & Collaboration

- *Fill-in the table below with a brief description or bullet-point lists of interactions with other WPs (successful ones & gaps) and propositions for risk mitigation.*

	Successful Interactions/Coordination with other WPs (specific actions concerned, frequency, tool sharing)	Gaps in Interactions/Coordination with other WPs: What is needed from other WPs? (NR = not relevant)	Risk mitigation: How to Improve (specific actions to be taken, frequency, tool sharing?)
WP1	We had very little interaction with WP1. Just a skype meeting and some e-mail exchanges.	WP1 in building an important database on farmers' varieties (location, use, culinary properties, etc.). This database is very valuable for genetic studies under the project and beyond it. Indeed, it can be used for diversity studies as well as the identification for candidate genes, GWAS panels or progenitors for breeding programs. Better communication with this WP is essential. It will prevent duplicating the work and consolidate information for RTBfoods, other bilateral projects and future research questions.	More frequent meetings with WP1 and WP4 partners that would result in: <ul style="list-style-type: none"> - A strategy of working together per crop, - Country meetings are also needed. The frequency of meetings should not be the same. That per crop can be done once or twice a year only. That by country can be done a little more frequently especially as researchers are often in the same institute or not very far geographically.
WP2	Few e-mail exchanges	More interaction is needed	Through annual and WP leaders' meetings.
WP3	Few interactions	Breeders need to interact with WP3 in order to prepare the plant material for NIRS calibration.	The annual meeting should be the opportunity to establish a timetable for the delivery of plant material to WP3 and to get feedback on the NIRS analyses carried out.
WP5	<ul style="list-style-type: none"> • None 	The breeders have varieties (see SOK document) that can be tested in farming systems. Better communication with WP5 would allow to begin their participatory evaluation.	Meetings and communication strategy.
WP6	<ul style="list-style-type: none"> • Meetings, Visit of Project leader, work with the PMU 	<ul style="list-style-type: none"> • NR 	<ul style="list-style-type: none"> • NR

Conclusion on Progress & Key Achievements:

- Please, Modify / Re-design / Annotate the WP4 flow chart from project proposal narrative hereunder.
- Indicate (e.g. circle or underline) the steps achieved or started in Period 1.



Perspectives for Period 2:

Activities, Publications, Planification of Interactions with WP2 & WP3, etc

Breeding activities: For period 2, field trials will be repeated. The trials will be resized to fulfil the objective of unravelling the genetic architecture of quality traits. The breeders have conducted a number of traits measures in 2018. The traits will be adjusted, after the annual meeting at Abuja, after discussion with WP2, 3 and other colleagues from WP4. The objective is to measure the more relevant traits and adjust them along the project before the HTP protocols and calibrations are made available for a routine use.

Data management: For each crop, the data produced will have to be stored in the database. Data storage and management will be in the agenda of the next RTBfoods annual meeting.

Communication within WP4 : One of the objectives of RTBfoods is sharing experience and create synergies between groups. In 2018, we had a cross-crops meetings. In 2019, we plan to start crop-based meetings (mainly on cassava and yam) to begin sharing approaches and experiences.

Communication between WP4 and other WPs: We plan to have more interactions with WP2 and 3 (how and when will be defined during the next RTBfoods annual meeting in Abuja). Increased interactions between breeders and food scientists is an overall objective within RTBfoods project and more widely. These interactions are particularly important and necessary to start adjusting the traits to be measured and not to end up with time-consuming but inefficient investment. Of course, a trade-off must be found between the frequency of the meetings and their contribution or added-value to the project success.