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ADVANCING ACHIEVEMENTS IN BREEDING FOR EARLY, RESILIENT, AND NUTRITIOUS POTATO AND SWEETPOTATO

14 November 2019

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October 2018–September 2019

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Duration: October 2018–September 2019

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ACRONYMS AND ABBREVIATIONS

ABMs	Accelerated breeding methods
ANOVA	Analysis of variance
ATW	Average tuber weight
AUDPC	Area under the disease progress curve
BLUP	Based on linear unbiased prediction
BW	Bacterial wilt
CC	Canopy cover
CIP	International Potato Center
CR	Canopy reflectance
CV	Cross validation
DAP	Days after planting
DArT	Diversity arrays technology
DI	Deficit irrigation
DICTA	Dirección de Ciencia y Tecnología Agropecuaria
DM	Dry matter
EiB	Excellence in Breeding
Fe	Iron
FW	Fresh weight
GCA	General combining ability
G x E	Genotype by environmental
GG	Genetic gains
GTDMS	Global trial data management system
ICP	Inductively coupled plasma
KALRO	Kenya Agricultural and Livestock Research Organization
KSU	Kansas State University
LAC	Latin America & the Caribbean
LB	Late blight
LBHT	LB-resistant, heat-tolerant potato population
LTVR	Lowland tropic virus-resistant potato population
METs	Multi-environmental trials

MTY	Marketable tuber yield
NARS	National agriculture research system
NDVI	Normalized difference vegetation index
NI	Normal irrigation
NIRS	Near-infrared reflectance spectroscopy
OFSP	Orange-fleshed sweetpotato
PCR	Polymerase chain reaction
PCCMCA	Programa Cooperativo Centro Americano para el Mejoramiento de Cultivos y Animales
PLRV	Potato leafroll virus
PVS	Participatory varietal selection
PVY	Potato Virus Y
SASHA	Sweetpotato Action for Security and Health in Africa
SCA	Specific combining ability
Sli	S-locus inhibitor
SNP	Single-nucleotide polymorphism
SPCSV	Sweet potato chlorotic stunt virus
SPFMV	Sweet potato feathery mottle virus
SPVD	Sweet potato virus disease
SSA	Sub-Saharan Africa
TCRC/BARI	Tuber Crops Research Centre, Bari
TGA	Total glycoalkaloids
TPS	True potato seed
TS	True seed
TTYNA	Total tuber yield no adjusted
UPLC	Ultra performance liquid chromatography
USAID	United States Agency for International Development
WAE	Wide adaptation and earliness
Zn	Zinc

EXECUTIVE SUMMARY

This report focuses on "Advancing Achievements in Breeding for Early, Resilient, and Nutritious Potato and Sweetpotato" project for October 2018–September 2019. The United States Agency for International Development (USAID) provided the funding for the International Potato Center (CIP).

There were four notable achievements in the 2018-2019 breeding work supported by USAID:

- Preparing CIP breeding programs to deliver novel, more effective breeding approaches, focused on increasing genetic gains (GG) and the fastest dissemination and adoption of new varieties.
- Expanding sources of resistance and selection to main pests, diseases, and traits affecting end-users' preferences.
- Enabling partners in developing countries to enhance and accelerate the delivery of improved varieties benefitting smallholders.
- Preliminary scientific data on the bioavailability in human subjects of Fe delivered through Fe-biofortified potato is encouraging beyond expectations. Once confirmed next year, it would convert potatoes into a very cost/effective tool to fight anemia in Africa, India/Bangladesh and Asian countries.

Report organization

"Advancing Achievements in Breeding for Early, Resilient, and Nutritious Potato and Sweetpotato" is necessarily a highly technical project that advances targeted and complex breeding programs for both crops. This document draws on the many components, activities, and results discussed in earlier deliverables and discusses progress.

Sections 2.1 and 2.2 entitled summarize the achievements of the potato and sweetpotato breeding programs, respectively. The two sections were organized into individual project outputs and the set of deliverables and milestones for each output. The potato breeding program consisted of four outputs; the sweetpotato program comprises five outputs.

The report concludes with supporting appendix material.

Preparing CIP breeding programs to deliver novel, more effective breeding approaches

The rate of GG expressed under farmer management in the form of farmer- and market-demanded product profiles and average area-weighted age of varieties in farmers' fields are the current high-level performance metrics used to evaluate CGIAR breeding programs. A modernization plan to raise breeding effectiveness based on assessments done with breeding program assessment tools and coordinated/supported by Excellence in Breeding (EiB) was discussed and partially implemented in 2019. CIP's breeding programs were evaluated by breeding program assessment tools in May 2018 and, based on the recommendations, major changes were proposed. Also, in response to the Crops to End Hunger Initiative, CIP has developed its breeding improvement plans for significant improvements in breeding operations and effectiveness achieved by capacities built by the internal teams and partners, which were submitted to EiB in September 2019.

Testing and implementing of new tools are important to remain competitive in breeding. CIP's Lima headquarters (HQ) has taken the lead to improve potato and sweetpotato field designs by p-rep designs;

data analysis with mixed models, including considering the covariance structure of genotypes, based on linear unbiased prediction (BLUP) estimates instead of lsmean estimates; and optimization of multistage selection in later breeding stages under the umbrella of the EiB platform. Such statistical upgrades are being rolled over into CIP's global breeding efforts. Molecular marker-assisted selection is available and used in potato breeding. In sweetpotato we expect to identify markers by our new bi-parental mapping populations for sweet potato virus D (SPVD). On potato molecular markers tagging genes Ry_{adg} and Rl_{adg} which provide tolerance to potato leaf roll virus (PLVR) and potato virus Y (PVY), respectively, have been successfully applied to the lowland tropic virus-resistant potato population gene pool. CIP–Mozambique has taken the lead to implement new tools in drought screening using canopy temperature by heat cameras and stable isotope composition. Public databases such as the "SweetpotatoBase" and the "Sweetpotato Knowledge Portal" have been updated for early-bulking clones and non–sweet clones after cooking. GG by regions and subregions have been documented. Current GG on an annual basis for sweetpotato storage root yield are estimated to be 0.8% (West Africa) to 2.5% (Amazon basin) and for beta-carotene root content 4.0% (Arid Pacific Coast) and 6.1% (West Africa).

CIP has started a diploid hybrid potato breeding program focused in Africa. Dihaploid genotypes from our main breeding populations have been developed and self-compatible 2x native germplasm has been self-pollinated to develop homozygous lines. 2X hybrid potatoes have the potential to provide easier access to clean seeds while dramatically diminishing the costs distributing and planting novel potato varieties. The breeding strategy has been designed as a network between countries in Africa, Latin America, and Asia, exploring great potential of the tropical genetic resources tested/selected globally by CIP over many years and partnering with advanced research institutes and the private sector.

Expanding sources of resistance and selection to main pests, diseases, climate resilience, and traits offering end-user preference and sustained genetic progress

Increasing the GG improvement in major CIP gene pools through recurrent selection scheme have proved to be a viable and important source of germplasm and advanced clones for tropical zones. These are (1) the lowland tropic virus-resistant potato population (LTVR) that combines resistance to the main viruses (PVX, PVY, PLRV); heat and drought tolerance, and early maturity; (2) late blight (LB)-resistant (B3) that confers quantitative LB resistance for highland tropics; (3) LB and heat tolerant (LBHT); and (4) high-Fe and high-Zn (zinc) from native landraces within a LTVR genetic background. The selection process is under accelerated breeding scheme, where one cycle of recurrent selection typically takes 5 years. Its main deliverables are novel parents for a next round of recurrent selection, and clones to be advanced for cultivar development/registration processes, which are to be tested in the target population of environments for which CIP and national agricultural research systems are breeding.

SPVD is the most severe disease in sweetpotato, which is a co-infection of sweetpotato chlorotic stunt virus and feathery mottle virus; high-yielding resistant clones are not available. Resistant clones to SPVD from our previous pre-breeding are reported and a new set of pre-breeding populations (89 families) is available for phenotyping and genotyping. In the offspring of the parents of these bi-parental populations we have observed previously segregation ratios of susceptible to resistant of less than 80% to more than 20%. Populations will also be used in Uganda in the context of other projects such as "SweetGains."

As a result of several recurrent selection cycles, Fe contents have been increased over 70% in advanced clones of potato. Preliminary results revealed that potato Fe absorption (as mentioned above). Complete results will be available by October, and a manuscript reporting these promising results will be submitted to a peer-reviewed, high-impact journal by the end of December 2019.

Furthermore, with EiB support, product profiles are being developed for the main TPEs, which specify key traits and traits levels that breeding progress will be measured against and the main current varieties to be replaced.

Enabling partners in developing countries to enhance and accelerate the delivery of improved varieties benefited smallholders

CIP is working on to expand and modernize its breeding operations in Africa toward a market-demand approach to increase GG and varietal adoption. The program is working from a regional breeding hub in Kenya, with Ethiopia as a secondary site under CIP's Potato Agri-food Systems Program. The program targets African highlands in Kenya, Ethiopia, Rwanda, Tanzania, Uganda, Malawi, Nigeria, Angola, Cameroon, Madagascar, the Democratic Republic of Congo, Mozambique, and Burundi. The regional potato-breeding effort is based on rational use of adapted African potato germplasm to exploit the power of heterosis and increase diversity by introducing new alleles from exotic germplasm into elite breeding populations to produce novel, locally adapted potato varieties.

An interesting recent experience involved a survey in 2019 of 300 potato growers in six counties in Kenya. This represented 70% of the national production area. Basically, yield and market demand dominated responses, followed by secondary factors such as disease resistance. The report indicated that the variety 'Sherekea', bred by CIP and released by the Kenya Agricultural and Livestock Research Organization (KALRO), has achieved a 9% total market share in 8 years following release. The CIP variety 'Unica' (released in 2016) is rapidly gaining market share, with CIP-bred varieties representing 86% of the total area. Through collaboration with a USAID-funded GDA project (PASTTA), some of these CIP/KALRO varieties have been licensed to local Kenyan seed companies and are already returning royalties to KALRO to provide a sustainable source of income to be re-invested in further local potato breeding. It is also hoped that this approach will provide much needed "market signals" on preferred traits to drive future breeding priorities.

Newly released modern varieties in Rwanda carry more robust, market-demanded traits than those currently grown, striking a balance in addressing farmers' limited ability to purchase inputs and meeting diverse market demands. New genetics and varieties, after a long time are pivotal to stimulate market interest and simultaneously uplift the system.

Sweetpotato population improvement has entered into population hybrid breeding for orange-fleshed sweetpotato (OFSP)—a new breeding scheme aiming to exploit heterosis in a systematic way for the first time in root, tuber and banana crops—to ensure medium- and long-term GG. The pre-breeding populations for SPVD resistance has been extended as well. The breeding team is moving 100 parents of hybrid population H1 into CIP's genebank. The true seed from elite crosses from OFSP hybrid populations for earliness is serving partners in Asia (Bangladesh, India, Vietnam, Philippines, Tajikistan, Turkey) and Latin America and the Caribbean (Brazil, Guatemala, Haiti, and Panama). The new set of pre-breeding populations for SPVD is available for phenotyping and genotyping, and during the past 2 years multistage selection in later breeding stages resulted in the release of various OFSP varieties.

Preliminary scientific data on the bioavailability in human subjects of Fe delivered through Fe-biofortified potato is encouraging beyond expectations.

One of the research highlights has been the preliminary study led by CIP and conducted in collaboration with ETH - Zurich in Switzerland and Nutritional Research Institute in Peru. The study looks at the bioavailability of iron (Fe) in human subjects, where women from local communities of Huancavelica—a

region in Peru with one of the highest levels of Fe deficiency—participated. This is the first time ever that the availability of Fe from potatoes in human subjects has been assessed. Preliminary results, to be further confirmed, indicate that potatoes have a higher Fe absorption than expected: 32% for the normally consumed yellow-fleshed potatoes and17% for purple-fleshed potatoes. This Fe absorption (bioavailability) from potato is much higher than that reported for other crops like pearl millet (7–10%), beans (3–5%), and sweetpotato (3–8%). Given these results, we expect that Fe-biofortified potatoes have more absorbable Fe than commonly consumed potato varieties and that they could significantly contribute to reduced malnutrition. If confirmed, such findings would enable the development of the first-ever potato biofortified product, namely Fe-enriched varieties. This could, for instance, represent a powerful tool to fight anemia in places such as Bangladesh, where currently over 40% of children are anemic.

Final remarks

USAID's investment in the potato/sweetpotato breeding project during the reported period has delivered value from several perspectives:

- Progress was achieved with important outputs, such as the first-ever assessment of Fe bioavailability in humans.
- Substantial breeding progress was achieved. In addition, the technological level of breeding activities has been increased as well as the likelihood of success (e.g., through a fast roll-out of linear mixed models to analyze breeding data).
- CIP fully embraced EiB and the Crops to End Hunger initiatives, which overall will increase its likelihood of success, ultimately expressed as improved livelihoods and outlooks for those smallholders and their families growing potato and sweetpotato.

1. PROJECT GOALS

The overall goal of the "Advancing Achievements in Breeding for Early, Resilient, and Nutritious Potato and Sweetpotato" project was to increase adoption by end-users, smallholders, and members of value chains based on potato and sweetpotato, through the genetic progress achieved by the International Potato Center's (CIP) breeding research and developments. During the past 2 years, CIP has increased the genetic progress of its breeding efforts, thereby understanding the quality drivers of end-users' adoption of cultivars and the climate resilience of its elite germplasm and derived varieties. CIP has rewritten the way engagement with local partners of national agricultural research systems (NARS) is done, so as to increase genetic gains (GG) by 20% and demonstrated actual adoption of improved varieties both in potato and sweetpotato.

1.1 Project Purpose

In the medium term, smallholder farms in Asia, Africa, and Latin America and the Caribbean (LAC) will have access to new, stable, and high-yielding potato and sweetpotato varieties that are disease and climate-change resilient and rich in iron (Fe) and vitamin A, respectively. This enables these farmers to improve their capacity to manage constraints affecting sustainability and household economy. The impacts of new varieties, when accompanied by functioning seed systems, successful crop management, and competitive value chains, can reduce poverty and malnutrition and enhance food security, farming, and food system resilience. CIP follows a comprehensive scheme for breeding, comprising variety development and population improvement (Gallais 2013). Variety development aims to select the best clones and maximizes the use of genetic variation. Population improvement aims to select the best parents to generate new genetic variation around an improved population mean. Variety development is relatively straightforward and done in cooperation with NARS. Population improvement is complex and has to be carried out for an agro-ecological zone—for example, potato for subtropical lowlands or tropical highlands, and/or orange flesh sweetpotato (OFSP) with short growing-season requirements. CIP's global potato and sweetpotato crop improvement programs emphasize improvement and dissemination of populations, whereas variety selection and releases from improved populations are carried out in cooperation with partners in target countries.

1.2 Overview of the Breeding Objectives and Outputs to Be Supported by the CIP Project

1.2.1 Breeding objectives

CIP's potato and sweetpotato breeding programs contribute to the following research-for-development products detailed in the center's Strategic Corporation Plan:

- Climate resilient, Fe-biofortified tetraploid potato varieties
- Seeds of change, toward diploid hybrid potato varieties
- Climate-resilient OFSP and other types of sweetpotato varieties
- OFSP + high-Fe sweetpotato varieties
- Seeds of change, hybrid sweetpotato varieties

1.2.2 Breeding outputs

Potato

- Alignment of breeding efforts with farmers' and end-users' preferences through increased awareness of market needs and opportunities.
- Nutrient-dense breeding populations available as sources of early-maturing, high and stable-yielding varieties with resistance to biotic and abiotic stresses and quality traits.
- Accelerated breeding methods (ABMs) and tools to help breeders select genotypes and parental lines.
- A modernized breeding information management system.

Sweetpotato

- Dynamic and nutrient-dense breeding populations developed as sources of early-maturing, high and stable-yielding varieties with resistance to biotic and abiotic stresses and quality traits.
- Farmers' and end-users' preferences integrated into varietal development and selection approaches.
- Accelerated breeding schemes and tools to help breeders select genotypes and parental lines in fewer years than with traditional clone-breeding schemes.
- New capacities for applying knowledge, tools, and modern breeding approaches developed for more efficient progress in variety-oriented breeding programs of NARS.
- Improved and shared breeding databases and knowledge management, including trait-specific protocols and catalogues to support the orientation of breeding products and facilitate decision-making and outcomes from breeding research.

2. FINAL REPORT

2.1 Summary of Achievements by Output—*Potato*

2.1.1 Output 1: Alignment of breeding efforts with farmers' and end-users' preferences through increased awareness of market needs and opportunities

DELIVERABLE 1.1: CURRENT LEADING VARIETIES USED BY SMALLSCALE FAMERS IN DEVELOPING COUNTRIES REPLACED WITH CIP VARIETIES

(Breeders: Thiago Mendes, Elisa Salas, Manuel Gastelo, and Neeraj Sharma)

Milestone 1: At least five product profiles defined in collaboration with NARS and other stakeholders (Q4 2019)

High adoption rates of the new varieties are fairly dependent on a well-designed product profile that can make the breeding effort to begin with a clear target and resources well allocated. CIP is working closely with Excellence in Breeding (EiB) platform (https://excellenceinbreeding.org/module1) to increase the significance of breeding products developed. It shares the mission on "sustainable transformation of how products are designed, created and managed within public sector breeding network" and the vision of "improving public sector breeding program impact by working transparently, methodically and professionally to increase rates of variety turnover."

CIP has used wide genetic resources to develop improved populations adapted to stressful conditions of the tropics. The aim is to generate improved populations and clones with resistance or tolerance to biotic and abiotic stresses as candidate varieties that can be easily adopted by farmers. To date, these efforts have resulted in two advanced populations that form the base of improved materials for developing countries: highland tropics-adapted late blight (LB)-resistant population (Population B) and the lowland subtropic virus-resistant population (Population LTVR).

To ensure that the breeding goals will be defined based on increased awareness of market needs and opportunities, CIP, with support of NARS potato breeders, have defined 12 product profiles targeting different countries in LAC, Africa, and Asia (Table 1). However, it is just a beginning, since the expectations is to develop more product profiles that will help to consolidate the global breeding strategy. A new series of 1-day workshops on potato variety (product) design have been planned, seeking input from stakeholders who directly or indirectly are engaged in the potato value chain for regions or countries that were not yet targeted.

TABLE 1. BASIC INFORMATION: SUMMARY OF POTATO PRODUCT PROFILE BY REGION, LIST OF VARIETIES TO BE REPLACED, AND THEIR FOUR BASIC TRAITS

#	Serial EiB	Breeder	Country	Region	Variety to be Replaced	Basic Traits			
						1	2	3	4
1	100159	Elisa Salas	Peru	LAC	Yungay	Excellent flavor	Dry matter (DM) 20–24%	Long dormancy	Oval shape
2	100180	Manuel Gastelo	Peru	LAC	Canchan	LB	Deep tuber eyes	French fries	Low glycoalkaloids
3	100191	Thiago Mendes	Ethiopia	Africa	Gudene	LB	DM > 20%	Round shape	White skin color
4	100206	Thiago Mendes	Rwanda	Africa	Kinigi	DM 20%	Red skin	Storability	Good taste
5	100207	Thiago Mendes	Kenya	Africa	Shangi	Short dormancy	Fast cooking time	Earliness	Multipurpose
6	100212	TBD	India	Asia	Kufri Chipsona-3	DM 18%	Moderate reducing		
7	100213	TBD	India	Asia	Lady Rosseta	Early maturing	DM >18%		
8	100218	TBD	India	Asia	Kufri Chipsona-1	DM 22%	Moderate reducing sugar	Mid maturity	
9	100219	TBD	India	Asia	Atlantic	Early maturing	DM > 20%		
10	100220	TBD	India	Asia	Kufri Jyoti	Shelf-life	Low reducing sugar		
11	100261	Neeraj Sharma	Vietnam	Asia	Atlantic	DM 21–23%	Low chip darkening	Low reducing sugar	Uniform tuber shape
12	100289	Neeraj Sharma	Vietnam	Asia	Granola	Tuber appearance	Marketing quality		

2.1.2 Output 2: Nutrient-dense breeding populations available as sources of early maturation, high and stable yields, resistance to biotic and abiotic stresses, and development of quality traits

DELIVERABLE 2.1: RECURRENT SELECTION OF THE MAIN BREEDING POPULATIONS OF POTATO WERE DEVELOPED. TRUE SEED (TS) FAMILIES THEN GENERATED MULTI-ENVIRONMENTAL TRIALS (METs) AND VARIETY SELECTION IN COUNTRIES OF INTEREST

(Breeders: Elisa Salas and Manuel Gastelo)

2.1.1: Development of a new cycle of selection of a LTVR population

Milestone 1: At least 25 true seed (TS) families from crosses between the best progenitors of a LTVR population with new sources of bacterial wilt (BW) available for international distribution by Q4 2019

BW, caused by *Ralstonia solanacearum*, is one of the most destructive diseases of potato. Modern varieties carrying resistance to the disease do not exist, but recently pre-breeding lines were developed at INIA Uruguay by crossing with wild species *S. commersonii*. These were introduced into CIP's genebank in a Crop Trust-funded project. Seven of these pre-bred lines were crossed with elite progenitors from CIP's LTVR population either as males (LTVR x BW) or as females (BW x LTVR). The berries will be harvested and the seed will be ready for international distribution by the end of 2019.

2.1.2: Recurrent potato hybrid selection pool for combining LB and virus resistance, heat and drought tolerance, and early bulking from populations LTVR and B3 (First (1) reciprocal recurrent selection cycle)

Milestone 1: At least 20 advanced clones from LBHT X LTVR population with resistance to LB, virus, heat and drought tolerance, high tuber yield, and quality for French fries and/or chips

With aims to exploit heterosis for tuber yield under high temperatures, a population originally developed by crossing elite clones from two divergent populations has been adapted to different agro-ecological zones through several cycles of recurrent selection. The first founder population, LBHT, resulted in clones combining resistance to LB, heat tolerance, and adaptation to mid-elevation and highland tropics and its germplasm consists mainly of *Solanum tuberosum spp. Andigena*. The second population, LTVR, consists of a combination to achieve resistance to virus, heat tolerance, earliness, and adaptation to lowland tropics using mostly germplasm of *S. tuberosum spp. tuberosum*.

After initial agronomical evaluations of a line by tester-mating design, 15 LBHT x 3 LTVR, 528 selected clones were tested in 2015 in San Ramon (11°08'S, mid-elevation at 800 masl, with average day–night temperatures of 28°C and 21°C) for heat tolerance. The best 240 clones were selected for LB-resistance evaluation in Oxapampa (10°35'S, 1,850 masl, 80% relative humidity, >2,000 mm of annual rainfall) and heat tolerance in San Ramon from 2015 to 2017.

Seventy-three clones with high levels of LB resistance were planted during 2017–2018 in Oxapampa and San Ramon to repeat the previous stress screening; in Huancayo (12° 07'S, 3,280 masl in the highlands) during 2018, to measure the yield potential under normal conditions for potato cultivation; in Majes (16°28'S, 1,294 masl, arid zone) during 2018–2019 to evaluate drought tolerance; and in Huancayo during the first half of 2019, to evaluate DM content and frying quality under low temperature conditions.

Of these experiments, 39 clones with high levels of LB resistance were identified. The area under the disease progress curve (AUDPC) of the clones (0–980) was significantly lower that that of the susceptible check 'Yungay' (1645). The tuber yield under the presence of LB (13.00–62.83 t/ha), which was notably higher than the checks 'Yungay' and 'Amarilis' (2.39 and 12.39 t/ha respectively). In absence of LB, yield was from 21.90 to 33.80 t/ha compared with the varieties 'Yungay', 'Amarilis', and 'Desiree', with 26.00, 26.50, and 22.60 t/ha, respectively. Under high temperatures yield was from 16.25 to 34.42 t/ha, which is higher than the varieties 'Amarilis' (not heat tolerant) and 'Desiree' (heat tolerant), with 4.27 and 12.95 t/ha, respectively.

The tuber yield of the test clones was higher than the average parental performance under high temperature conditions, suggesting a heterotic effect when crossing two genetically divergent sources with heat tolerance. In Majes after analysis with mix models, the BLUP values for yield under normal irrigation were in the range of 27.99–42.72 t/ha. Yields of the control varieties 'Canchan', 'Desiree', and

'Yungay' were 28.96, 27.09, and 26.00 t/ha, respectively. Under restricted irrigation the yields of the clones were from 0.85 to 15.58 t/ha; the same control varieties showed yields of 2.39, 1.83, and 0.84 t/ha, respectively.

Twenty-eight clones with tolerance to heat also had good tuber yield in Huancayo, showing adaptation to these contrasting environments and can be planted under both conditions (Fig. 1). Ten clones have reasonable yields under restricted irrigation, whereas 10 clones have extreme resistance to potato virus X (PVX) and 11 to PVY. Ten clones have good quality for frying when grown under low temperature conditions, which increases the content of reducing sugars and determines the color of the frying. The DM content in percentage was 19.40–24.74% compared with the commercial varieties 'Amarilis', 'Yungay', and 'Canchan', with 20.31%, 22.00%, and 22.04%, respectively (Appendix A1_Potato).

After testing for resistance to LB and virus, tolerance to heat and drought, and adaption to mid-elevation and highlands, 39 resilient clones were selected for their resistance to LB and tuber yield. They are now being introduced into CIP's genebank to obtain the adequate health status for international distribution.

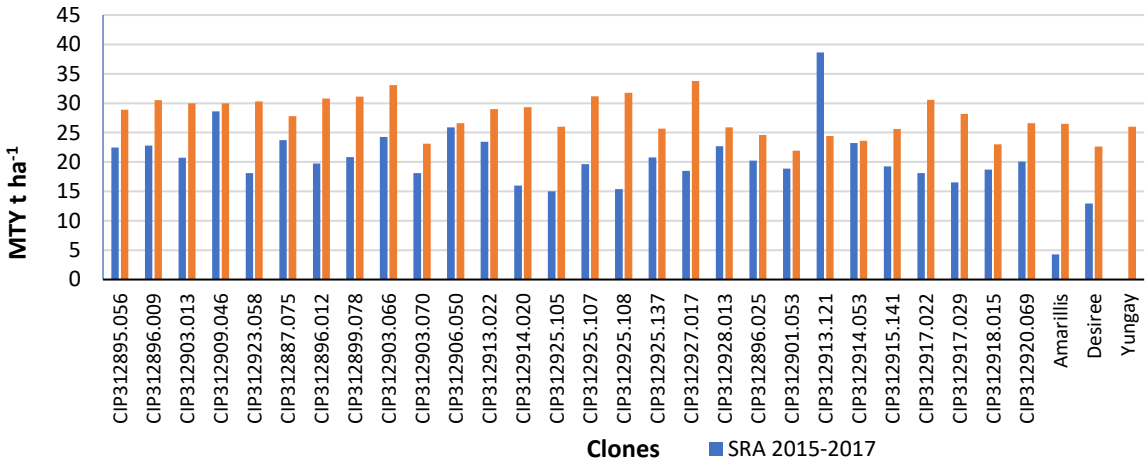

Figure 1. Marketable tuber yield per hectare in clones LBHT x LTVR in San Ramon and Huancayo. (This is the first time the information has been reported.)

2.1.3 Development of a new cycle of selection in highland tropics-adapted LB-resistant population (Population B) for tropical highland and mid-elevation agro-ecologies

Milestone 1: At least 20 clones from recurrent selection cycle 3 of the B3 population with high levels of LB and virus resistance, high tuber yield, drought and heat tolerance, low glycoalkaloid content, and good quality for French Fries and/or chips

Recurrent selection cycle 3 of the B3 resulted in crosses between the elite clones from the previous cycle of the same population made in 2011. Selection based on agronomic characteristics (skin and flesh color, tuber shape, eye depth, plant vigor, uniformity of tubers) and LB-resistance evaluation under the high endemic disease pressure in Oxapampa in 2012–2015 have since narrowed down the number of clones to 181. These elite clones were evaluated from 2016 to 2019 for yield in multilocation trials in Oxapampa, Huancayo, San Ramon, and Majes (see previous deliverable for detailed description of the environments and trial designs). In addition, the quality for frying (chips) was evaluated from tubers harvested in Huancayo and for resistance to PVX and PVY under greenhouse conditions, with artificial virus inoculations. Parental values and phenotypic stability for LB resistance and tuber yield were estimated.

A total of 51 clones with high levels of LB resistance were selected in Oxapampa and good tuber yield in Huancayo, both better than in the control varieties. AUDPC values are in the range of 17.50–705.83, lower than the AUDPC values of the 'Yungay' and 'Amarilis' control varieties (1,586.67 and 1,534.17, respectively). The tuber yield on average in highlands was from 20.67 to 56.41 t/ha compared with the 'Yungay' and 'Amarilis' varieties at 26.29 and 35.66 t/ha, respectively. Under high temperature conditions, the tuber yield in the heat-tolerant clones was ranged from 16.32 to 33.71 t/ha, higher than the 'Desiree' and 'Amarilis' varieties with 13.39 and 5.24 t/ha, respectively. All the collected data were uploaded at Dataverse Open Access CIP repository (Click here). Six clones were selected in 2019 that have some potential for drought tolerance; but further trials are required to confirm these results.

The DM content of the elite clones is in the range of 17.94–26.92%, and 33 clones have good frying quality. Twenty-eight clones showed extreme resistance to PVX and 17 to PVY. Fifteen clones have a high parental value to be used as parents in a new selection cycle or in improvement programs in the regions or countries of LAC, Africa, and Asia. Fifteen clones show phenotypic stability for tuber yield (Fig. 2, Appendix A2_Potato). These clones are being introduced into CIP's genebank for international distribution.

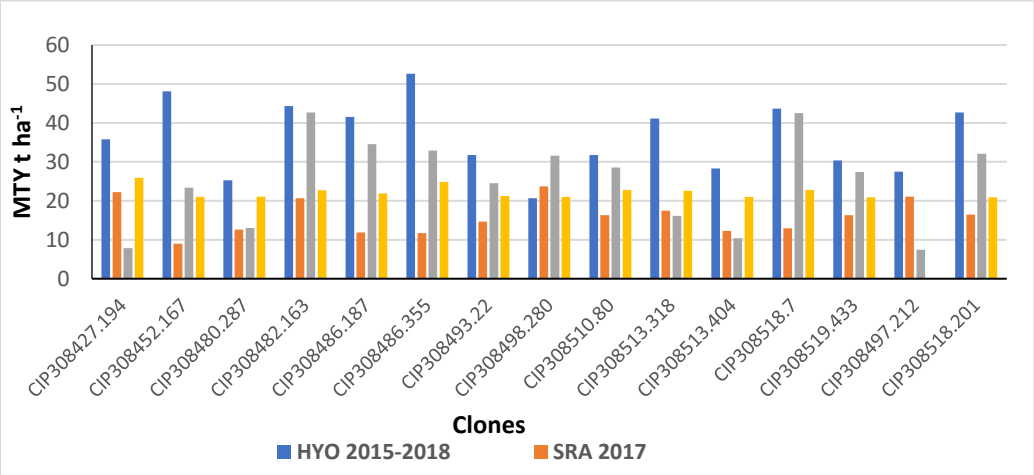

Figure 2. Marketable tuber yield in clones with phenotypic stability Milestone 2: At least 10 potato clones with LB resistance from B3C3 population with high parental value for tuber yield components.

The parental value for tuber yield was studied in 39 elite clones. In 2016–2018 these clones were crossed to four testers, the varieties 'Desiree', 'Katahdin' (*Solanum tuberosum spp. tuberosum*), 'Huagalina' (*S. tuberosum spp. Andigena*), and the clone CIP-308480.292 from the B3C3 population, using the mating design line (clones) by tester, obtaining 117 progenies. From November 2018 to May 2019, these progenies were evaluated in three experiments under field conditions in Huancayo using randomized complete block statistical design with three repetitions of 40 plants each. Tubers were harvested at 120 days after planting (DAP), the number and weight of commercial and noncommercial tubers were collected and used to estimate the commercial yield per hectare and the average tuber weight.

The parental value was estimated by general combining ability (GCA) and specific combining ability (SCA) for marketable tuber yield (MTY) per plot (10.80 m^2), per hectare MTY/ha, and average tuber weight (ATW).

In 2019 an experiment was planted to determine the parental value for tuber yield under high temperature conditions in San Ramon (11°08'S, 800 masl), a warm environment where day–night average temperatures are 28°C and 21°C. This experiment was planted in August and will be harvested in November at 90 DAP.

The analysis of variance (ANOVA) for MTY, MTY/ha, and ATW show significant statistical differences for the lines (clones) associated with the GCA and additive effects and the interaction line x tester associated with the SCA and the non-additive effects (Table 2).

TABLE 2. ANOVA FOR MTY, MTY/HA, AND ATW IN THREE EXPERIMENTS IN HUANCAYO, 2018–2019

		Mean Square Set 1				Means Square Set 2				Mean Square Set 3		
Sources of variation	df	MTY	MTY/ha	ATW	df	MTY	MTY/ha	ATW	df	MTY	MTY/ha	ATW
Replications	2	8.19	7.03	4.56	2	38.97	33.55	23.62	2	308.21*	264.14*	2162.69*
Lineas	9	99.33**	85.15**	135.12**	8	172.11**	147.33**	492.56**	19	180.74**	154.99**	2449.34**
Testers	2	1285.68**	1102.06**	456.12**	2	993.00**	851.15**	1503.21**	2	4551.66**	3902.33**	82104.03**
Lines x Testers	18	43.88**	37.62**	78.87**	16	120.92**	103.67**	578.34**	38	52.22	44.76	955.81
Error	58	5.03	4.31	28.62	52	14.83	12.73	56.29	118	49.91	42.79	856.81
C.V.%		25.45	25.45	28.43		28.27	28.28	24.58		28.3	28.3	27.29

Eighteen clones had high parental value: GCA ($p < 0.01$) for MTY and MTY/ha, 14 clones for ATW. Twelve clones combine significant effects of GCA for MTY, MTY/ha, and ATW (Table 3). Fifty progenies had significant effects of SCA ($p < 0.01$) for MTY/ha and 30 for ATW (Table 4).

The clones with high parental value (GCA) are recommended as parents for breeding programs in Africa, Asia, or LAC. The progenies with high SCA are the most promising as potential new varieties.

TABLE 3. GCA FOR MTY, MTY/HA, AND ATW IN ADVANCED B3C3 CLONES

#	Clone	Female	Male	Resistance			GCA					
				LB	PVX	PVY	MTY (kg)		MTY (t/ha)		ATW (g)	
1	CIP308433.160	CIP395109.29	CIP395011.2	R	ER		3.77	*	3.49	*	-2.11	
2	CIP308476.16	CIP395077.12	CIP395011.2	R	ER	ER	1.13	*	1.05	*	-0.32	
3	CIP308479.56	CIP395096.5	CIP395017.242	R		ER	2.32	*	2.15	*	1.77	*
4	CIP308480.287	CIP395109.29	CIP395017.242	R	ER		2.93	*	2.72	*	-7.58	
5	CIP308480.299	CIP395109.29	CIP395017.242	R			3.05	*	2.83	*	-1.92	
6	CIP308480.334	CIP395109.29	CIP395017.242	R	ER		3.03	*	2.81	*	27.37	*
7	CIP308486.187	CIP395112.32	CIP396012.288	R	ER		1.58	*	1.46	*	15.75	*
8	CIP308486.220	CIP395112.32	CIP396012.288	R			5.53	*	5.13	*	12.81	*
9	CIP308486.314	CIP395112.32	CIP396012.288	R	ER		0.67	*	0.62	*	5.76	*
10	CIP308486.328	CIP395112.32	CIP396012.288	R	ER	ER	3.69	*	3.42	*	1.15	*
11	CIP308486.355	CIP395112.32	CIP396012.288	R	ER	ER	4.43	*	4.10	*	-4.80	
12	CIP308487.163	CIP395112.32	CIP396264.14	R	ER	ER	10.04	*	9.30	*	50.02	*
13	CIP308487.374	CIP395112.32	CIP396264.14	R			4.03	*	3.73	*	9.19	*
14	CIP308488.198	CIP395112.36	CIP396004.337	R	ER		-0.58		-0.54		17.77	*
15	CIP308494.368	CIP395123.6	CIP396240.23	R	ER		8.14	*	7.53	*	0.62	*
16	CIP308499.334	CIP396004.263	CIP396038.107	R		ER	1.07	*	0.99	*	2.56	*
17	CIP308499.76	CIP396004.263	CIP396038.107	R			1.27	*	1.17	*	0.19	*
18	CIP308501.211	CIP396004.309	CIP396240.23	R			4.29	*	3.97	*	0.96	*
19	CIP308503.39	CIP396009.207	CIP395017.242	R	ER	ER	1.91	*	1.77	*	-5.25	
20	CIP308513.318	CIP396033.102	CIP395152.16	R	ER		-5.09		-4.72		8.44	*

TABLE 4. SCA FOR MTY, MTY/HA, AND ATW IN B3C3 PROGENIES

#	Progeny	Female	Male	SCA					
				MTY (kg)		MTY (t/ha)		ATW (g)	
1	CIP316532	CIP308486.355	CIP308480.292	5.54	*	5.13	*	1.78	*
2	CIP316533	CIP308486.355	Huagalina	-1.84		8.03	*	3.02	*
3	CIP316535	CIP308487.163	CIP308480.292	10.10	*	22.26	*	47.39	*
4	CIP316632	CIP308498.326	Huagalina	-0.10		3.22	*	1.84	*
5	CIP316641	CIP308519.81	Huagalina	1.58	*	4.27	*	6.86	*
6	CIP316643	CIP308515.48	CIP308480.292	6.50	*	6.02	*	25.03	*
7	CIP318003	CIP308489.367	CIP308480.292	3.24	*	2.21	*	-1.78	
8	CIP318004	CIP308493.195	CIP308480.292	1.26	*	4.62	*	0.36	*
9	CIP318005	CIP308486.220	CIP308480.292	-0.70		8.09	*	20.95	*
10	CIP318007	CIP308493.195	Huagalina	3.20	*	8.43	*	-1.23	
11	CIP318008	CIP308476.16	CIP308480.292	2.04	*	6.55	*	12.86	*
12	CIP318011	CIP308494.211	Huagalina	0.90	*	5.82	*	33.62	*
13	CIP318015	CIP308480.287	CIP308480.292	0.52	*	6.81	*	-4.32	
14	CIP318017	CIP308480.287	Huagalina	1.36	*	9.60	*	-2.92	
15	CIP318019	CIP308480.334	Huagalina	1.11	*	9.47	*	-8.37	
16	CIP318021	CIP308503.312	Huagalina	5.76	*	6.16	*	8.49	*
17	CIP318023	CIP308503.39	CIP308480.292	-0.12		5.27	*	-31.13	
18	CIP318024	CIP308503.39	Huagalina	1.42	*	8.71	*	3.73	*
19	CIP318027	CIP308513.318	Huagalina	2.64	*	3.36	*	14.55	*
20	CIP318031	CIP308480.334	CIP308480.292	-1.68		4.87	*	4.12	*
21	CIP318032	CIP308486.328	CIP308480.292	-2.04		5.14	*	13.82	*
22	CIP318033	CIP308433.160	CIP308480.292	-1.06		6.12	*	-0.12	
23	CIP318034	CIP308486.328	Huagalina	1.90	*	10.81	*	-3.88	
24	CIP318036	CIP308433.160	Huagalina	-0.74		8.43	*	-7.19	
25	CIP318039	CIP308486.220	Huagalina	2.29	*	12.88	*	-9.49	
26	CIP318040	CIP308487.157	Huagalina	1.97	*	6.27	*	8.65	*
27	CIP318043	CIP308488.198	CIP308480.292	-0.93		2.21	*	7.77	*
28	CIP318044	CIP308488.198	Huagalina	3.58	*	8.40	*	-6.92	
29	CIP318046	CIP308476.16	Huagalina	0.26	*	6.92	*	-14.04	
30	CIP318049	CIP308486.187	Kathadin	5.04	*	5.51	*	27.40	*
31	CIP318050	CIP308489.415	Desiree	3.56	*	3.30	*	-2.38	
32	CIP318051	CIP308489.415	CIP308480.292	1.50	*	1.40	*	3.73	*
33	CIP318053	CIP308486.187	Huagalina	2.70	*	3.34	*	-6.57	
34	CIP318055	CIP308486.314	CIP308480.292	6.89	*	6.38	*	4.74	*
35	CIP318058	CIP308479.56	CIP308480.292	3.45	*	3.19	*	-1.03	
36	CIP318059	CIP308509.221	Huagalina	3.75	*	3.48	*	4.46	*
37	CIP318068	CIP308480.174	Huagalina	3.63	*	3.37	*	8.40	*
38	CIP318073	CIP308520.145	Desiree	2.53	*	2.34	*	1.03	*
39	CIP318074	CIP308518.7	Kathadin	5.21	*	4.82	*	3.02	*
40	CIP318075	CIP308518.7	CIP308480.292	1.18	*	1.10	*	-1.03	
41	CIP318078	CIP308499.334	CIP308480.292	1.62	*	1.50	*	1.64	*
42	CIP318079	CIP308480.299	CIP308480.292	6.08	*	5.62	*	-6.35	
43	CIP318084	CIP308499.76	Huagalina	3.17	*	2.94	*	3.11	*
44	CIP318088	CIP308478.123	Desiree	2.01	*	1.86	*	-1.32	
45	CIP318092	CIP308486.133	Huagalina	4.96	*	4.60	*	7.81	*
46	CIP318093	CIP308494.368	CIP308480.292	0.87	*	0.78	*	-0.26	
47	CIP318094	CIP308487.374	CIP308480.292	1.64	*	1.52	*	13.43	*
48	CIP318096	CIP308487.374	Huagalina	1.84	*	1.71	*	-7.96	
49	CIP318097	CIP308494.368	Huagalina	8.57	*	7.95	*	12.22	*
50	CIP318099	CIP308488.142	Huagalina	5.38	*	4.99	*	4.94	*

2.1.4 Consolidation of biofortified populations with high nutrient content and health-promoting traits

Milestone 1: Phenotypic stability for tuber yield components, minerals, sensorial test in advanced clones from tetraploid biofortified population (Q4 2020), and yield stability trials for biofortified cycle I clones

A group of 269 biofortified tetraploid cycle I genotypes, three biofortified diploid cycle III, and four commercial varieties ('Yungay', 'Ccompis', 'Serranita', and 'Canchan') were planted in November 2018 for multi-environment trials in the Peruvian Andes in four locations (Table 5). The trial design was row and column design with three replications. Each plot of five plants had a size of 1.08 m^2, considered one row 1.2 m long and 0.9 m between rows. Nitrogen, phosphorus, and potassium (180-180-160) and organic amendment ("guano de corral") were applied before planting. Soil samples of 1 kg each were collected before planting and sent to the agricultural chemistry laboratory Valle Grande–Cañete for soil, salinity, and micronutrient content analysis. The data for the yield trial were collected following the protocol set forth in the "Procedures for Standard Evaluation and Data Management of Advanced Potato Clones" (https://research.cip.cgiar.org/potatoknowledge/yield.php). Variables such as length of stolon, tuber appearance, uniformity and size, and agronomical variables for yield component as number of harvested plants, total number of tuber, and total tuber weight per plot were recorded in the fieldbooks. After harvest, samples from every plot at each location were collected for analysis of mineral content (Fe and Zn). The samples were sent to the University of Nottingham for determination of mineral content using the inductively coupled plasma (ICP) method. Postharvest evaluations were made for DM content, soluble solids content, and frying quality. Organoleptic tests for boiled potato from every location were conducted with a trained panel of evaluators, who evaluated appearance (darkness), texture, flavor, and strange flavors.

The LB-resistance trial, planted in October 2018 and harvested in May 2019, consisted of a group of 279 biofortified tetraploid cycle I genotypes, three biofortified diploid cycle III, and four commercial varieties ('Yungay', 'Ccompis', 'Serranita', and 'Canchan') planted in 576 plots of five plants, using an incomplete block design (α design) of 24 blocks of 12 genotypes by each repetition. Soil samples were collected before planting and sent to the Laboratory for Soil, Plant, Water and Fertilizer Analysis Universidad Nacional Agraria-La Molina, for soil analysis.

The LB-resistance evaluation was conducted following the protocol "Field assessment of resistance in potato to *Phytophtora infestans*" (https://research.cip.cgiar.org/potatoknowledge/lateblight.php). At the harvest in January 2019, agronomical traits, such as total tuber number and total tuber weight of each plot and DM content, were evaluated. The detailed data analysis is ongoing, and the results will be reported during the next reporting period.

TABLE 5. SITES OF THE MULTILOCATION TRIALS FOR YIELD STABILITY OF THE BIOFORTIFIED CYCLE I CLONES

#	Geographical Location	Department	Locality	Altitude (masl)	Trial
1	Northern Andes	La Libertad	Chugay	3,789	Yield and minerals
2	Central Andes	Cerro de Pasco	Paucartambo	2,904	Yield and minerals
3		Cerro de Pasco	Oxapampa	1,810	LB
4	Southern Andes	Apurimac	Huanacopampa	3,922	Yield and minerals

Participatory varietal selection (PVS) trials. Thirty tetraploid biofortified clones and four commercial varieties were evaluated in multilocation trials in nine field experiments in five departments of Peru using PVS (Table 6, Fig. 3).

TABLE 6. THE EXPERIMENT SITES PLANTED FOR PVS TRIALS

#	Geographical Location	Department	Locality	Altitude (masl)
1	Northern Andes	Cajamarca	Cutervo	2,666
			Chulec	3,480
		La Libertad	Chugay	3,789
			Pataz	3,530
2	Central Andes	Junín	Chulec	4,054
			La Victoria	3,219
		Huancavelica	Paucara	4,184
3	Southern Andes	Cusco	Leocpata	4,054
			Apacheta	3,998

Trials were planted according to local practices using 40 plants per plot with a randomized complete block design with three replications at each location. The plot size was 9.72 m^2, with four rows 2.7 m long and 0.9 m between rows. Nitrogen, phosphorus, and potassium (180-180-160) and organic amendment ("guano de corral") were applied before planting. Soil samples of 1 kg each were collected before planting and sent to the agricultural chemistry laboratory Valle Grande–Cañete for soil, salinity, and micronutrient content analysis. PVS evaluations were conducted following the protocol outlined in the "Participatory Varietal Selection of Potato Using the Mother & Baby Trial Design: A Gender-responsive Trainer's Guide" (https://research.cip.cgiar.org/potatoknowledge/pvs.php). The data were collected using the highly interactive data analysis platform software. Evaluations at the flowering, harvest and post-harvest (storage) phase were performed. Farmers identified and ranked characteristics of potato that they considered important, and afterwards they selected the genotype they preferred. Each farmer's varietal selection and the criteria for selection were recorded.

Figure 3. PVS trials in the Peruvian Andes. Clockwise from left: experimental field in Chulec, Junín; evaluation at flowering stage in Chugay, La Libertad; evaluation at harvest in Paucara, Huancavelica; and organoleptic test under field conditions in Chugay, La Libertad.

The yield assessment was performed following the protocol "Procedures for Standard Evaluation and Data Management of Advanced Potato Clones" (https://research.cip.cgiar.org/potatoknowledge/yield.php). Fourteen variables were collected at field level for the yield trial, including marketable and nonmarketable number and weight of tubers and morphological data. The DM content, reducing sugars, soluble solids content, and frying quality were evaluated. Sensorial evaluations were conducted using a trained evaluation panel. Samples from all the trials were evaluated for Fe, Zn, vitamin C, and glycoalkaloid content. In addition, freeze-dried tuber samples (three per genotype from every field) were sent to the University of Nottingham for determination of mineral content using the ICP method. The data analysis is still ongoing, and full results will be reported in the next reporting period.

2.1.5 Smart trait combination for increased GG using adapted African potato germplasm: improving yield, LB, earliness, and quality attributes

(Breeder: Thiago Mendes)

Milestone 1: Designing an accelerated potato breeding scheme for Ethiopia and generate tuber seeds from at least 19 TS families comprising 150 clones each (Q2 2019)

An accelerated breeding scheme was developed reflecting the local capacity building in Ethiopia to increase GG aligned with the recently developed product profile. Nineteen true potato seed (TPS) families derived from crosses using adapted African germplasm with different attributes were planted (Table 7). The breeding scheme and selection strategy are presented in Figures 4 and 5.

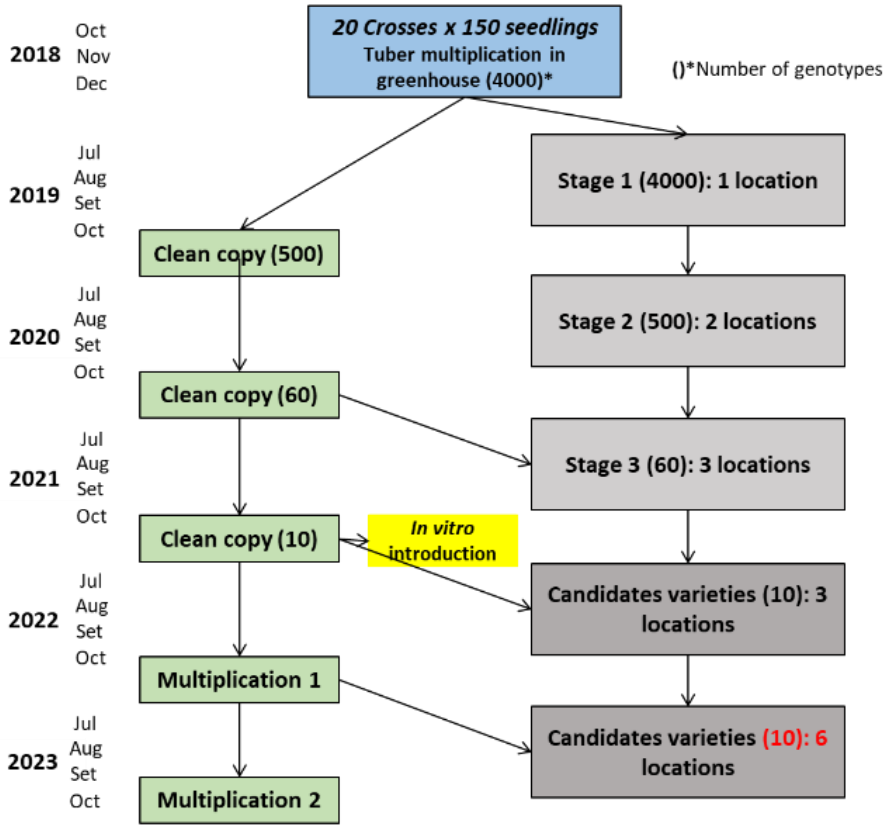

Figure 4. Accelerated breeding scheme applied to Ethiopian Potato Breeding Program, Holetta, Ethiopia.

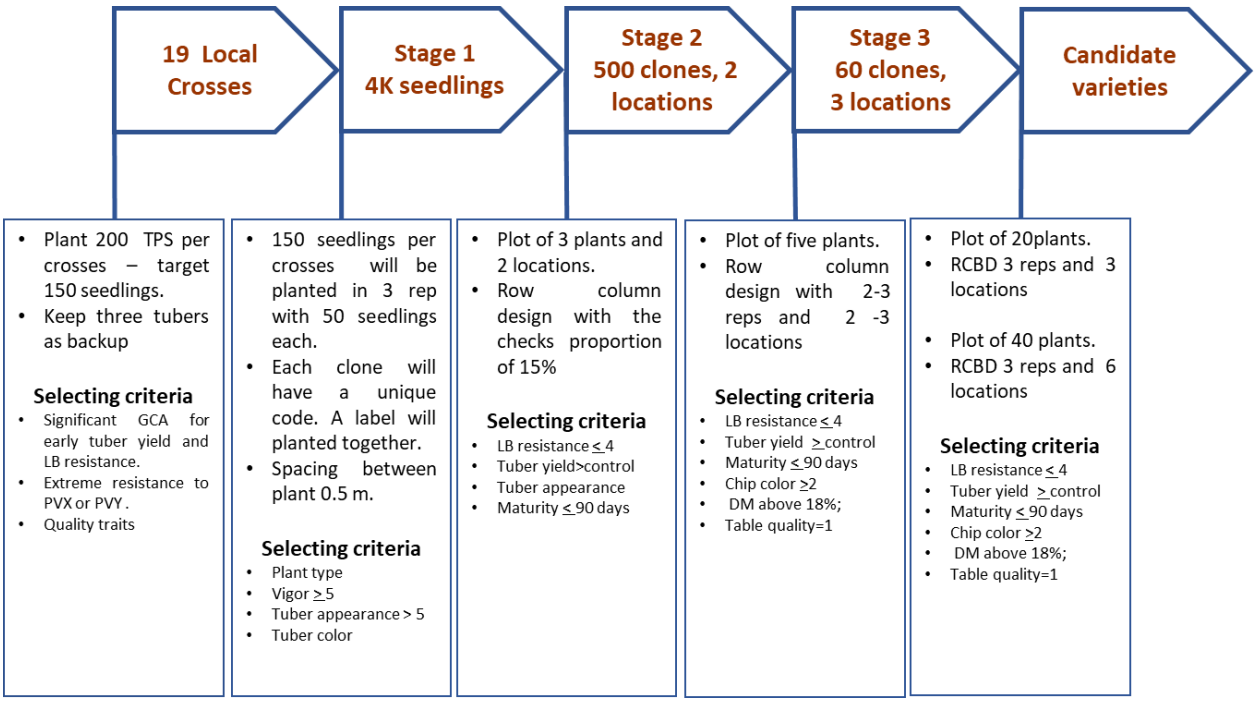

Figure 5. Selection strategy aligned with the product profile recently developed at Holetta, Ethiopia.

TABLE 7. THE 19 TPS FAMILIES FROM CROSSES USING ADAPTED AFRICAN GERMPLASM IN 2019, HOLETTTA, ETHIOPIA

No.	Crosses	Attributes	No. of Clones Generated
1	Akime x Awash	Early maturing, good shape	231
2	Akime x CIP391046.14	PVX-R, PVY-ER	100
3	Belete x Awash	LB, PVX-ER "x" early maturing, good shape	211
4	Belete x CIP393077.159	LB, PVX-ER "x" PVX-R, PLRV-HR, LB-R	133
5	Feleke x Awash	Early maturing, good shape	216
6	Feleke x Belete	LB, PVX-ER	102
7	Feleke x CIP391046.14	PVX-R, PVY-ER	192
8	Gudene x Awash	LB, good taste "x" early maturing, good Shape	197
9	Gudene x CIP393536.13	LB, good taste "x" Fe	80
10	Gudene x CIP398180.292	LB, good taste "x" PVX-ER, LB-R	265
11	Holland x CIP391046.14	PVX-R, PVY-ER	76
12	Holland x CIP398192.41	PVX-ER, LB-R	310
13	Nech Abeba x CIP391046.14	PVX-R, PVY-ER	160
14	Nech Abeba x CIP398180.292	PVX-ER, LB-R	121
15	Rejim-China x Awash	Early maturing, good shape	146
16	Rejim-China x CIP398192.41	PVX-ER, LB-R	135
17	Shangi x Belete	Early, early cooking "x" LB, PVX-ER	299
18	Shangi x CIP398180.292	Early, early cooking "x" PVX-ER, LB-R	194
19	Siquare x CIP391046.14	PVX-R, PVY-ER	235
	Total		**3,403**

*'Belete' (CIP393371.58), 'Awash' (CIP378501.3), and 'Gudene' (CIP386423.13)

TPS was sown in sterilized media composed of sand, forest soil, and compost at a ratio of 1:2:1, respectively, from September to November 2018. The seedlings were transplanted to individual pots after 40 days. Approximately 3 months after transplanting, genotypes containing at least four tubers were selected and stored in diffused light store for about 5 months (Table 10). A maximum of 200 clones per family were planted in the field at Holetta Agricultural Research Center in June 2019. Each clone was presented by one plant and three tubers of a clone were kept as back-up. The trial will be harvested in October 2019 and about 500 best performing clones will be selected.

Milestone 2: Assessment of 81 advanced potato clones selected from crosses of adapted African germplasm (Q2 2019)

In 2015 crosses of adapted African germplasm were introduced to Ethiopia. The best clones have been selected in order to develop high-yielding and LB-resistant clones for tropical highlands under rainfed condition. The crosses were made in Kenya in 2013 and 2014 using local cultivars and CIP's advanced clones adapted to tropical highlands of east Africa. In 2017, 820 clones were planted in augmented block design. No fungicide was sprayed during the growing season. Eighty-one clones were selected, representing about 10% of the tested clones that had an AUDPC < 2300 or susceptibility scale ≤ 5 (where 9 is most susceptible and 1 is highly resistant); total yield per plant ≥ 0.45 kg and marketable yield per plant ≥0.41 kg; and free from virus symptoms and external tuber defects. The selection of the 10% best clones increased tuber yield twofold, the marketable tuber yields more than fourfold, and reduced the disease severity by half as compared with the original population planted in the 2017 growing season. The selected 81 clones plus three check varieties were planted in 12 x 7 alpha lattice design in two replications and 10 plants/plot at Holetta from June to October 2018 for further selection. Single spray of contact fungicide (i.e., Mancozeb) was applied at 30 DAP during the growing season, and tubers were harvested 110 DAP. There was a significant difference among the clones for total and marketable tuber yield (Table 8). Eighteen clones were identified that displayed over 10% total and marketable tuber yield advantage as compared with the existing best check cultivar 'Belete' (Table 9).

TABLE 8. ANOVA ON TOTAL AND MARKETABLE YIELD OF POTATO TUBERS OF CLONES FROM CROSSES OF ADAPTED AFRICAN GERMPLASM DURING 2018 GROWING SEASON IN 2018 AT HOLETTA, ETHIOPIA

Source of Variation	d.f.	Total Tuber Weight (kg)	Marketable Tuber Weight (kg)
Replication	1	0.0002	0.016
Genotype	71	0.1404***	0.1194***
Residual	71	0.0208	0.0155
CV		24.4	22.5
Mean		0.59±0.14	0.48±0.12

TABLE 9. YIELD PERFORMANCE OF SELECTED LB-RESISTANT CLONES FROM CROSSES OF ADAPTED AFRICAN GERMPLASM IN 2018 AT HOLETTA ETHIOPIA

Rank	Clone	Status	Total Tuber Yield (ha)*	Marketable Tuber (ha)	Above Best Check
1	CIP314022.23	Selected	56.76	47.52	68%
2	CIP314035.21	Selected	53.68	44.88	58%
3	CIP314022.22	Selected	53.24	49.72	57%
4	CIP314005.39	Selected	51.92	42.24	53%
5	CIP314035.12	Selected	45.76	38.72	35%
6	CIP314035.1	Selected	44.00	40.04	30%
7	CIP314035.5	Selected	43.56	33.00	29%
8	CIP314005.6	Selected	42.24	37.84	25%

Rank	Clone	Status	Total Tuber Yield (ha)*	Marketable Tuber (ha)	Above Best Check
9	CIP314030.2	Selected	41.80	37.84	23%
10	CIP314022.11	Selected	39.60	33.88	17%
11	CIP314030.14	Selected	39.16	32.56	16%
12	CIP314030.32	Selected	39.16	32.12	16%
13	CIP314005.20	Selected	38.72	33.00	14%
14	CIP314022.6	Selected	38.28	30.36	13%
15	CIP314022.13	Selected	38.28	35.20	13%
16	CIP314005.23	Selected	37.84	34.32	12%
17	CIP314022.29	Selected	37.84	34.76	12%
18	CIP314005.1	Selected	37.40	30.80	10%
	Belete	Check	33.88	29.04	
	Gudene	Check	32.12	28.60	
	Jalene	Check	28.60	24.20	

* Contrast scale: "dark to light gray color" reflecting the yield performance "high to low" across clones.

A preliminary variety trial is planned for the five selected clones from LBHT x LTVR population and 18 selections from SSAP population to identify at least three high-yielding (>40 t/ha), LB-resistant varieties (better than resistant variety 'Belete') with best cooking quality for traditional potato-growing areas (altitude >1,800m) with one or no spray of fungicide.

Milestone 3: Evaluation of CIP potato clones for suitability to Rwandan potato growing agro-ecologies

Five potato clones (CIP393280.64, CIP393371.58, CIP393077.159, CIP396018.241, and CIP398190.615) were selected among 43 clones introduced in 2013 from CIP–Lima. These clones were evaluated under the National Performance Trials in 2018 and tested in different agro-ecological areas, including the mid-altitude and warmer areas; they have proved to be suitable. They were also evaluated by all the stakeholders, including farmers (producers), restauranteurs, processors (users), and consumers. The ANOVA of yield data reveals significant effects of clones, sites, and genotype by environmental (G x E) interaction (Tables 10 and 11).

TABLE 10. PARAMETERS ESTIMATE FROM ANOVA OF SEVEN CLONES OF POTATO ASSESSED FOR TUBER YIELD IN MULTILOCATION TRIALS IN 2018, RWANDA

Source	DF	SS	MS	F	Probability
Genotype (G)	6	7429.0	1238.2	42	0.00001
Environment (E)	14	21863.5	1561.7	53	0.00001
Rep/E	30	971.3	32.4	1.1	0.34033
G x E	84	6900.0	82.1	2.8	0.00001
Error	180	5304.6	29.5		
Total	314	42468.5			
Mean	17.6				
Std. Error	5.4				
CV%	30.8				
LSD5%	9.0				
G/GGE	51.9				

NOTE: Tuber yield is measured in t/ha.

TABLE 11. ENVIRONMENTAL STATISTICS ESTIMATE FROM SEVEN CLONES OF POTATO ASSESSED FOR TUBER YIELD IN 2018, RWANDA

	Sites	Gen	Rep	Mean	Max	SE	LSD5%	SD	Heritability	CV%
1	Rwamagana	7	3	34.92	49.05	6.61	11.97	8.72	0.81	18.93
2	Kayonza*	7	3	19.34	27.51	10.31	18.67	7.41	0.35	53.32
3	Cyuve	7	3	38.60	51.90	6.75	12.21	12.75	0.91	17.47
4	Kinigi	7	3	9.80	17.55	1.91	3.46	5.49	0.96	19.49
5	Ruhunde	7	3	10.47	13.24	2.21	4.01	2.56	0.75	21.15
6	Kisaro	7	3	13.27	18.07	3.00	5.42	4.59	0.86	22.57
7	Uwinkingi	7	3	16.86	28.65	2.46	4.45	6.79	0.96	14.57
8	Kigeme	7	3	13.30	19.29	3.42	6.20	4.11	0.77	25.74
9	Karongi	7	3	12.75	19.00	3.67	6.64	4.18	0.74	28.76
10	Busasamana*	7	3	16.43	40.63	7.35	13.31	14.16	0.91	44.73
11	Kabatwa*	7	3	7.71	12.43	6.39	11.57	3.07	0.00	82.83
12	Mukura	7	3	20.67	28.66	5.98	10.82	4.94	0.51	28.93
13	Nyabimata	7	3	17.90	26.62	4.59	8.32	5.63	0.78	25.67
14	Nyabirasi	7	3	13.76	20.50	3.17	5.74	5.31	0.88	23.03
15	Jenda	7	3	18.51	28.32	6.01	10.88	8.38	0.83	32.46

* Poor precision, for further decision it must be discarded.

Across 15 sites, among the newly tested potato clones, the highest yield was 22.03 t/ha, and of observed on CIP393371.58. However, this yield was low compared with local checks 'Kirundo' and 'Kinigi', with 24.39 and 21.26 t/ha, respectively. The yields of 16.96, 16.48, 11.33, and 10.89 t/ha were observed on clones CIP393077.159, CIP393280.64, CIP398190.615, and CIP39601.241, respectively (Table 12).

TABLE 12. MEAN OF POTATO TUBER YIELD OF SEVEN CLONES TESTED AT 15 RWANDA LOCATIONS IN 2018

Sites	Clone							Site mean
	CIP393077.159	CIP393280.64	CIP393371.58	CIP396018.241	CIP398190.615	Kinigi	Kirundo	
Cyuve	51.90	48.98	40.13	24.87	17.67	40.43	46.23	38.60
Rwamagana	29.55	32.18	49.04	21.39	37.85	34.17	40.25	34.92
Kayonza	22.59	21.32	27.51	7.82	12.00	17.23	26.88	19.34
Jenda	21.30	16.75	28.32	9.76	5.42	22.23	25.76	18.51
Busasamana	17.40	4.43	25.61	2.47	3.36	21.11	40.62	16.43
Mukura	15.75	28.66	22.01	17.49	16.14	25.52	19.08	20.67
Nyabimata	13.98	15.64	18.62	15.01	11.19	24.22	26.62	17.90
Uwinkingi	13.30	13.96	18.87	9.68	11.29	22.29	28.65	16.86
Kigeme	12.07	8.62	14.11	10.64	10.14	19.29	18.24	13.30
Nyabirasi	11.37	10.09	18.35	8.01	8.98	20.50	19.03	13.76
Kisaro	10.46	13.28	18.07	5.09	12.17	16.52	17.33	13.27
Karongi	9.83	11.96	16.73	8.90	8.07	14.78	19.00	12.75
Ruhunde	9.81	12.41	13.02	7.78	6.77	13.24	10.25	10.47
Kinigi	8.26	4.16	13.00	4.99	5.20	17.55	15.45	9.80
Kabatwa	6.81	4.71	7.01	9.46	3.71	9.87	12.43	7.71
Clone mean	16.96	16.48	22.03	10.89	11.33	21.26	24.39	17.62

However, potato clones CIP398190.615, CIP393371.58, and CIP393280.64 showed the lowest score of LB (9%, 13%, and 14 %, respectively) compared with local checks 'Kinigi' and 'Kirundo' (19% and 20%, respectively). The clones CIP398190.615, CIP393077.159, and CIP393280.64 showed lowest virus incidence (6%, 10%, and 12%, respectively) compared with the virus incidence of local checks 'Kirundo' (13%) and 'Kinigi' (17%) (Table 13).

TABLE 13. MAIN CHARACTERISTICS OF SEVEN CLONES ASSESSED DURING THE PERIOD OF VEGETATIVE DEVELOPMENT AT 15 SITES IN 2018, RWANDA 2018

Clones	Characteristics				
	PGH	Uniformity	Vigor	LB (%)	Virus (%)
CIP393077.159	Decumbent	Uniform	Vigorous	28	10
CIP393280.64	Decumbent	Intermediate	Medium	14	12
CIP393371.58	Decumbent	Uniform	Vigorous	13	17
CIP396018.241	Semi-Erect	Intermediate	Medium	27	32
CIP398190.615	Decumbent	Uniform	Medium	9	6
Kinigi	Decumbent	Uniform	Vigorous	19	17
Kirundo	Decumbent	Uniform	Vigorous	20	13

PGH = plant grow habit; vigor = plant vigor; LB (%): percentage of LB incidence; Virus (%) = percentage of virus incidence.

It was observed that clones CIP393077.159 and CIP398190.615 reveal a high stability with the lowest absolute number of instabilities mean compared with local checks 'Kinigi' (1.7) and 'Kirundo' (4.1) (Table 14 and Fig. 6).

TABLE 14. PREDICTED MEAN AND INSTABILITY PARAMETER OF SEVEN CLONES FOR TUBER YIELD ACROSS 15 ENVIRONMENTS IN 2018, RWANDA

Entries	Measured	Predicted	Instability*	Integrated
Kirundo	24.1	26.2	4.1	24.1
Kinigi	22.2	23.6	1.7	22.7
CIP393371.58	21.9	23.5	-2.1	22.4
CIP393280.64	16.4	15.8	-5.7	18.6
CIP393077.159	15.9	15.5	-0.7	15.9
CIP398190.615	11.4	9.6	0	9.6
CIP396018.241	11.4	9.2	2.6	10.5

* A greater absolute value of Instability means greater contribution to GE and less stable.

All the new tested potato clones revealed a DM content that is above 18% of total fresh weight except CIP396018.241 which has 17.1% of fresh weight. This dry matter content was comparable with the dry matter content of Kinigi. Based on color of crisps, clones CIP393077.159, CIP393280.64, CIP396018.241, CIP398190.615 showed the same trend as local check Kinigi. The crisps from these clones were ranked as good or very good for taste and crunch (Table 15).

TABLE 15. PROCESSING ASSESSMENT OF FIVE NEW POTATO CLONES AND LOCAL VARIETIES, RWANDA 2018.

Clone	Shape	Eyes	Sp. Gr.	DMC (%)	Taste	Crunch	General Comments
CIP393077.159	Round	Deep	1.06	18.2	Good	Good	Good
CIP393280.64	Round	Shallow	1.07	18.4	Good	Good	Good
CIP393371.58	Round	Shallow	1.07	18.4	Bad	Bad	Bad
CIP396018.241	Round	Deep	1.06	17.1	Good	good	Very good
CIP398190.615	Long	Shallow	1.07	18.4	Bad	Good	Very good
Kirundo	Round	Shallow	1.06	16.9	Good	Bad	Bad
Kinigi	Round	Deep	1.08	19.2	Good	Very good	Very good

The adaptation of clones CIP393280.64, CIP393077.159, CIP396018.241, and CIP398190.615 was as low as 'Kinigi', and recommendation by region should be considered due to the G X E effect observed (Figs. 6–8). The results of this study highlight that the clones of CIP393371.58 and CIP393077.159 are candidate for new varieties for high tuber yields, whereas clones CIP398190.615, CIP396018.241, and CIP393280.64 are candidates for new potato varieties for chipping and French fries. These five varieties

were released in early 2019 and are the first new released varieties since 1996 in Rwanda. They will revitalize the potato value chain (Table 14). These varieties are market-oriented compared with those currently grown, striking a balance in addressing farmers' limited ability to purchase inputs and meeting diverse market demands. New genetics and varieties, after such a long time, are pivotal to stimulate market interest and simultaneously uplift the seed system.

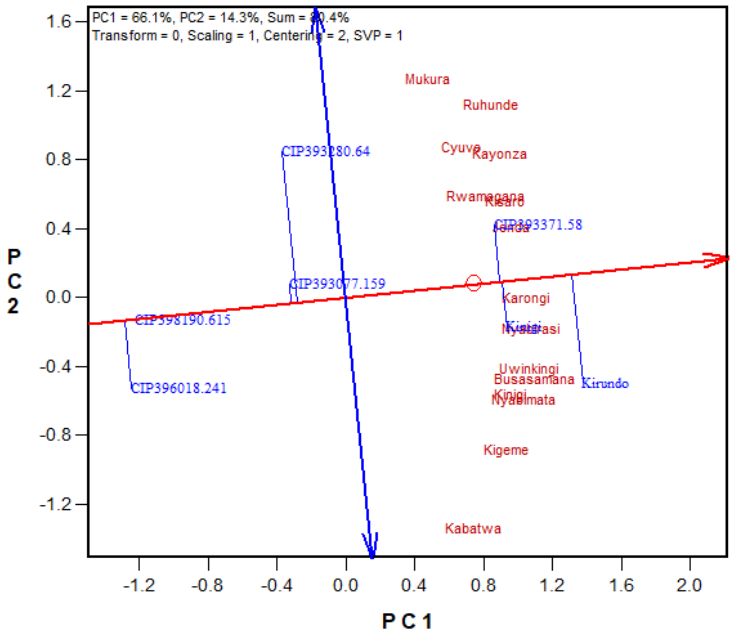

Figure 6. The "mean vs. stability" view of the GGE (genotype main effect (G) plus G x E interaction) biplot based on the G × E data. The biplot is appropriate for visualizing the *similarities among genotypes*. It explained 80.4% of the total G + GE. The genotypes are labeled in blue and the environments are labeled in red.

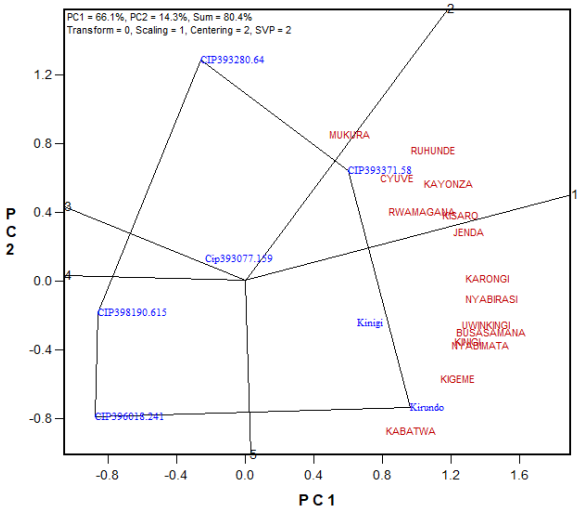

Figure 7. The "which-won-where" view of the GGE biplot based on the G × E data. The biplot is appropriate for visualizing the relationships among environments and genotypes. It explained 80.4 % of the total G + GE. The genotypes are labeled in blue and the environments are labeled in red.

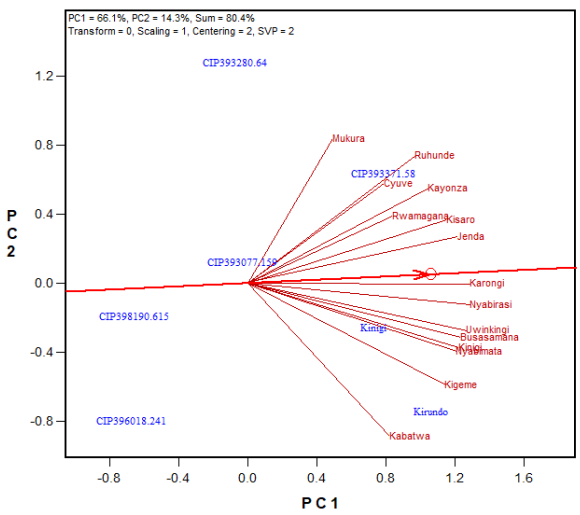

Figure 8. The "discriminating power vs. representativeness" view of the GGE biplot based on the G × E data. The biplot is appropriate for visualizing the relationships among environments. It explained 80.4% of the total G + GE. The genotypes are labeled in blue and the environments are labeled in red.

Milestone 4: Breeding new elite potato clones combining yield, LB resistance, earliness, mid-dormancy, and cooking quality for African highlands

CIP is working to expand and modernize its breeding operations in Africa toward a market-demand approach to increase GG and varietal adoption. The focus of the regional-breeding program is on integrated breeding strategies that use the knowledge of scientists as well as farmers and other actors in the potato value chain, particularly strategies that pay attention to gender-differentiated preferences of producers and consumers of all ages. The program works from a regional breeding hub in Kenya. Ethiopia serves as a secondary site under CIP's Potato Agri-food Systems program targeting African Highlands in Kenya, Ethiopia, Rwanda, Tanzania, Uganda, Malawi, Nigeria, Angola, Cameroon, Madagascar, the Democratic Republic of Congo, Mozambique, and Burundi.

The potato-breeding goals in Africa include developing (1) durable resistance to predominant diseases (LB, virus, BW), (2) stable yields and quality with less water and under warmer temperatures, and (3) varieties matching cropping system requirements; and (4) improving nutritional and market traits.

The regional potato-breeding effort is based on rational use of adapted African potato germplasm to exploit the power of heterosis and increase diversity by introducing new alleles from exotic germplasm into elite breeding populations, producing novel, locally adapted potato varieties (Table 16).

TABLE 16. POTATO BREEDING PIPELINE FOR AFRICA (PRODUCT PIPELINE)

Variety to be Replaced	Geographic Targets	Agro-Climatic Zone Being Targeted	*Stage 1*	*Stage 2*	*Stage 3*	*Stage 4*	*Stage 5*	*Stage 6*
			Development & Early Product Testing	*Early Product Testing*	*Late Product Testing*	*Late Product Testing*	*External Testing*	*Product Introduction*
Gudene	Regions Amahara and Oromia (Ethiopia)	Highland	2,850 (SAP)	57 (Biofortified)	18 (SAP)	8 (LBHT)	CIP312921.654 CIP312930.557 CIP312930.509 CIP312922.508 CIP312922.626	
TBD	Melkasa, Koga, Gode, Diredawa (Ethiopia)	Mid-elevation			64			
Shangi	Kenyan Highlands	Highland	3,100 (SAP)	57 (Biofortified)	77 (SAP)	CIP312284.737 CIP312084.731 CIP313001.649 CIP313011.28 CIP314938.14		CIP392797.22 (Unica) CIP393371.157 (Wanjiku)
Sherekea	Sub-Saharan Africa (SSA)	Mid-elevation		20 (LTVR)				CIP392797.22 (Unica) CIP398208.704 (Chulu) CIP398190.200 (Nyota)
TBD	African highlands	Highland		215 (B)				

*Source of breeding materials displayed on the table: SAP = crosses of adapted African potato germplasm, biofortified = tetraploid advanced clones derived from crosses of LTVR vs. diploid biofortified parents. The numbers within the table refer to the number of clones selected.

Advanced clones have been selected under local African conditions over the last 5 years and are potential candidates to replace the existing varieties were identified (Fig. 9).

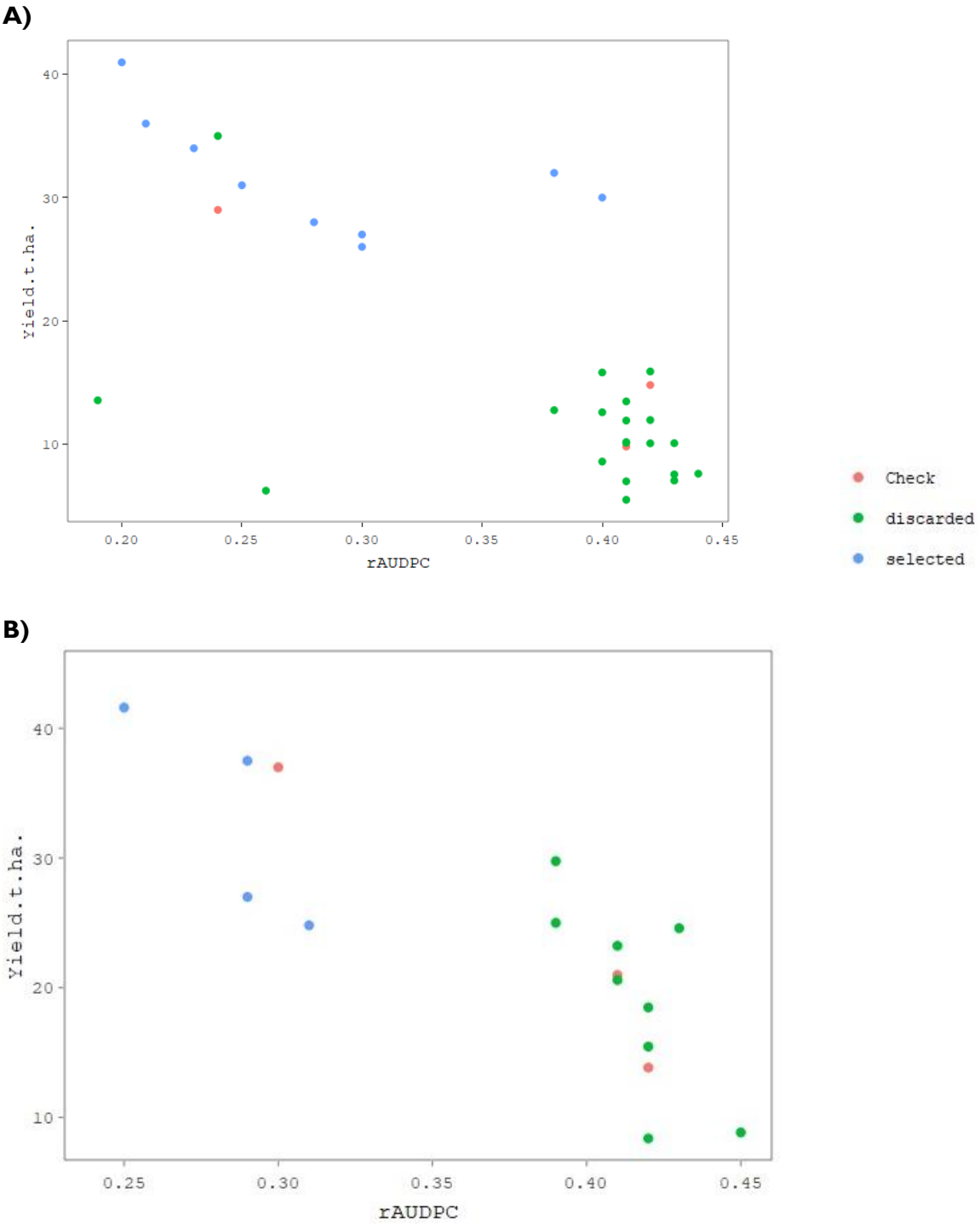

Figure 9. Performance of advanced potato clones under natural LB pressure—Kenya 2017 and 2018. A) Clones from crosses of adapted African potato germplasm and B) clones from LTVR x LBHT crosses made in Peru.

The following populations and clone sets are being evaluated in the field in Kenya: (1) advanced inter-cross (LTVR x LBHT) population introduced as TS families from HQ in 2013; (2) SAP (SSA population) crosses made in Nairobi from 2013 to 2017; (3) advanced clones selected at Peruvian highland tropical regions under LB pressure. The most advanced clones were introduced to tissue culture lab for cleaning. They will be shared across African highland countries and will be tested in the National Performance Trials.

The next step to improve the relevance and effectiveness of the potato product pipeline for Africa (Table 1) will be the annual advancement meeting of a cross-functional team (breeders, pathologists, social scientists, farmers, seed producers, etc.) from the potato value chain, validating the clones selected in the breeding trials.

Milestone 5: At least five advanced clones (out of 69) from LBHT x LTVR population with resistance to LB, high tuber yield, earliness, and cooking quality for Ethiopian highlands (Q1 2019)

In the 2017 growing season, about 442 progenies derived from crossing of LBHT x LTVR populations were tested at Holetta Agricultural Research Center for LB resistance and yield under LB pressure. About 63 clones that showed 46% and 63% yield and LB resistance advantage, respectively, over the entire population were selected. Seventy-two clones, including the 63 selections from the previous year, 6 advanced cones from LBHT x LTVR population, and three Ethiopian cultivars, were planted in 9 x 8 alpha lattice design in two replications and 10 plants/plot at Holetta from June to October 2018. Tubers were harvested 110 DAP. There was significant differences among the clones for all the traits assessed (Table 17). Five clones were identified that displayed over 10% total and marketable tuber yield advantage as compared with the existing best check cultivar 'Belete'. Figure 10 shows the potential of the selected clones against the main checks for yield. Table 18 displays the selected clones with checks and elite clones from LBHT x LTVR population that were evaluated together.

TABLE 17. ANOVA INVOLVING 72 CLONES IN 2018 GROWING SEASON, HOLETTA ETHIOPIA

Source	d.f.	Traits*				
		TTWPL (kg)	MTWPL (kg)	AUDPC (g)	ATW (g)	ATMW (g)
Replication	1	0.0029	0.0093	90902	1506.37	82.1
Genotype	71	0.0634**	0.0402**	447189**	612.6**	991.4**
Residual	71	0.0099	0.0101	24999	95.05	234.3
CV		16.2	22.5	16	16	19
Mean		0.6±0.1	0.4±0.1	985.5±158.1	61±9.8	80.4±15.3

*TTWPL=Total tuber weight/plant; MTWPL = Marketable tuber weight/plant; ATMW = Average marketable tuber weight.

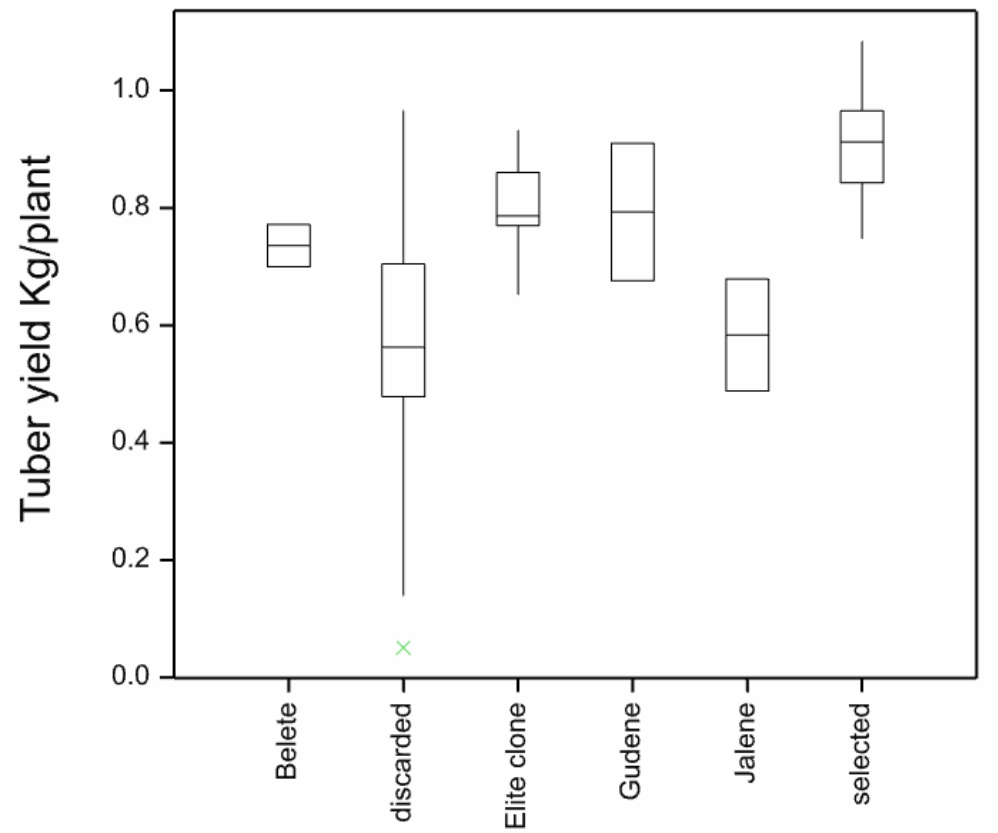

Figure 10. Yield distribution of 72 clones evaluated in 2018 growing season at Holetta, Ethiopia.

TABLE 18. SELECTIONS FROM LBHT X LTVR POPULATION PLUS CHECKS AND ELITE CLONES AND THEIR YIELD AND LB SEVERITY AT HOLETTA (2017–2018)

Clone	Status	TTWPL[1]		MTWPL[2]		AUDPC	
		2017	2018	2017	2018	2017	2018
CIP312921.654	Selected	0.75	0.97	0.57	0.69	2692	611
CIP312930.557	Selected	0.91	0.96	0.59	0.66	1487	514
CIP312930.509	Selected	1.27	0.90	1.27	0.75	1372	333
CIP312922.508	Selected	1.30	0.89	1.15	0.64	1627	791
CIP312922.626	Selected	0.98	0.82	0.96	0.64	1240	495
CIP312927.593	Elite clone		0.86		0.75		610
CIP312922.528	Elite clone		0.78		0.58		635
Gudene	Check	0.75	0.79	0.68	0.68	1251	460
Belete	Check	0.63	0.74	0.61	0.58	1671	1236
Jalene	Check	0.36	0.58	0.25	0.49	3091	1260

[1]Obtained by dividing total tuber weight per plot with number of plants harvested per plot (kg/plant), [2]computed by dividing the weight of healthy and >30-mm tubers in diameter (marketable tubers) per plot by number of plants harvested per plot (kg/plant).

Milestone 6: At least three high-yielding (>40 t/ha), LB-resistant varieties (better than resistant variety 'Belete' or 'Gudene') with best cooking quality for traditional potato-growing areas (altitude >1,800 masl) and farmers' preferred traits identified

Over the past 5 years, 15 best materials were selected in Ethiopia from LBHT x LTVR population initially obtained from TPS imported from CIP–Lima. The selection was based on tuber yield, LB

resistance, and organoleptic characteristics (mainly boiled tuber taste and texture). In 2018 gender-disaggregated PVS by farmers was started in order to identify the most promising clones as a variety preferred by farmers.

Fifteen clones and 3 local checks ('Dagim', 'Gudene', and 'Jalene') were planted in randomized complete block replications and 40 plants/plot from June to October 2018 at two research stations in Ethiopia: Holetta (Oromia region, 2,400 masl, latitude 8.88333, longitude 38.38333) and Adet (Amhara region, 2,238 masl, latitude 11.265838, longitude 37.488772). Clones were evaluated at flowering, harvesting, and after harvest for the farmers' preferred traits. In addition, data were collected for yield and LB severity.

Twenty-five (14 female, 11 male) potato-growing smallholder farmers from Welmera district were invited to Holetta Research station to evaluate the materials at flowering, harvest, and 10 days after harvest for organoleptic characteristics (taste and texture). Before the evaluation, men and women were organized into separate groups for focused group discussion to account for gender differences in trait preference. Supported by facilitators who spoke their local language, farmers listed their selection criteria at different stages of the plant. The criteria were classified as production and market traits (Table 19).

TABLE 19. LISTS OF TRAITS IDENTIFIED BY FARMERS

Gender Group	Production Related/Agronomic Traits	Market/Consumption Related Traits
Trait mentioned by both gender group	Disease resistance Large number of stems Thick and strong stem Broad leaves Deep green foliage High tuber yield	Tuber flesh color (preferably white), Medium-sized tuber Tubers free from cracks Easy to peel (shallow eye depth) Floury taste when cooked Tubers don't crack when boiled Tubers do not have bitter or metallic tastes
Traits mentioned only by women	Abundant leaves that stays longer in the plant Uniformly flowering Medium plant height/no lodging	Long storability Smooth skinned tuber Tubers hold their shape in stew
Traits mentioned only by men	White flowers require longer to drop Vigor Medium maturing	Oval shape Not sticky when boiled Needs short time to cook

At flowering and harvesting, farmers selected their most preferred clones. To differentiate men and women's choices, men were each given six corn kernels and women six bean seeds each. A covered container was placed at the end of each plot (per clone). The male and female farmers were to select the preferred clones by placing three corn kernels or three bean seeds in the container for their most preferred clone, two corn kernels or bean seeds for the second most preferred clone, and one corn kernel or bean seed for the third choice. Farmers used all the three replications for their selection. Tuber yield and yield-related traits were measured at both locations.

The best 11 clones in terms of yield and farmers' preference at harvest and flowering stage were selected for organoleptic testing (appearance, taste, and texture) along with the check variety 'Gudene'. 'Gudene' is a well-known variety for its acceptable organoleptic property and for its resistance to LB in Ethiopia. The selection was made using a 5-point scale, with 1 implying that the clone has very low quality, and 5 signifying that the clone is of a very high quality.

One-way ANOVA were used to analyze the data. Mean of the treatments was compared using Fisher's least significant difference at 0.05 level of significance.

Farmers listed their preferred characteristics through focus group discussions and helped to identify traits that need to be added to varietal selection criteria. Farmers' criteria for selection differed by gender. At flowering, women farmers selected materials with disease resistance, more stems per plant, thick and strong stems, broader leaves, and those with more abundant green foliage (in order of importance). Male farmers went for medium-maturing, white-flowered materials that maintain their flower longer, more stems per plant, disease resistance, and thick and strong stems. At harvest the top three preferred selection criteria for both men and women were the same: high tuber yield, medium tuber size, and tuber flesh color (market preferred).

Quality traits in the boiled potatoes—important for both men and women—were floury texture, tubers that do not crack when boiled, and do not have a bitter or metallic taste. In addition, women mentioned tubers that hold their shape in stew as an important trait—a clear indication of women's responsibility in food preparation. Tables 20 and 21 summarize traits more preferred by men and women. Both genders are equally important.

TABLE 20. SUMMARY OF GENDER-BASED FARMERS' TRAIT PREFERENCES

Traits Mentioned Only and/or Ranked Higher by Women	Traits Mentioned Only and/or Ranked Higher by Men	Traits Mentioned and/or Ranked the Same by Women and Men
Disease resistance	White flowers and that take long to drop	Large number of stems
Thick and strong stem	Vigor	High tuber yield
Broad leaves	Medium maturing	Tuber flesh color (preferably white)
Abundant leaves that stay longer on the plant	Oval shape	Medium-sized tuber
Uniformly flowering	Not sticky when boiled	Tubers free from cracks
Medium plant height/no lodging	Tubers need short time to cook	Floury taste when cooked
Easy to peel (shallow eye depth)		Tubers do not crack when boiled
Long storability		Tubers do not have a bitter or metallic taste
Smooth-skinned tuber		
Tubers hold their shape in stew		

TABLE 21. CHARACTERISTICS OF CLONES PREFERRED BY FEMALE AND MALE FARMERS AT FLOWERING AND HARVEST

Selection Criteria	Women			Men	
	Frequency	Rank		Frequency	Rank
Flowering					
Disease resistance	53	1		8	4
Large number of stems	47	2		17	3
Thick and strong stems	26	3		4	5
Broad leaves	21	4		3	7
Abundant leaves that stays longer in the plant	20	5		-	-
Uniformly flowering	16	6		-	-
Deep green foliage	16	7		4	5
Medium plant height/no lodging	11	8		-	-
White flowers and that take long to drop	-	-		18	1
Plant vigor	-	-		3	7
Medium maturing	-	-		18	1
Harvesting					
High tuber yield	61	1		53	1
Tuber flesh color (preferably white)	58	2		30	3

Selection Criteria	Women			Men	
	Frequency	Rank		Frequency	Rank
Medium-sized tuber	40	3		34	2
Free from crack s	28	4		14	5
Long storability	20	5		-	-
Easy to peel (shallow eye depth)	3	6		5	6
Oval shape	-	-		29	4

Farmers identified their most preferred clones that had the traits they need. The participative selection approach can reduce the time for uptake by increasing likelihood of acceptance through early exposure of farmers and consumers, including gender preferences. Results showed no statistically significant differences by gender for organoleptic characteristics evaluation, thus the data were not disaggregated by sex. Both women and men identified their best three clones, among which CIP312927.593 and CIP312927.610 were the most frequently selected by both gender groups at the flowering stage. The female group uniquely selected CIP312922.528 as their second most preferred clones; the reason for this could probably be attributed to women's sole selection criteria listed in Table 22. At harvest, likewise, farmers identified their best three clones. Of these CIP312920.532 and CIP312920.515 were most frequently selected by both gender groups. CIP312921.525 was uniquely selected by female farmers as their second-best clone.

TABLE 22. YIELD, LB SUSCEPTIBILITY SCALE VALUES, AND TUBER DM CONTENT OF EIGHT SELECTIONS FROM LBHT X LTVR POPULATION

Clone	Yield (t/ha)					LB Score			DM (%)
	Holetta		Combined[1]	Average		Holetta			
	2016	2017	2018			2016	2017		2018
CIP312920.515	40.0	35.6	38.4	38.0		2	6		19
CIP312927.593	48.0	45.8	36.6	43.0		1	4		22
CIP312922.528	41.3	47.6	34.0	41.0		1	3		21
CIP312921.525	26.2	34.7	29.3	30.0		2	4		22
CIP312927.618	36.9	43.1	25.7	35.0		1	3		18
CIP312921.603	23.1	33.8	25.7	28.0		1	5		19
CIP312920.532	16.0	27.6	24.3	23.0		3	5		22
CIP312923.634	41.8	50.2	23.0	38.0		0	2		19
Gudene	26.2	26.2	20.8	24.0		1	4		20
Jalene	10.7	16.3	24.2	17.0		7	7		19
Mean square	240**	368**	208**			525987**	1969956**		11**
N. plants/plot	5	10	16			5	10		16
Rep	2	3	3			2	3		3
N. clones	83	21	18			83	21		18
Mean	20.0	30.4	26.2			922	2199		20
CV (%)	25	19	20			24	15		5

[1]Combining Holetta and Adet trials, 1Computed by converting the total weight of all the tubers harvested in a plot to t/ha,**P <0.001.

Organoleptic quality is one of the most important factors that affects end-user's preference and, eventually, varietal adoption. The same farmers tasted the best 11 clones in terms of yield and farmers' preference at harvest and flowering stage along with the check variety 'Gudene'. From the clones evaluated, farmers identified two clones with bitter taste and soggy texture, namely CIP312921.651 and

CIP312927.610. Thus, these two clones will be dropped from next season's evaluation regardless of their yield performance and farmers' selection score at harvest and flowering.

In general, CIP312920.515, CIP312923.634, and CIP312927.618 are the best three clones that combined yield, farmers' preference, and organoleptic quality. They showed 30–65% yield increments over 'Gudene', fairly to overwhelmingly selected by both gender groups at harvest, and had fair to excellent organoleptic taste. See Table 23 for summary data on the selected clones for the traits assessed.

TABLE 23. FREQUENCY OF SELECTION AND ORGANOLEPTIC TASTING BY FARMERS OF EIGHT CLONES FROM LBHT X LTVR POPULATION IN THE 2018 GROWING SEASON AT HOLETTA, ETHIOPIA

Clone name	Frequency of Selection by Gender of Farmers								Organoleptic Tasting[1]		
	Flowering				Harvest				Appearance	Taste	Texture
	Women	Men	Total		Women	Men	Total				
CIP312920.515	1	6	7		12	20	32		4.5	3.3	2.5
CIP312927.593	19	16	34		0	6	6		3.0	3.0	2.6
CIP312922.528	15	1	16		0	0	0		3.6	3.1	2.9
CIP312921.525	2	2	4		12	1	13		4.7	4.0	3.8
CIP312927.618	10	9	19		4	5	9		3.8	3.7	3.5
CIP312921.603	0	0	0		6	1	7		3.8	3.2	2.2
CIP312920.532	0	1	1		13	7	19		4.7	3.6	2.9
CIP312923.634	0	0	0		6	6	12		4.6	4.5	4.0
Gudene	5	5	12		9	0	9		4.0	4.0	3.3
Mean square									10.4*	9.2*	26.6*
Mean									3.9±0.3	3.4±0.4	5.8±0.6

[1] 5 is excellent and 1 is poor taste and texture; **P <0.001.

DELIVERABLE 2.2: OPTIMIZED BREEDING PIPELINE FOR SELF-COMPATIBLE INBRED LINES

(Breeders: Monica Santayana, Hannele Lindqvist-Kreuze, and Thiago Mendes)

The potential of using TPS in developing uniform 4x families was tested at CIP in the 1990s, but the approach was put on hold due to genetic constraints and low market potential. Important breakthrough research on the genetics of potato self-incompatibility 1 and the subsequent identification of self-compatible diploid wild accessions 2 or landraces 3 has re-opened the possibility of turning potato into a seed-propagated crop. Breeding at diploid level enables combining of traits in a single variety much faster than at tetraploid level, and recent reports suggest that yield of diploids is comparable to that of tetraploid cultivars. CIP has long experience in working with the technologies required for ploidy and fertility manipulation, and has been developing dihaploid genotypes from its best tetraploid clones during the last 10 years.

In this project we have started a systematic effort to develop the first CIP-bred diploid hybrid potatoes. The goal is to develop the first (nearly) homozygous lines by the end of 2021 and the first hybrid candidate varieties that would be distributed as TS for variety testing in Africa in 2022.

2.2.1 Identification of fertile dihaploids from most promising LTVR, TPS, and B3 populations

Milestone 1: At least 10 dihaploids with the best reproductive traits identified from the breeding populations LTVR and B3

CIP's breeding populations adapted for different agro-ecologies and containing valuable traits such as abiotic and biotic stress tolerance and good nutritional qualities are considered cornerstones of the hybrid breeding program. The goal is to develop dihaploid genotypes that combine the favorable agronomic and stress-tolerance alleles as well as alleles favorable for reproductive traits to ensure profuse flowering and good seed set. During the last 10 years, 1,440 dihaploid genotypes originating from 49 tetraploid clones have been identified (Table 24).

To identify the genotypes with best potential as female and male progenitors, the dihaploids were evaluated for the reproductive characteristics including flowering degree, pollen quantity, and pollen viability following previously published protocols. Those with moderate to profuse flowering (degree of flowering > 4) and low pollen quantity or viability were considered as potential female progenitors, whereas those with good pollen quality (>2) and pollen viability (>60%) were considered as potential male progenitors. See Appendix A3_Potato for details of the reproductive characteristics of the dihaploids.

Development of the dihaploids is a continuous activity of the hybrid potato breeding project and will continue in order to identify at least 10 dihaploid genotypes with good reproductive traits every year. In the next step the dihaploids will be altered from self-incompatible to self-compatible plants by introducing the S-locus inhibitor gene (Sli) to enable cycles of selfing and development of homozygous diploid lines.

TABLE 24. POTATO DIHAPLOID (DH) POPULATIONS FOR 2X BREEDING

Population	Main Traits of Interest	Tetraploid Progenitors	DHS Evaluated	DHS Selected
B3	Highland and mid-elevation adaptation, LB resistance	5	22	9
BW	BW resistance	1	30	6
LBHT-1	LB resistance, heat tolerance	4	20	2
LTVR	Lowland adaptation, virus resistance, heat tolerance	36	1,327	38
Released varieties	Various traits	3	39	1
Total		**49**	**1,438**	**56**

NOTE: The inducers were *S. phureja* IVP-101, IVP-35 or C96HI-01.4.

2.2.2 Development of self-compatible and homozygous lines

Milestone 1: At least five self-compatible dihaploids developed from each of the main breeding populations (Q4 2019)

To restore the self-compatibility in the dihaploids these are pollinated with different Sli-donors available. So far, the genotypes CIP819002.6 (97H32-6) and CIP819002.14 (97H32-14) have been successfully crossed with eight selected dihaploids from LTVR, B3, and varieties groups, producing a total of 449 berries (Table 25). On average, 50% of all flowers crossed resulted in berry formation. The seed from these crosses will be evaluated for self-compatibility to select the genotypes for subsequent cycles of selfing. The first self-compatible dihaploids are expected to be identified by the end of 2020; hence this milestone will not be achieved according to the plan. However, this activity is also continuous, and the annual goals will be adjusted based on experience gained during the first year of this project.

The self-compatibility restoration of the remaining dihaploids will continue using the same Sli-donors as well as two additional Sli-donors developed by CIP. These so called BSli genotypes CIP511008.122 (BSli-008.122) and CIP511007.005 (BSli-007.005) are hybrids between diploid landraces and the above mentioned Sli-donors.

TABLE 25. CROSSES MADE BETWEEN DIHAPLOIDS AND SLI-DONORS AND SUCCESSFUL FERTILIZATIONS RESULTING IN BERRIES

			Male CIP No. (Sli-donors)					
			CIP819002.14			CIP819002.6		
Pop.	Dihaploid CIP No.	Dihaploid Breeder Code	Attempts	Flowers	Fruits	Attempts	Flowers	Fruits
BW	CIP315040.004	PL-DT5.004	29	136	106	36	148	95
LTVR	CIP315047.053	PL-DT8.053	0	-	-	1	3	3
LTVR	CIP315048.004	35-DT8.004	0	-	-	1	6	1
LTVR	CIP315048.048	35-DT8.048	21	99	61	25	106	47
Varieties	CIP315052.002	PL-DT10.002	2	13	12	2	10	9
LTVR	CIP316618.010	35-HT2.010	6	33	30	7	45	33
LTVR	CIP316620.002	35-HT1.002	1	2	2	2	7	5
B3	CIP515521.002	PL-HT13.002	24	139	23	27	151	22
	Total		**83**	**422**	**234**	**101**	**476**	**215**

Milestone 2 (New): Workflow optimized for the development of the homozygous lines (Q4 2020)

While the self-compatible dihaploids are being developed, we are using other self-compatible diploids to develop a workflow for the development of homozygous lines. Most of the diploid potatoes are self-incompatible, but spontaneously self-compatible landraces have been previously identified at CIP from the cultivar groups Phureja, Andigena, and Stenotomum and these are being used to develop homozygous lines. These materials are valuable sources for fertility restoration because they are cultivated landraces with acceptable tuber quality. The mechanism of self-compatibility in these genotypes will be tested through reciprocal crosses to confirm whether it is pollen specific like Sli.

Each landrace started with a single parent (1 *in vitro* accession), and each generation was obtained from a single seed descendant. None of the donors are homozygous for the locus (or loci) that determine the ability for self-pollination; hence the trait is segregating after every cycle of selfing. The parents for each cycle of selfing were selected based on flowering degree, pollen quality, 2n pollen, seed set, and total number of seeds. In every generation 200–600 seeds were planted. After the first cycle of selfing, the percentage of self-compatible progenies varied significantly among the lines, with the lowest in the *S. phureja* line and highest in the *S. stenotomum* subsp. *goniocalyx* line (Table 26).

Continuous selfings allow us to increase homozygosity. As a result, many deleterious alleles can be expressed causing inbreeding depression. To trace this effect some additional traits will be evaluated: percentage of germination, percentage of atypical plantlets, tuber yield, and tuber shape. In addition, level of homozygosity will be evaluated by diversity arrays technology (DArT) markers and compared with phenotypic data.

TABLE 26. PERCENTAGE OF SELF-COMPATIBLE PROGENIES FOUND IN THE DIFFERENT LINES AFTER THE FIRST AND SECOND CYCLES OF SELFING

		% Self Compatibility	
Species	**Genotypes**	**S1**	**S2**
S. phureja	1	0.9	Data not available
S. stenotomum subsp. *goniocalyx*	1	26.9	Data not available
S. tuberosum subsp. *Andigena*	1	12.2	6.08
S. stenotomum subsp. *stenotomum.*	2	21.4	Data not available

2.2.3 Output 3: Accelerated breeding methods and tools to help breeders select potato genotypes and parental lines

DELIVERABLE 3.1: STRATEGIES AND TOOLS TO ENHANCE SELECTION AND TRAIT TRANSFER IN AND AMONG GENE POOLS

3.1.1 Routine estimation of GG from the breeding program

In a breeding program, it is important to base the selection strategy on clearly defined required criteria (or product profiles) and on reliable predictions for the traits of interest, in order to obtain a maximized real GG. To achieve the first prerequisite, we decided to start transforming to a stage-gate breeding approach. To minimize the uncertainty of predictions of genotypes for the concerned traits, it is indispensable to use optimal experimental designs and the appropriate phenotypic analysis methods, both considering possible field heterogeneity. Resulting reliable predictions also allow as estimate of GG achieved by the breeding program.

Milestone: Rolling out new field designs (row and column design) and statistical analysis methods using linear mixed models (Q1 2019) (Breeder: Bert de Boeck)

Field trials conducted to obtain reliable trait predictions of the genotypes in a breeding population often suffer from the problem of field heterogeneity, confounding the real genetic signal. This problem particularly arises in the early breeding stages where the number of tested genotypes is considerable, although it is not excluded for smaller trials. To deal with field heterogeneity, a spatial analysis filtering out of non-genetic field noise can be incorporated into the phenotypic data analysis if the row and column coordinates of each plot in a rectangular grid structure are recorded. To anticipate the existence of such likely field effects, (resolvable) row–column designs are rolled out in the potato-breeding programs. Such designs consider a two-dimensional blocking structure (i.e., random row and random column blocks) with respect to a rectangular grid on the plot level, which is more granular and often more realistic than the one-dimensional random blocking of alpha designs. The row–column designs are optimal under the assumption of significant random row and column effects in the linear mixed model describing the phenotypic data. To analyze the phenotypic data, a linear mixed model is fitted, testing for these random row–column effects but also for linear and quadratic row or columns trends in the field and for AR2 x AR2-correlated residual errors. Significance of these row–column effects, or of the residual correlations, means that the spatial analysis filters out present field noise and improves the true genetic signal that is obtained. Consequently, the corresponding linear mixed model leads to more reliable trait predictions of the genotypes. Currently, the randomization of row–column designs and the discussed phenotypic data analyses, using linear mixed models, are custom made; but as outlook it is considered to automate these processes where possible.

3.1.2 Point of contact for genomic prediction in the potato breeding program (Breeder: Hannele Lindqvist-Kreuze)

Potato breeding is challenging because of the high number of traits that need to be considered during variety development. Most of the traits are governed by several loci with small effects and are highly affected by the environment. Therefore, in a conventional breeding program genotypes need to be screened during several clonal generations and in many locations. This means that it can take more than 10 years before a variety is ready for release. Early-generation visual selection is used to reduce around 50% of the materials. It has been suggested that the intensive early visual selection may explain the absence of improvement of yield over time because the visual attributes are not highly correlated with final yield performance but, rather, are more influenced by the seed tuber weight. Low heritability of the visual traits makes the selection of best parent combinations difficult. This can be significantly improved by incorporation of the pedigree information and genomic marker data in the data analysis to estimate the breeding values of the genotypes BLUP estimates. Recent research suggests that incorporating genomic prediction as a part of the breeding process can significantly improve GG in autotetraploid potato. Genomic prediction uses genome-wide set of molecular markers together with the phenotypic data in a training set to develop a model, which can then be used to estimate the breeding value of related individuals with fewer phenotypic data. This proof of concept will be conducted at CIP–Peru because of the availability of the historical phenotypic data on the breeding populations. CIP's potato-breeding program was centralized and advanced clones are mainly sent to the regions, there are therefore no data available on the performance of entire breeding populations, or even the founders of those in the target environments outside Peru. In parallel, phenotypic evaluation of the new breeding populations will be conducted in Kenya, and the staff will be trained on sampling and sample tracking.

Milestone: Collaboration established with Wisconsin University and a post-doctoral fellow hired for the development of statistical models for genomic prediction in potato (Q3 2019)

For the point of contact of the methodology collaboration was established with Dr. Jeffrey Endelman, associate professor at the University of Wisconsin–Madison, Department of Horticulture, Plant Breeding & Plant Genetics Graduate Program. This partnership brings valuable insight in the field of quantitative genetics of autotetraploid potato, including genomic prediction, genotype calling, genetic mapping, and G x E interaction. In September 2019 CIP finalized the competitive recruiting process for a new post-doctoral fellow in quantitative genetics of potato. The selected candidate is expected to join the team during Q4 of 2019.

Milestone: Mid-density molecular marker system developed for potato genotyping (Q4 2019)

One of the requirements for the applicability of genomic selection in the breeding program is the affordable cost of genotyping. EiB module 3 (genotyping services) is driving this process to identify partnerships with private sector, keeping in mind that the price per unit decreases as the number of users increases. Potato is one of the first CGIAR crops participating in the development of a set of markers that represents the entire genome, has acceptable allele frequency in the target population, and enough in numbers for using in genomic selection. Potato markers for the DArT Tag custom amplicon marker system were selected from SolCap and genotyping by sequencing single-nucleotide polymorphism (SNP) based on minor allele frequency and chromosome coverage. The potato genome was divided into 1 cM bins of and 2 SNP, with the highest minor allele frequency separated by at least 1 kb was selected. This produced 1,587 genomic markers with good coverage of the genome. After quality testing by the service provider, the final number of markers was reduced to 862. Initial tests with the DNA of the double monoploid as a control show that the markers are producing reproducible results and that

clustering of samples from tetraploid families are meaningful (Fig. 11). So far, the allele dosage calls are not included in the assay (the three heterozygous classes AAAB, AABB, and ABBB are collapsed into a single class AB), but initial bioinformatics analysis indicate that dosage calling will be possible with higher read depths.

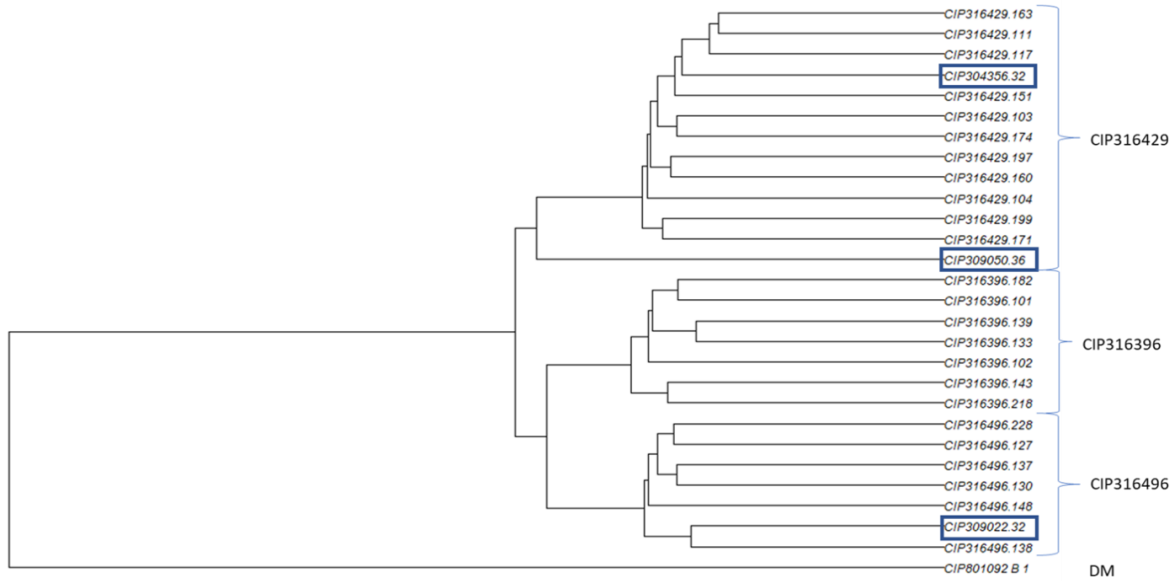

Figure 11. Unweighted Pair Group Method with Arithmetic mean dendrogram of randomly selected progenies from three tetraploid potato families using 862 genome-wide SNP markers. The parents (when available) are indicated by blue borders. The double monoploid genotype DM was used as a control.

3.1.3 Fe content measurement and bioavailability from biofortified potatoes in humans

Milestone 1: Potato samples of diploid biofortified potatoes analyzed for minerals using ICP, for vitamin C using spectrophotometry, and for individual phenolics and glycoalkaloids using ultra performance liquid chromatography (UPLC) (Q3 2019) (Breeder: Gabriela Burgos)

The Fe, Zn, vitamin C, phenolics, and glycoalkaloid concentrations of seven Fe-biofortified potato clones and two local potato check varieties grown in four locations of Huancavelica were determined by using ICP-Mass spectrometry for Fe and Zn. Vitamin C (a promoter of Fe absorption), phenolics (an inhibitor of Fe absorption), and the glycoalkaloid concentration (a potentially toxic antinutrient) were determined by using spectrophotometric methods.

The concentrations of Fe, Zn, vitamin C, phenolics, and glycoalkaloids were affected by the location and the interaction between the clone and the location. The mean Fe and Zn concentrations were higher in Yanamachay and Paltamachay, localities with acidic soils and high organic matter content. They were lower in Tacsana, which has low percentage of organic matter and high proportion of sand.

The mean vitamin C concentration was lower in Castillapata, a locality with lower levels of Mg and K in the soil and higher levels of total nitrogen than in the other localities. The mean phenolic concentration was lower in Yanamachay, which has lower levels of calcium than the other localities. The mean glycoalkaloid concentration was higher in Castillapata and Yanamachay. These two localities not only have higher levels of nitrogen and high organic matter content in the soil, they also have the most likely higher stress factors such as increased temperatures, drought, and/or pest pressures. Acidic soils with high organic matter content can favor the uptake of Fe in potato tubers.

Milestone 2: Feeding trial in Huancavelica, including the daily preparation of potato meals including the stable isotopes, and collection of blood samples before and after the feeding trial (Q3 2019)

Milestone 3: Isotopic analyses in the whole blood samples from the participants in the feeding trial, to determine Fe absorption (Q3 2019)

Under the USAID subproject, "Evaluating Potato Iron Bioavailability in Humans Using Stable Isotopes," bioavailability of Fe in humans from a yellow-fleshed potato variety compared with a purple-fleshed Fe-biofortified potato clone was determined. Stable isotopes were used in Fe-deficient volunteer women from Huancavelica, a region of Peru with high levels of Fe deficiency in local communities. The study involved women because they are one of the most vulnerable group in terms of anemia and malnutrition. This subproject was performed through a collaboration with ETH-Zurich in Switzerland and the Nutritional Research Institute in Peru.

Thirty-six participants successfully completed the stable isotope Fe absorption study conducted in Huancavelica between May and August 2019. Every woman received two different types of potato meals in series of 10 servings for 5 days each. The order of the two different series was randomized. One potato meal was based on a yellow-fleshed potato (local variety 'Peruanita') and the other in a purple-fleshed biofortified potato (CIP-306417.79). Servings of one potato meal types were always labeled with the same isotope: ^{57}Fe was used for the yellow-potato meal and ^{58}Fe for the purple-potato meal.

Blood samples were drawn at Days 1, 15, 26, and 40. The samples (whole blood and plasma) from 17 participants have been shipped from Huancavelica to Zurich at the end of July 2019. The samples from the remaining 19 participants were shipped at the end of August.

The whole blood samples from the first batch of 17 participants have been processed at ETH Zurich, and the isotopic composition of their Fe was measured by multi-collector inductively coupled mass spectrometry. Fractional Fe absorption has been calculated based on isotopic ratios, hemoglobin concentrations in blood, body height and weight, and amounts of administered stable isotopes.

Mean fractional Fe absorption from the yellow-fleshed local variety was higher (32%) than in the purple-fleshed biofortified potato clone (17%). It seems that the reduced percentage of Fe absorption in the purple potatoes is because of its high phenolic concentration compared with that of the yellow potato. However, for both types of potato, the Fe absorption is higher than expected (10%) and higher than what has been previously reported for pearl millet (7–10%), beans (3–5%), and sweetpotato (3–8%).

The total Fe absorbed in the purple-fleshed biofortified potato clone is not significantly different than in the yellow-fleshed local variety. But the fact that the yellow-fleshed control has a very high Fe absorption (32%) indicates that most likely the Fe absorption in a yellow-fleshed biofortified clone will also be very high. Therefore we expect that the total absorbed Fe from yellow-fleshed biofortified potatoes will be significantly higher than from the yellow-fleshed local variety. We will confirm that in 2020 under a project funded by the Biotechnology and Biological Sciences Research Council that will compare Fe absorption from a yellow-fleshed biofortified clone with the same yellow-fleshed control variety ('Peruanita').

Considering 8 mg of Fe as the estimated average requirement for women and 500 g of potato intake/day, the biofortified clone CIP-306417.79 would contribute 31% to the Fe estimated average requirement.

Complete results will be available by October. A manuscript reporting these promising results will be submitted to a peer-reviewed, high-impact journal by the end of December.

3.1.4 High throughput phenotyping for improved trait evaluation

(Breeder: David Ramirez)

Milestone: Point of contact for remote sensing biotic and abiotic stress in field conditions (Q4 2020)

A field trial with 1,585 potato genotypes (1,542 belonging to LVTR cycle 7, 41 parental lines, and two checks) were planted at Majes-Arequipa, Peru, from November 2018 to February 2019. The experimental design was an incomplete block design (alpha design) with 264 blocks of 12 genotypes each. The experimental unit (plot) was formed by four plants, with the distances between plants and rows 0.3 and 0.9 m, respectively. Two irrigation treatments were applied, normal irrigation (NI, inter-daily watering) and deficit irrigation (DI, bi-weekly watering). A plant-scale phenotyping consisted of canopy reflectance (CR) assessed by a Green Seeker-handheld crop sensor in three dates ranges: 45–51 DAP, 64–68 DAP, and 79–82 DAP. The total tuber yield no adjusted (TTYNA) was expressed as the fresh tuber biomass obtained in the experimental unit area. With the aim to accelerate the phenotyping measured at land scale, two multispectral aerial images acquired by a camera (Tetracam) assembled to an octocopter (drone) were taken at 66 and 81 DAP. Normalized difference vegetation index (NDVI) and canopy cover (CC) calculated from drone were calculated. The results from the second assessment (NDVI_EV2 and CC_EV2) were compared with CR measurements taken in the third assessment (CC_EV3).

All the collected data were uploaded at Dataverse Open Access CIP repository (click here). Water restriction treatment promoted a global average reduction of -64.6, -39.9, -29.3, and -55.8% in TTYNA, CR_EV3, NDVI_EV2, and CC_EV2, respectively (Fig. 12). The relationship between drone-based NDVI were mainly related to the plant-scale CR under well-water conditions, whereas this correlation was low under DI (Fig. 13). Early drone-based NDVI assessments (66 DAP) showed the maximum correlation with TTYNA under NI and DI (Table 27). Similarly, early assessment of plant-based CR showed higher correlation with TTYNA under DI, but under well-water conditions the average value of CR presented the higher correlation with tuber biomass. As a preliminary conclusion, under well-irrigated condition drone-assessment during close to the maximum CC phenological stage (66 DAP) shows as the most appropriate moment for phenotyping, allowing an important process acceleration. The spatial variability is increased under water-restricted conditions reducing the relationship between NDVI and CR – TTYNA. Under this condition it is pending a genotype clustering exercise (precocity, senescence delay, etc.) to fine-tune the relationship of drought-tolerant physiological traits and remote sensing proxies like NDVI.

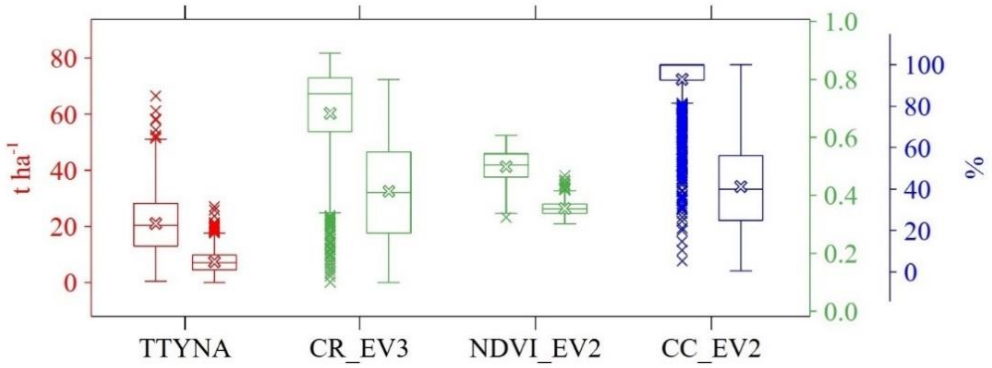

Figure 12. Boxplots of the TTYNA, the CR_EV3, the NDVI_EV2, and the CC_EV2. For each variable, the boxplot on the left and right sides corresponds to control (NI) and stress (DI) treatment, respectively.

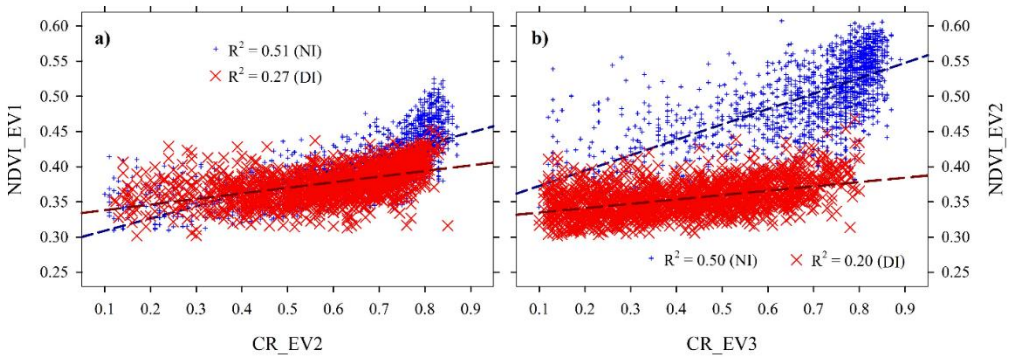

Figure 13. Scatter plot and linear regression of the second evaluation of canopy reflectance (CR_EV2) vs. the first evaluation of the normalized difference vegetation index (NDVI_EV1) (a) and the third evaluation of CR (CR_EV3) vs. the second evaluation of NDVI (NDVI_EV2) (b) under normal (NI, blue) and deficit (DI, red) irrigation. Each point corresponds to the average value of each genotype.

TABLE 27. PEARSON'S CORRELATION COEFFICIENT BETWEEN THE TTYNA AND PLANT-BASED CR AND DRONE-BASED NDVI OBTAINED UNDER NI AND DI

	TTYNA	
	NI	**DI**
CR_EV1	0.66	0.57
CR_EV2	0.69	0.43
CR_EV3	0.58	0.29
CR_AV	0.74	0.52
NDVI_EV1	0.71	0.33
NDVI_EV2	0.54	0.17
NDVI_AV	0.64	0.29

NOTE: Average values (AV) and temporal assessments correlations are shown (EV1, EV2, and EV3). Maximum values of correlation were marked with gray color.

3.1.5 Postharvest quality characterization

Milestone 1: Fast protocol for total glycoalkaloid estimation published and available in the Global trial data management system (GTDMS) (Q2 2019) (Breeder: Thomas zum Felde)

Glycoalkaloids are secondary plant metabolites that serve as natural defenses against bacteria, fungi, viruses, and insects. They can be toxic for humans when present in high concentrations and can impart a bitter taste to potatoes. Although there are many glycoalkaloids, α-chaconine and α-solanine make up 95% of the total glycoalkaloids present. Glycoalkaloid levels vary greatly in different potato varieties and may be influenced by factors such as light exposure, mechanical injury, and storage time. They are also influenced by stress such as heat and drought during production. Given the importance of potato glycoalkaloids, every potato-breeding program needs to include the evaluation of them. However, the evaluation of thousands of samples produced as a part of a breeding program by the conventional UPLC method would be very expensive and time consuming. Therefore, a need exists for objective, rapid, sensitive, and selective analytical techniques. The aim of the study was to examine the potential of near-infrared reflectance spectroscopy (NIRS) as a rapid method to estimate chaconine and solanine in freeze-dried potato samples. In a diverse set of 50 potato clones, chaconine and solanine concentrations were analyzed by an UPLC method.

The concentration of chaconine ranged from 0.46 to 12.73 mg/100g FW (fresh weight), whereas the concentration of solanine ranged from 0.26 to 9.52 mg/100g FW. The sum of chaconine plus solanine ranged from 0.78 to 22.23 mg/100g FW and for all the cases was significantly lower than the total glycoalkaloid concentration (TGA) as determined by spectrophotometer. NIRS calibration results were disappointing. Mean values, standard deviations, and ranges of the reference values as well as the statistics of the NIRS calibration and of the cross-validation are shown in Table 1 (page 3). All four NIRS calibration equations for chaconine, solanine, the sum of both and TGA (measured by photo spectrometer) showed very low coefficients of determination for the calibration curve (0.36, 0.17, 0.25, and 0.22, respectively) and consequently low coefficients of determination in cross-validation (0.28, 0.05, 0.14, and 0.13, respectively) Table 28. The standard errors of calibration and the standard errors in cross validation were high for all traits.

TABLE 28. VARIATION OF CONCENTRATIONS, NIRS-CALIBRATION, AND CROSS VALIDATION STATISTICS FOR CHACONINE, SOLANINE, THE SUM OF BOTH, AND TGA IN 50 DIVERSE POTATO SAMPLES

Trait	Reference Values			Calibration		Cross Validation	
	Estimated Range[a]	Mean[a]	SD[a]	R^2c	SEC[a]	R^2cv	SECV[a]
Chaconine	0.00–35.71	13.15	7.52	0.36	6.03	0.28	6.33
Solanine	0.00–55.72	17.28	12.81	0.17	11.64	0.05	12.35
Sum Chaconine + Solanine	0.00–100.9	32.46	22.80	0.25	19.74	0.14	20.97
TGA	0.00–209.3	71.48	45.92	0.22	40.62	0.13	42.41

R^2_c = coefficient of determination in calibration, SEC = standard error of calibration, R^2_{cv} = coefficient of determination in cross validation, SECV = standard error of cross validation, [a] = mg/100g in dry weight.

Unfortunately, this study showed that NIRS technology so far cannot be applied for fast and cost-effective TGA assessment in potato. NIRS has been applied for the quantitation of the three main alkaloids caffeine, theobromine, and theophylline in roasted coffee and alkaloids in green tea leaves. It seems that the TGA concentrations in potato are below the NIRS detection limit.

Milestone 2: Sensorial characterization (focusing on taste and texture) of 45 elite, LB- and virus- resistant and biofortified potato clones performed from a minimum of three diverse environments (Q3 2019)

This milestone was postponed until 2020.

Sensory evaluation, which includes a trained panel, allows us to measure consumer acceptance and therefore is supposed to increase adaptation of new varieties. Sensorial analysis will focus on the evaluation of texture and taste. Variations in sensorial properties of potato tubers are strongly correlated with the biochemical composition. For example, some potato varieties present a sweet flavor after storage that is related to conversion of starch to sugars. Furthermore, secondary metabolite accumulation such as glycoalkaloids and phenolics is a plant's reaction to stress conditions. This not only could affect the taste but also make tubers unsafe for human consumption.

Milestone 3: Protocol for assessing postharvest traits in potato developed, published, and available in GTDMS (Q4 2019)

The primary objective of evaluating postharvest traits is to obtain information about the potential or aptitude of intermediate and advanced clones for diverse end-uses, ranging from fresh consumption to processed products. The interpretation of these evaluations provides important information to guide potato-breeding and -selection programs, as well as for the variety recommendation for specific uses of the product. Therefore, CIP has adopted standard procedures for determining the following: specific

gravity, DM content, chipping, French fry test, oil content, and texture and flavor components of cooking quality. Most of these tests constitute routine procedures at CIP's potato-breeding programs and may be adapted in order to determine parental value for postharvest parameters. The first version of this protocol is available in the GTDMS (Protocol for Assessment of Post-Harvest Traits).

2.2.4 Output 4: Modernized breeding information management system

DELIVERABLE 4.1: TOOLS AND METHODS FOR THE INTEGRATION OF GENOTYPIC, PEDIGREE, AND PHENOTYPIC INFORMATION IN DATA ANALYSIS TO INFORM DECISION-MAKING IN BREEDING OPERATIONS

4.1.1. Mechanized and digitized phenotyping and data collection systems that increase accuracy and throughput while reducing costs

A modern breeding program with advanced phenotyping and genotyping technologies has the potential to create vast amounts of data. Integrated data and bioinformatics tools are needed to manage and convert these data into valuable information in a timely manner.

Milestone 1: Adoption of the digital template (Coordinate App) in sampling for DNA analysis (Q2 2019) (Breeder: Hannele Lindqvist-Kreuze)

Marker-assisted selection and genomic prediction programs generate large quantities of genotypic data, typically from thousands of samples. It is of fundamental importance that the samples collected are properly tracked and their correct identity maintained throughout the whole breeding process. The current genotyping assays for potato breeding consist of a set of SNP markers using the KASP assays available at Intertek, and mid-density genotyping using DArT-Tag targeted amplicon sequencing technology. In both cases, leaf discs are collected from potato leaves using 96-well format and sent for DNA extraction and subsequent genotyping. The leaf samples are bar-coded using unique CIP numbers; these codes are then used to directly generate the data collection template using Coordinate mobile Android application (Fig. 14). The template is then used by the genotyping service provider to return the marker information. This mobile application was developed by PhenoApp to enable breeding and research programs to rapidly collect and manage data and is used at both CIP and in other CGIAR breeding programs participating in the EiB module Bioinformatics, biometrics, and data management. In 2019 we adopted the Coordinate App and used it to sample and track leaf tissue from the breeding populations. In total 1,500 samples were collected for KASP marker assays, 5,000 for mid-density genotyping (DArTtag), and 800 for DArTSeqLD genotyping. The leaf samples were desiccated and stored using silica gel. The genotyping assays were planned for Q4 2019 or Q1 2020. The genotypic data can be directly linked through the GOBii into the PotatoBase (i.e., BreedBase for potato).

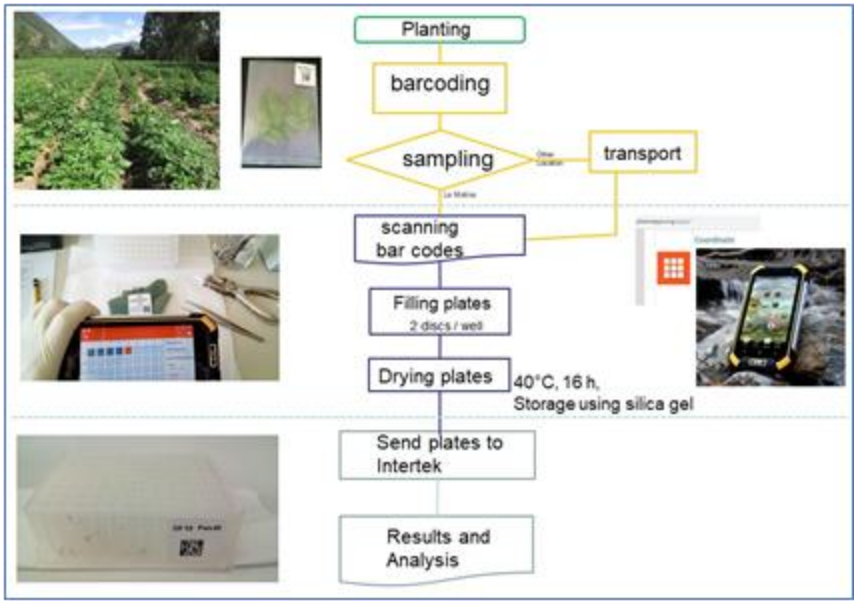

Figure 14. Schematic presentation of the workflow from sampling in the field and preparing the plates using Coordinate App to define the sampling layout. The plates with dried leaf discs are sent for genotyping.

Milestone 2: Migration of Mobile Fieldbook in Android System (Q3 2019)

The Mobile Fieldbook App, developed by Kansas State University (KSU), facilitates field data collection, removes transcription errors, and replaces hard-copy field books. Currently, the App supports 12 languages.

These are the main features of the App:

- Managing fields. Additional fields can be selected from the list. The App can import traits to capture data by accession and can import the material list.
- The user can create new traits and choose the trait format and other information if required. Traits can be reordered, hidden from the main screen, and edited.
- Since September 2019 the App can import a file with unique ID primary and secondary order = plot_id, plot row and plot column. Also, extra columns can be added such as seed_id, seed_name, and pedigree.

The use of the Fieldbook App still must be further integrated into the CIP breeder's data management workflow, which is a pending task since the final state of this workflow will depend on the new database management system that will be used. The Fieldbook App then needs to be tested in the new workflow, and the printing feature of the App needs to be improved.

4.1.2. Database for storing phenotypic and genotypic data, pedigree information, and crossing records

A modern breeding program with advanced phenotyping and genotyping technologies has the potential to create vast amounts of data. A performant and versatile data management system is crucial to make the bridge between data recording in the greenhouse, laboratory, or field and the data analyses necessary for decision-making. Currently, phenotypic data can be stored in CIP's Biomart database. Nevertheless, to modernize breeding and obtain higher GG, a transition must be made to the inclusion

of pedigree and genotypic information into the analyses for decision-making. To link all these different sources of information accordingly, a more versatile and linked database system is therefore needed. A possibility that is currently considered is the switch to PotatoBase, developed by the Boyce Thompson Institute. This database has the advantage of hosting as well phenotypic, genotypic, and pedigree data in a linked way. An additional advantage is that this transition would increase efficiency by streamlining our data management workflows for potato and sweetpotato, because the global sweetpotato breeding team already uses SweetPotatoBase (i.e., BreedBase for sweetpotato).

Milestone 1: Trait dictionaries of the protocols for PVS, chemical and quality analysis, sensorial analysis, abiotic stress tolerance, and high throughput phenotyping aligned with the crop-ontology platform (Q4 2019)

Trait dictionaries are developed to carry out experiments effectively. They are the first step in the correct collection, analysis, storage, and reporting of data. In this context all research held at CIP is standardized and reflected in protocols. This documentation allows for variables used in these experiments to be described and detailed extensively.

Furthermore, in a breeding program, it is very important to standardize the way field data are collected. This way data characterization and evaluation are compatible with international ontologies and vocabularies. A common and controlled vocabulary of the potato domain that describes concepts, attributes, and the relations between them in a formal way using a standardized knowledge representation language was developed. In this context CIP developed an ontology of PVS, a method that provides key information on farmers' preferences that are useful to accelerate the release and acceptance of new potato candidates. The PVS ontology provides a common set of standardized variables for institutions, trainers, and facilitators involved in PVS. It is based on the protocol: "Participatory Varietal Selection of Potato" https://research.cip.cgiar.org/potatoknowledge/pvs.php. There are a total of 45 presented variables identified in each of the growing stages of the potato crop. In the flowering stage, there are 10 variables that describe farmers' preference; 14 variables of biotic stress; and 15 variables that focus on tuber characteristics, marketable and organoleptic qualities, votes by gender, and farmers' global votes for clone preference. Finally, in the postharvest stage, 6 variables were considered for tuber organoleptic characteristics after cooking and farmers' preference as well.

The ontology of the chemical and quality analysis has been updated. The variables were gathered and revised, and the information was curated by breeders and researchers at CIP. In total there are 34 new variables. Analysis of ascorbic acid, analysis of total and individual carotenoids, analysis of total phenolics compounds, analysis of total anthocyanins, evaluation of hydrophilic antioxidant activity, analysis of individual phenolic acids, and analysis of ß-carotene (and others) were considered.

On the other hand, CIP is working on the abiotic stress ontology. The variables are based on the "Practical Guide to Assessing Potato Clone Drought Tolerance under Field Conditions." This information is being revised with breeders and specialists—we are considering 100 variables—and is being examined in Microsoft Excel. (It is available through this link.) By the end of the year all the information should be available on the crop ontology page.

CIP is working to reflect the information of trait dictionaries in the potato ontology. Currently, this page holds 197 variables for potato (see https://www.cropontology.org/ontology/CO_330/Potato).

Milestone 2: Web access to information on breeding populations, advanced clones, progenitors, and TS families with associated phenotypic information (Q4 2019)

The data generated by the CIP potato-breeding program are stored in a "Global Roots & Tubers Base" utilizing the free BioMart software https://research.cip.cgiar.org/gtdms/biomart/. Storage of phenotypic, genotypic, pedigree, geographical, and environmental data is possible. Through the metadata and the search function using filters, the user can retrieve data from the experiments conducted by CIP scientists or NARS partners using CIP materials. The availability of the data is managed in conjunction with the Dataverse portal following CGIAR's open-access guidelines. Currently, the database holds data from 548 experiments conducted from 2002 to 2019 in 12 different countries and 75 localities. The phenotypic data include important potato traits such as healthy tuber yield, LB resistance, and vitamin and mineral composition. The genotypic data consist of approximately 3,000 SNP marker genotypes on a set of 103 B3 population breeding lines using the SolCAP Infinium Potato SNP platform. Stakeholder preference data from PVS trials are also included in the database: biochemical evaluation (153 field books), physiology (3 field books), LB exposure (157 field books), healthy tuber yield (179 field books), PVS (46 field books), dormancy (4 field books), and bulking (6 field books) (Fig. 15).

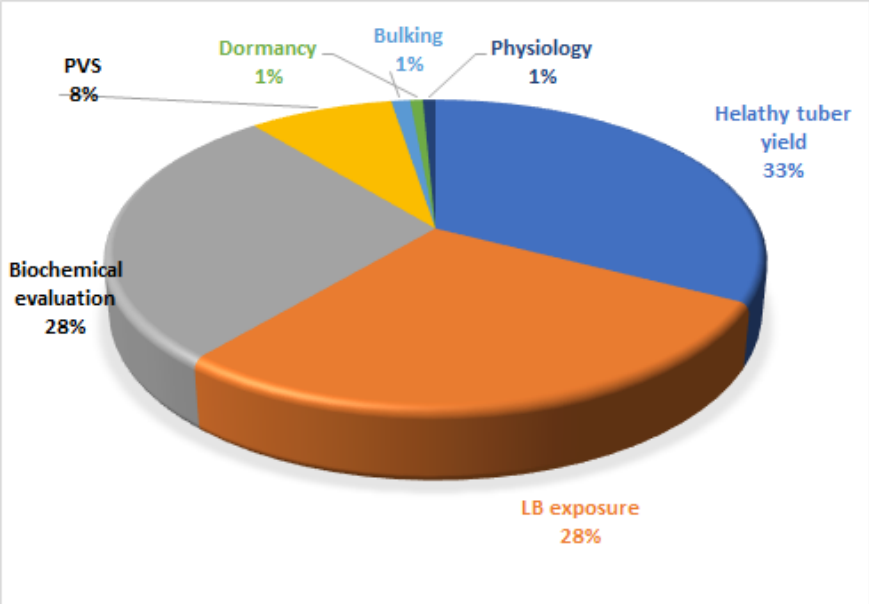

Figure 15. Number of field books registered in Global Roots & Tubers Base by experimental trial.

Milestone 3: CIPCROSS system for botanical seed inventory adapted in Android System (Q4 2020)

CIP, together with the Boyce Thompson Institute and KSU, organized a "hackathon" on 13–17 May 2019 to align databases and tools for crop improvement and to streamline development efforts. One of the tools that will be adopted for all Breedbases is Intercross (developed by KSU). When crosses are made, Intercross tracks parental and cross IDs, who makes the cross, and where the cross is made. Cross labels can be printed to Zebra label printers, and lists of crosses can be exported to local files. Intercross is part of the broader PhenoApps initiative, an effort to modernize plant breeding and genetics data collection and organization by developing new strategies and tools for data capture.

After discussions at the hackathon, the following activities will be implemented with Intercross. (These are the activities still pending to be achieved in 2019–2020.)

- General changes:
  - The APK will be loaded in GitHub
  - CIPCROSS should to be reflected in Intercross
  - Intercross should allow data collection for each flower, pollination events, collection events, and family totals. Once the data are collected with Intercross, the raw (flower#, fruit #) data will go to Breedbase, where they will be summarized (crossing events).
  - The Crossing event and the Seed Count event should be separated
  - Batch print depending on number of flowers
- Once Potatobase is running at CIP–Lima, there should be a connection with Intercross to create crossing plans.
- Parental printing:
  - Implement an Android tab like CIPCROSS parental page
- Crossing changes:
  - Implement backend for storing various counts and dates
- Cross page changes:
  - Replace current page with label preview and data entry
  - Add pedigree visualization
- Cross block manager:
  - Create static headers
  - Implement backend
  - Implement gradient algorithm for cell coloring

Because the Intercross crossing tool will be suitable for both potato and sweetpotato crosses (among others) and is Android based, the adaptation of CIPCROSS to Android is no longer needed.

Milestone 4: Online data repository (PotatoBase) for combined analysis and reports of clonal evaluation data across years and locations (Q4 2020)

At the hackathon we discussed the possibility of creating a CIP–PotatoBase, based on the Breedbase framework. The advantage of such a web-based database is that it allows the linked storage of phenotypic, pedigree, and genotypic data, making the extraction of necessary data for analyses for decision-making more straightforward. With the advancement of new high-throughput phenotyping and genotyping technologies, and the corresponding more modern analysis methodologies (e.g., genomic prediction), data have grown in quantity and complexity. Better data management and storage facilities are needed. Breedbase can be a solution for this need and stores linked trait ontologies, crosses, pedigrees, images, and sequencing data. Together with PhenoApps (http://phenoapps.org/) and the breeding API (https://brapi.org/), Breedbase offers plant-breeding communities a digital ecosystem to support their experimental activities.

CIP will decide about the new potato database system as soon as possible, to enable the achievement of this milestone before the stated deadline.

DELIVERABLE 4.2. METHOD FOR RECORDING AND TRACKING THE DISTRIBUTION DATA OF THE BREEDING PRODUCTS

4.2.1. Database of globally released CIP related varieties

Milestone 1: Updated version of the online catalogue of advanced clones and variety catalogue detailing the materials from CIP's breeding program available for international distribution through the genebank (Q4 2019)

CIP's interactive 2019 online catalogue includes a compilation of CIP's advanced potato clones and varieties, with 506 advanced potato clones and 70 varieties (registered by the end of 2018). Each catalogue accession contains information divided among four categories: (1) identification, consisting of the institutional number, breeder code, the direct parental information, and the name of the population; (2) visual characterization, comprising photographs of up to six characteristics of a genotype; (3) fingerprint, a repository that includes a genomic characterization obtained by the low-density DArTseq analysis; and (4) description, a section subdivided into five groups of information that includes morphological characteristics, resistance traits, agronomical performance, postharvest performance, and nutrient concentration in tubers.

During October 2018–September 2019, the online catalog had 352 page views from 16 different countries (mainly Peru, Kenya, Ecuador and Asian countries). To increase both visibility and our customer reach, CIP needs to develop other materials like DVDs and brochures, share the catalog on social media and CIP's website, and translate the catalog into different languages.

New catalog updates performed during the first half of the current year include (1) implementation of an internal mirror catalog that will support the selection processes; (2) a user-oriented search tool that includes a search engine with three categories of search (by parameters or characteristics, by list of genotypes, and by population); (3) creation of a curation group to verify the quality of the content within the online catalog; and (4) a new update for 39 biofortified advanced clones, which have been fully uploaded to the catalog, including photographs for plants, tubers, sprouts, flowers, leaves, and chips.

Several new improvements for the second half of the year are planned: (1) the addition of a full-resolution link for all photographic descriptors; (2) a friendly pdf print-out option to enable fast complied information on a single page; (3) the development of the internal mirror catalog for genotypes characterization and data management, with means to improve traceability of varieties and to reduce release time; and (4) the transition of the developed catalog to be compatible with a wide range of mobile devices and desktop computers with Android mobile operative system in all current available languages (i.e., English, Spanish, French, Chinese, Korean, Russian, German, Portuguese, and Hindi).

2.2 SUMMARY OF ACHIEVEMENTS BY OUTPUT—*SWEETPOTATO*

2.2.1 Output 1: Dynamic and nutrient-dense breeding populations developed as sources of early-maturing, high, and stable-yielding varieties with resistance to biotic and abiotic stresses and quality traits

DELIVERABLE 1.1 GLOBAL OFSP BREEDING POPULATION FOR WIDE ADAPTATION AND EARLINESS

1.1.1 Moving 100 parents for OFSP wide adaptation and earliness into *in vitro* at San Ramon and then into CIP's genebank (75% achieved)

To secure the large GG for earliness and wide adaptation in our hybrid population 1 for the future—69.7% more storage root yield at 90 days (18.5 t/ha on average in the hybrid breeding population 1

compared with the foundation of 80 grandparents at 90 days harvest of 10.9 t/ha)—we are incorporating all parents of hybrid population 1 (42 PJ' and 42 PZ' parents for wide adaptation and earliness [WAE]) into CIP's genebank. Note: the set of grandparents (N=80) and parents of hybrid population 0 are already in CIP's genebank. (The parents of hybrid population 1 are given in detail in Appendix A4_Sweetpotato.) This is breeding material that for the first time can enter into the very short crop duration season (90 days) in the potential rice-sweetpotato-rice farming systems of Asia (selections from this hybrid population are described under output 2).

1.1.2 Elite crossings for OFSP for wide adaptation and earliness in San Ramon for Asia and LAC (Bangladesh, India, Vietnam, The Philippines, Tadzhikistan, Turkey, Brazil, Guatemala, Haiti, and Panama)

CIP–Lima is distributing TS from six low DM OFSP elite crossings and six high DM OFSP elite crossings tracing back to hybrid population 0. The low DM OFSP elite crossings are estimated to have for number of commercial storage roots per plant, storage root yield, foliage yield, and DM content an average of 3.0, 25.1 t/ha, 30.8 t/ha, and 26.7%, respectively. The high DM OFSP elite crossings are estimated to have for number of commercial storage roots per plant, storage root yield, foliage yield, and DM content an average of 2.3, 21.2 t/ha, 28.3 t/ha, and 30.1%, respectively (see the October 2017 report). We have sent TS elite crosses to Bangladesh (N=22,591), India (20,000), Panama (3,000), Turkey (N=5,000), and Canada (N=800). Until December 2019 we are planning to conduct further TS elite crossing shipments to India, Vietnam, the Philippines, Tajikistan, Brazil, and Haiti. At present we have 100,000 TS from elite crossings in our seed stocks for distribution (Appendix A5_Sweetpotato). (The performance estimates of each of these elite crossings is given in Appendix A6_Sweetpotato). Note: We have stopped elite crossings from hybrid population 0 (100 days harvest) because we are starting elite crossings with hybrid population 1 (90 days harvest).

DELIVERABLE 1.2 PRE-BREEDING POPULATION FOR SPVD

1.2.1 Selection of 10 SPVD-resistant clones for further recombination programs

On the basis of enzyme linked immune-sorbent assay tests for sweet potato chlorotic stunt virus (SPCSV), symptoms observed in greenhouse, virus response in the field (including offspring tests), and the total storage root yield (tons/hectare), we selected a set of clones to be crossed in a complete diallel. These clones are CIP105086.1, CIP194540.5, CIP110019.21, CIP112240.7, CIP107548.5, CIP107729.9, CIP107734.5, CIP107577.23, CIP107581.1, and CIP107582.3 and have shown virus resistance in different experiments including offspring. The accessions CIP107729.9 and CIP107734.5 are also parents of the virus resistance population VJ13 and produced more than 50% of resistance in offspring in field tests. They are parents of families 112186 (CIP189151.34 x CIP107729.9), 112208 (CIP110019.17 x CIP107729.9), 112240 (CIP110019.2 x CIP107734.5), and 112185 (CIP189151.34 x CIP107734.5). Four VZ08 clones included are estimated to have storage root yield in the range of 9–24 t/ha. Additionally, CIP110019.21 was included, which is a clone that after grafting onto infected material responded similarly to a virus-clean check control. Note: clone CIP112240.7, which is a cross of CIP110019.2 x CIP107734.5, has shown no virus symptoms in field experiments and has a storage root yield of 11 t/ha. The diallel recombination 21,913 TS were obtained (89 families; 83 families with more than 3 seeds (Appendix A7_Sweetpotato). Note: Several successful self-fertilizations were obtained that are very useful for studying the inheritance of SPVD resistance because this resistance is supposed to be recessively inherited (sweetpotato is hexaploidy). The material will be used by the project "SweetGains"

starting on 1 October 2019 by germinating 30 TS *in vitro* (about 2,000 genotypes) to test each family in Uganda and under controlled screenhouse conditions at CIP–Lima.

2.2.2 Output 2: Farmers' and end-users' preferences integrated into varietal development and selection approaches

DELIVERABLE 2.1: VARIETIES AS WELL AS FARMERS' AND END-USERS' PRIORITIES AND PREFERENCES DOCUMENTED AND INTEGRATED INTO VARIETAL BREEDING

2.1.1 CIP–Lima in 2019 selects a new generation of OFSP clones; these clones are tracing back to hybrid population 1 (three OFSP wide adaptation and earliness/90 days harvest, one OFSP for low sweetness after cooking, and two OFSP for high Fe to register for 2020)

Varieties to replace are 'Benjamin' and 'Shokhin' for low DM OFSP at 90 days harvest and 'Dagga' for high DM OFSP. The varieties have been registered or released in Peru ('Benjamin'/CIP 105085.2); Panama, Guatemala, and Haiti ('Shokhin'/CIP106603.1); Tadzhikistan ('Benjamin/CIP 105085.2, 'Shokhin'/ CIP106603.1); and South Africa, Ghana, and Haiti ('Dagga'/CIP199062.1). During the past 2 years, 11 clones have been released in LAC which can be traced back to CIP's program: CIP106603.1 (Panama); CIP440185, CIP440132, CIP106496.1, CIP187016.2, and CIP106603.1 (Guatemala); CIP199026.1 and CIP192033.50 (Nicaragua); CIP199026.1 and CIP106603.1 (Haiti); and CIP106906.1 (Brazil). An additional evaluation to launch varieties is ongoing in Honduras. Furthermore, three high DM dual-purpose varieties (food and animal feed) are being disseminated: 'Abigail' (CIP194540.5), 'Isabel' (CIP189153.18), and 'Sumy' (CIP105523.1). A new generation of OFSP clones has reached final breeding stages. All selections are hybrid clones from crossings of PJ x PZ (N= 400 for OFSP WAE; N=200 for OFSP non-sweet after cooking; N=135 clones for OFSP high Fe, which evaluated in p-rep designs at three locations, Huaral, San Ramon, and Satipo). Table 29 shows the GG achieved relative to checks 'Dagga' and 'Cemsa'. We are beginning to select 32 OFSP clones for WAE, 16 OFSP clones for non-sweet after cooking, and 12 OFSP clones for high Fe for the second selection step, to be conducted in a row–column design at eight locations. The target will be to register for 2020 3 OFSP clones for WAE (90 days harvest), 1 OFSP clone for non-sweet after cooking (120 days harvest), and 2 OFSP clones for high Fe (120 days harvest).

TABLE 29. MEANS OF SELECTED MATERIAL RELATIVE TO CHECK CLONES ('DAGGA' AND 'CEMSA' FROM HYBRID POPULATION 1 IN LATER BREEDING STAGES IN ORDER TO REGISTER SIX NEW OFSP CLONES

Mean H1 Breeding Lines & Checks	Root Yield (t/ha)	No. Comm. Roots/Plant	Foliage Yield (t/ha)	ß-Carotene (mg/100 g FW)	Root DM (%)	Sweetness Taste Score	Fe ppm (dry weight)
WAE (N = 400) 90 days harvest	30.2	3.70	49.0	6.44	26.2	-	-
Dagga (check)	26.8	2.44	49.1	1.16	26.4	-	-
Cemsa (check)	15.9	1.53	55.5	0.08	28.4	-	-
Non-sweet (N = 200) 120 days harvest	44.4	3.69	71.6	6.2	25.2	4.1	-
Dagga (check)	41.1	2.64	72.6	1.11	25.7	5.1	-
Cemsa (check)	61.7	3.20	115.6	0.88	25.6	6.8	-
High Fe (N = 135) 120 days harvest	40.7	3.48	46.9	11.2	23.9	-	26.2
Dagga (check)	51.5	3.12	37.0	1.52	28.8	-	15.1
Cemsa (check)	39.2	2.15	48.4	0.0	32.8	-	12.2

2.2.3 Output 3: ABMs and tools to help breeders select genotypes and parental lines in fewer years than with traditional clone-breeding schemes

DELIVERABLE 3.1: ABMs DEVELOPED BY IMPROVED STRATEGIES FOR SELECTION AND TRAIT TRANSFER IN EARLY-BREEDING STAGES AFTER APPLYING FIELD SURFACE/NEAREST NEIGHBOR MODELS

3.1.1 Field surface/nearest neighbor models implemented at two breeding platforms to achieve higher precision in hybrid population trials and other trials with very large number of genotypes by August 2016, extended in 2018–2019

Field heterogeneity in large trials with more than 100 clones (often thousands of clones) is a critical issue. Options to adjust for soil heterogeneity are alpha lattice designs or spatial analysis using splines. For the second option, the R package is used to fit generalized additive models. Moreover, package SpATS is available for spatial analysis using spline functions. We are also testing commercial software such as ASReml and AGROBASE (www.agronomix.com). ASReml can fit models for AR1 x AR1 correlated errors, polynomial models, or smoothing splines trends in fields. AGROBASE fits the more traditional nearest neighbor adjustment. Unfortunately, AGROBASE provides only adjusted means across major blocks and not adjusted values for each major block. For all methods it is essential to have a row–column mapping for fields. A freely accessible R package st4gi (https://github.com/reyzaguirre/st4gi) was made available to create field books with row–column mapping for several statistical designs. It also creates randomizations with row–column mapping in nonreplicated trials (often carried out in early breeding stages). A standard design in nonreplicated trials has been implemented in the highly interactive data analysis platform (https://research.cip.cgiar.org/gtdms/hidap/), which is a free software developed by CIP to support breeders.

DELIVERABLE 3.2 (NEW DELIVERABLE): MULTISTAGE SELECTION PROCEDURES OPTIMIZED FOR LATER BREEDING STAGES AND P-REP DESIGNS IMPLEMENTED IN LATER BREEDING STAGES

3.2.1 Analysis of different breeding scenarios with VarComp estimates and documentation of optimum resource allocation in later breeding stages (in process)

Analysis of different breeding scenarios. To allocate breeding test capacity (usually the total number of plots), a comparison of different breeding scenarios is required. Variance component (VarComp) estimates for METs in later breeding stages are needed to compare breeding scenarios (we estimated these from METs across 3 years from the Amazon region). Provided VarComp estimates are available (often historical data), formulas from Cochran's approach are available to calculate the response to selection. For one-, two-, or three-stage selection, we have implemented the corresponding formulas in R and SAS to determine the response to selection. (Both of these programs are available on https://www.sweetpotatoknowledge.org/files/the-stage-selection-gain-1to3/.) A manuscript, entitled "Selection of High Dry Matter Orange-Fleshed Sweetpotato [*Ipomoea batatas* (L.) Lam.] and Allocation of Breeding Resources in the Humid Tropics of Peru" for the journal *Theoretic and Applied Genetics* has been completed. Co-authors are from the Institute of Plant Breeding, Seed Science and Population Genetics, University of Hohenheim, Germany (with more than 50 years of experience in model calculations), and the Universidad Nacional Agraria–La Molina in Peru.

3.2.2 Randomization and analysis of (augmented) p-rep designs at first stage of later breeding stages (fully achieved)

Randomization and analysis of (augmented) p-rep designs. In the first stage of the later breeding stages, experiments are constrained because a reasonable number of genotypes must be tested with a limited amount of planting material per genotype. There is a trade-off of the number of test locations with the plot replications per location. A p-rep design is a useful tool to maximize the amount of locations without going to the more extreme situation of unreplicated designs.

P-rep designs with additional blocking (incomplete one-dimensional alpha design type blocks, or incomplete two-dimensional row–column blocks) have been implemented for the first time at CIP. These designs were done with the material described above in Table 29 in the first selection stage of later breeding stages (four-plot replications across the three locations for each genotype). Only the checks 'Abigail', 'Arne', 'Benjamin', 'Cemsa', 'Dagga', 'Isabel', 'Jonathan', and 'Sumi') are replicated more often (three times in the N = 400 METs, five times in the N = 200 METs, and four times in the N = 135 METs).

DELIVERABLE 3.3: ABMs DEVELOPED BY USING DArT MARKERS

3.3.1 Renamed currently avaible DArT markers for SPCSV and SPFMV validated by December 2019 former name "At least the currently available amplified fragment length polymorphisms and SSR markers for SPCSV and SPFMV validated by June 2017"

The activity has been be out-sourced and only DArT markers for SPCSV and sweet potato feathery mottle virus (SPFMV) are used (Diversity Arrays Technology Pty Limited, Australia; Service: SP DArTseq). As for the previously used amplified fragment length polymorphisms and simple sequence repeat markers two groups are used comprising 30 susceptible and 11 resistant clones from the pre-breed population VJ08. Five DArT markers were found to be associated with the two groups "susceptible" (N=30) versus "resistant" (N=11) within VJ08 clones, namely 7548044, 7574925, 7573123, 7572542, and 7563062 (Appendix A8_Sweetpotato). In a second population, VZ08 (related to VJ08), 444 clones were phenotyped for resistance after SPCSV inoculation in a screenhouse experiment. On the basis of results of enzyme-linked immunosorbent assays, positive and negative responses to SPCSV were determined using non-infected genotype 'Tanzania' as a healthy control. Two groups of resistance were formed in the validation population PZ08: 33 susceptible and 30 resistant clones. Susceptible clones tested positive at 60 and 90 days after infection; resistant clones tested negative at 90 days after infection exhibited a titer mean <1.2 times (titer of the healthy control 'Tanzania'). The five markers were found to have R^2> 0.34 and R^2<0.48 in the population VJ08, but for none of these five markers was an association observed in the validation population VZ08 (one marker even was not detectable within 63 VZ08 clones). These five DArT markers are useless in SPVD-resistance screening for applied sweetpotato breeding. But in these 63 VZ08 clones, 47,889 SNPs from the DArTseq service were obtained. Two groups "susceptible" (N = 33) versus "resistant" (N = 30), which were scored "AA" for reference allele homozygotes, "BB" for SNP allele homozygotes, "AB" for heterozygotes, and "NN" for double null/absence of SNP. The trait-marker association analysis (software Tassel 4.3.15) indicated six new DArT markers within R^2> 0.250 and R^2< 0.310 (Appendix A5_Sweetpotato). The very small genetic basis for resistance might cause the very poor association of markers in the validation population VZ08—all resistant clones are tracing back to two parents and most are derived from selfings of CIP107729.9 (breeding code VJ08.330). For this reason, we created a larger set of potential bi-parental mapping populations by diallel crossings (see Output, Deliverable 2). These bi-parental mapping populations will be used for further research and development on markers for SPVD.

DELIVERABLE 3.4 (NEW DELIVERABLE): ACCELERATE BREEDING FOR DROUGHT AND USE OF NEW BREEDING TOOLS FOR DROUGHT-PRONE AREAS IN MOZAMBIQUE

3.4.1 Implementation canopy temperatures and stable isotopes 13C and 15N as new breeding tools in drought-screening studies in Mozambique (partially achieved)

3.4.2 Determination of heritabilies, average phenotypic correlations, and genetic correlations among commercial root yield, noncommercial root yield, vine yield, canopy temperature, and stable isotope composition (13C and 15N) under different types of drought stress (partially achieved)

CIP–Mozambique carried out two experiments aiming to apply new tools (canopy temperature by cameras and stable isotope composition by ^{13}C and ^{15}N) for breeding in drought-prone areas. The first experiment was carried out at Umbeluzi Research Station with 24 genotypes with five drought treatments and two-plot replications. The second experiment was carried out at two locations with two drought treatments and two-plot replications. The two locations are Chilembene, with 200 genotypes, and Umbeluzi Research Station, with 120 genotypes (subset from the 200 genotypes planted at Chilembene). The trial at Umbeluzi Research Station has not been harvested at the time of reporting. Agronomic and canopy temperature data were analyzed in R using the spatial modeling engine SpATS. In a preliminary data analysis of commercial root yield, total root yield, and vine yield, we observed yield reductions in early-season drought and mid-season drought in the range of 14–29% for total storage root yield, 11–29% for commercial storage root yield, and 15–35% for vine yield. However, the 24 genotypes planted at Umbeluzi were not affected by late-season drought. At Chilembene, with late-season drought, the total storage root yield was reduced by 23%, and commercial root yield and vine yield were reduced by 41% and 15%. Genotypes of early-maturing varieties 'Irene' and 'Bela' exhibited overall highest total storage root yield under early-season drought. We assume that in these varieties root initiation was advanced when early-season drought was imposed. The terminal drought had no effect on these genotypes. Early- and late-season drought exhibited in yield traits high positive correlations. We concluded therefore that early maturity is a very important trait in sweetpotato for semi-arid and arid regions. Moreover, the farmer variety 'Xiadlaxakau' exhibited good yields in most drought treatments. It is worth noting that the number of commercial roots per plant as a yield component is very high in 'Xiadlaxakau' (previous studies with 42 genotypes at CIP–Lima estimated average phenotypic correlations and genetic correlation of $r = 0.811$ and $r = 0.957$ between number of commercial roots per plant and storage root yield). Canopy temperatures were significantly higher in late-drought treatment than in optimum irrigation and optimum irrigation + fertilizer treatments (150 DAP). The same trend was observed for mid-season drought treatment but less pronounced compared with late-drought treatment. Data on stable isotopes ^{13}C and ^{15}N are being processed. In further data analysis we will determine heritabilities for yield traits, canopy temperature, and stable isotopes ^{13}C and ^{15}N by treatments. Heritability and correlations are the two parameters needed to determine the value of new breeding tools for direct and indirect selection, which can be determined by the formulas of the response to selection. This has been done before at CIP for a number of commercial roots per plant and responses to selection for storage root yield.

2.2.4 Output 4: New capacities for applying knowledge, tools, and modern breeding approaches developed for more efficient progress in variety-oriented breeding programs of NARS

DELIVERABLE 4.1: REGIONAL BREEDING HUBS STRENGTHENED

4.1.1 Capacity building for OFSP breeding in LAC—at least eight countries work with *in vitro* OFSP clone introduction and at least three countries with TS introductions (90% achieved)

The HarvestPlus program and the Dirección de Ciencia y Tecnologia Agropecuaria (DICTA) in Honduras invited CIP to train for evaluation of OFSP clones for future variety releases in Honduras from 19 July to 25 August 2018. Federico Diaz (assistant sweetpotato breeder at CIP–Lima) conducted the training. The evaluation in Honduras was based on 13 OFSP clones introduced from CIP–Lima in 2017 in a MET series across six environments. For such breeding scenarios a well-elaborated manual and paper is in the process of being submitted. All OFSP clones exhibited high yields, and local farmers and companies were highly interested in the material. Technicians from DICTA were trained in planting and harvest, storage root yield, number of commercial root determination, characterization of foliage, identification of virus symptoms, identification of nematode damage, and other procedures to select clones. The department of Comayagua (~600 masl) in Honduras (near the capital) is the area with the highest potential for sweetpotato production. A presentation entitled "Production and Management of Sweetpotato" was given to 60 participants from DICTA. The emphasis was on virus symptoms and production of clean planting. The leader of research at DICTA, Narcizo Meza, and CIP management are looking to collaborate more closely. Moreover, HarvestPlus and CIP are aiming to introduce new OFSP with high root DM and dual-purpose use (food and feed) further into the LAC regions.

CIP participated at the HarvestPlus annual meeting for LAC and the Programa Cooperativo Centro Americano para el Mejoramiento de Cultivos y Animales (PCCMCA), which conducted a congress in Honduras from 27 April to 4 May 2019. Participants from seven countries presented sweetpotato results nearly exclusively based on sweetpotato clones introduced by CIP–Lima in previous years. CIP's presentation at the PCCMCA was "Maintaining Biofortified OFSP Clean of Virus from *In Vitro* Germination" of sexual seeds. This is new technology developed at CIP to provide virus-free material rapidly within 12 months to partners, and it avoids cumbersome cleaning-up of clones at CIP–Lima. In total 250 delegates from different LAC countries participated in the PCCMCA congress. The current sweetpotato breeding network in LAC comprises nine countries: Panama, Guatemala, Nicaragua, Honduras, Haiti, Jamaica, Brazil, Ecuador, and Peru. They mainly operate with national funds but also with material and knowledge introduced from CIP–Lima. (For sweetpotato variety releases in the LAC region see Output 2 deliverable 1.)

4.1.2 Capacity building for OFSP breeding in Asia—establishment of one breeding hub in Bangladesh and a sweetpotato breeding network of six countries (90% achieved)

Strengthening the Bangladesh breeding platform to serve Asia. The breeding platform in Bangladesh hired a national recruited staff, Mir Ali, a breeder; two technicians will join the program. The main task is to foster TS production from predominantly grown varieties (2 clones) and new releases (12 clones) in Bangladesh, GG trials, and improving germination and multiplication of TS introductions. Handling TS is still the major bottleneck in Bangladesh. In October 2018 the Tuber Crops Research Centre, Bari (TCRC) received about 22,500 TS (12 elite crossings); but only 5,828 TS were used for germination in polybags because TCRC cannot handle more seed. Seeds were not scarified with sulfuric acid but was instead soaked overnight with GA_3 treatment. Only 583 seeds germinated (in contrast, the

germination rate at CIP–Lima is >90%). The NARS, through TCRC and BARI, conducts preliminary and advanced yield trials. They have a substantial number of variety releases based on *in vitro* introductions from other countries, which are combined with intensive vine multiplication for bilateral projects. However, there is nearly no impact from new releases as more than 95% of the sweetpotato production in Bangladesh (265,000 t, harvested area of 26,000 ha) is covered by two local farmer varieties. (This contrast with Peru, which produced 256,000 t on a harvested area of 14,000 ha.)

2.2.5 Output 5: Improved and shared breeding databases and knowledge management, including trait-specific protocols and catalogs to support the orientation of breeding products and facilitate decision-making and outcomes from breeding research

DELIVERABLE 5.1: DATABASE FOR EARLY BULKING (THE <100-DAY SWEETPOTATO)

5.1.1 Documentation about early-bulking genotypes in Southwest and Southeast Asia available by June 2016 (milestone achieved)

5.1.2 Heritability estimates for early bulking and outline the strategy to breed for 90-day sweetpotato determined by April 2016 (milestone achieved)

Early bulking. Information on 48 early-bulking released/launched varieties was uploaded onto a database on the Sweetpotato Knowledge Portal. Early maturing (time from planting to harvest of 2.5–3.5 months) is an attribute to be found across all sweetpotato production zones: Arid Pacific coast (1 variety); humid tropics of the Amazon Basin (2 varieties); humid tropics of South Asia (7 varieties), Indian subcontinent (8 varieties); temperate West Pacific, Korea, and Japan (7 varieties); west Africa (2 varieties); east Africa (9 varieties); and semi-arid Southern Africa (12 varieties). The database has reporting gaps for Southeast Asia, but recent information claims that selection for 90-day OFSP clones for variety release was very promising in Indonesia. Certainly, the attribute of 90 days to harvest is relatively easy to incorporate into OFSP-breeding populations. Early-maturing OFSP varieties for the humid tropics are considered to be a funding opportunity with low risk of failure.

New early-bulking breeding clones from CIP's global program. These will be disseminated in the future, mainly by TS through **elite crossing**s (see Deliverable 1). The clones in *in vitro*, registration, and virus cleaning at CIP–Lima are divided in two groups. **(1) Moist and sweet** comprises 31 clones: Z06.077, PZ06.085 ('Arne'), PH09.718, PZ08.127, PZ08.018, PH09.5176, PJ07.609, PJ07.057, PJ07.586, PJ07.522, PZ08.008, PJ05.212, PH09.2294, PZ08.048, PH09.2582, PH09.893, PH09.3534, PJ07.660, PJ07.119, PZ08.017, PH09.5313, PZ08.174, PJ07.096, PH09.1609, PH09.4137, PZ08.011, PJ07.305, PH09.1687, PH09.3314, PJ07.508, and PJ07.678. **(2) Dry and starchy** comprises 22 clones: PJ05.236, PJ05.052, PJ05.312, PZ08.053, PH09.3323, PZ06.698, PH09.753, PJ07.588, PJ07.602, PH09.2616, PJ07.084, PJ07.544, PJ07.028, PJ05.324, PZ08.153, PJ07.147, PJ07.061, PJ07.064, PZ06.050, PH09.4543, PJ07.079, and PH09.1699.

DELIVERABLE 5.2: DATABASE FOR NON-SWEET SWEETPOTATO AFTER COOKING

5.2.1 Zero amylase activity or non-sweet after cooking sweetpotato tested (zero/low amylase activity identified) and documented by January 2017 (milestone achieved)

Non-sweet sweetpotato. Information for 21 non-sweet sweetpotato clones have been uploaded onto a database on the Sweetpotato Knowledge Portal. The information contains CIP-code, accession name/ variety name/breeding code, aroma, and taste. The quality of information and material in the database

for non-sweet sweetpotato is poor compared with that in the early-bulking database. CIP–Lima has larger numbers of clones considered as low in sugar after cooking, but we had to realize that there are issues with our screening methods for sweetness after cooking and the determination of beta-amylase activity after cooking. The sweetpotato breeding group at CIP–Lima decided that all clones need to be evaluated for taste and aroma in order to decide about non-sweet sweetpotato after cooking.

DELIVERABLE 5.3: DATABASE FOR GG BY MODIFIED DEMO TRIALS

5.3.1 GG estimates for OFSP in humid tropics determined based on modified demo trials (comprising about 10 OFSP and 10 varieties from the past in Peru) available and documented by September 2017 (milestone achieved)

5.3.2 GG estimates for OFSP in semi-arid tropics/subtropics under terminal drought conditions (no irrigation after 80 days) determined based on modified demo trials (comprising about 10 OFSP and 10 varieties from the past in Peru) available and documented by September 2017 (milestone achieved)

Estimates for GG across years are important for predicting yield developments for the decades and for demonstrating value of investments into breeding. GG studies became available for four climatic zones mainly on basis of modified demo trials funded by the Gates Foundation in the context of the Sweetpotato Action for Security and Health in Africa project (Appendix A9_Sweetpotato).

DELIVERABLE 5.4: DATA IN SWEETPOTATOBASE FOR MANAGING SWEETPOTATO BREEDING RESEARCH

5.4.1 Multistage selection data for stages 1, 2, and 3 uploaded onto the SweetPotatoBase

Data from a national OFSP MET series for 42 genotypes with three seasons (2011, 2012, and 2013) and nine locations in the humid Amazonian lowlands of Peru were available in the SweetPotatoBase database: https://sweetpotatobase.org/folder/1578. With these data, variance components for genotypes, seasons, locations, and interactions were computed using mixed models. These variance components were used to evaluate the efficiency of different breeding scenarios. The data have potential to serve further research on both multistage and index selection (selection for several traits simultaneously).

APPENDIX

TABLE A1_POTATO. ADVANCED CLONES LBHT X LTVR

#	Clone	Skin color	Flesh color	Tuber shape	Eyes depth	Marketable tuber Yield th^{-1}					Resistance				Tolerance		Dry Matter % Huancayo 2018-2019	Chips color	TGA mg/100gr FW SRA2016-2017	Maturity days
						SRA 2015-2017	HYO 2017-2018	OXA 2017-2018	Majes NI 2018-2019	Majes RI 2018-2019	LB AUDPC 2017-2018	Scale	PVX	PVY	Heat	Drought				
1	CIP312887.075	Rd	Cr	El	S	23.72	27.80	21.00	32.15	5.01	520	2.00	ER	ER	T	NT	23.25	Good	7.41	90-110
2	CIP312887.141	Pi	Cr	Ob	S	13.54	22.00	35.93	35.01	7.87	18	0.06			NT	T			12.89	90-110
3	CIP312890.040	Rd	Cr	Ob	S	13.04	33.60	24.44	36.30	9.16	18	0.06			NT	T	21.17			90-110
4	CIP312894.008	Rd	Cr	Ov	S	15.93	27.02	35.26	37.21	10.07	210	0.73			NT	T	24.38		2.85	90-110
5	CIP312895.056	Cr	Cr	Ob	S	22.47	28.90	40.96	34.83	7.69	368	1.29	ER	ER	T	T	23.84	Good	2.65	90-110
6	CIP312895.102	Cr	Cr	El	S	17.76	30.60	28.15	29.48	2.34	228	0.80			NT	NT	21.75		19.73	90-110
7	CIP312896.009	Cr	Cr	El	S	22.81	30.50	22.22	36.53	9.40	228	0.80			T	T	24.27	Good	17.41	90-110
8	CIP312896.012	Cr	Cr	El	S	19.74	30.80	19.33	32.64	5.50	438	1.13	ER	ER	T	NT	22.91	Good		90-110
9	CIP312896.025	Cr	Cr	El	S	20.20	24.60	30.00			980	3.43	ER	ER	T		22.04			90-110
10	CIP312896.133	Rd	Cr	El	S	11.89	30.80	19.56	34.12	6.98	228	0.80	ER	ER	NT	T	20.10			120
11	CIP312899.078	Rd	Ye	Ov	S	20.83	31.10	30.00	30.85	3.71	105	0.37	ER	ER	T	NT	24.74	Good	15.26	90-110
12	CIP312900.155	Rd	Wh	Ob	S	11.56	28.10	28.22	34.35	7.21	140	0.49			NT	T	24.32			90-110
13	CIP312900.156	Cr	Cr	Ov	S	14.41	30.40	39.10	38.89	11.75	18	0.06			NT	T	23.75			90-110
14	CIP312901.053	Cr	Cr	Ov	S	18.84	21.90	19.80			910	3.00			T					90-110
15	CIP312903.013	Rd	Cr	Ob	S	20.74	30.00	40.96	34.40	7.26	88	0.31			T	T	20.13	Good		120
16	CIP312903.066	Cr	Cr	Ob	S	24.23	33.10	39.11	32.32	5.19	70	0.24			T	NT	22.02	Good		90-110
17	CIP312903.070	Cr	Ye	Ro	S	18.09	23.10	37.26	31.25	4.11	88	0.21			T	NT			16.04	120
18	CIP312906.044	Cr	Cr	Ob	S	13.81	25.10	33.85	28.94	1.81	193	0.67			NT	NT	19.98		4.99	90-110
19	CIP312906.050	Cr	Cr	El	S	25.88	26.60	21.86	32.45	5.41	755	2.63		ER	T	NT	20.49		3.67	120
20	CIP312906.102	Cr	Wh	Ov	S	14.39	27.80	56.44	33.57	6.43	88	0.31			NT	T	21.12			90-110
21	CIP312909.046	Rd	Wh	El	S	28.60	30.00	24.81	42.72	15.58	648	2.27			T	T	20.03		5.38	90-110
22	CIP312913.022	Cr	Cr	El	S	23.43	29.00	20.74	29.38	2.24	245	0.86	ER	ER	T	NT	21.75	Good	15.49	120
23	CIP312913.121	Cr	Cr	Ob	S	38.66	24.40	23.00			58	0.19			T				2.66	120
24	CIP312914.020	Rd	Ye	Ob	S	15.97	29.30	54.59	32.07	4.93	35	0.12			T	NT	23.16		7.17	120
25	CIP312914.053	Pi	Cr	Ob	S	23.22	23.60	41.83			840	2.98			T		21.40		7.89	90-110
26	CIP312915.141	Cr	Cr	Ob	S	19.27	25.60	47.93			35	0.12			T		22.26		6.34	90-110
27	CIP312917.022	Cr	Cr	Ob	S	18.11	30.60	25.85			53	0.18		ER	T		23.13		19.19	120
28	CIP312917.029	Cr	Cr	El	S	16.51	28.20	38.37			175	0.61			T		19.40		11.52	90-110
29	CIP312917.096	Cr	Cr	Ob	S	12.40		36.00			0	0.00			NT		20.82			120
30	CIP312918.015	Cr	Cr	El	S	18.69	23.00	30.67			0	0.00			T		22.29	Good		90-110
31	CIP312920.069	Cr	Cr	El	S	20.09	26.60	9.41			945	3.31			T		23.39			150
32	CIP312923.058	Pi	Cr	Ov	S	18.10	30.30	20.22	40.99	13.85	263	0.92	ER	ER	T	T	21.87			120
33	CIP312925.105	Cr	Cr	Ov	S	15.01	26.00	41.00	27.99	0.85	105	0.30			T	NT	23.85			120
34	CIP312925.107	Cr	Cr	El	S	19.63	31.20	30.44	30.08	2.94	123	0.43			T	NT	23.38		19.47	120
35	CIP312925.108	Cr	Cr	El	S	15.37	31.80	48.00			123	0.43			T	NT	23.42			120
36	CIP312925.137	Cr	Cr	El	S	20.76	25.70	62.83	30.12	2.99	105	0.30	ER		T	NT	21.40		9.31	120
37	CIP312927.017	Cr	Cr	Ob	S	18.48	33.80	4.59	28.97	1.83	18	0.06			T	NT	20.91		19.47	120
38	CIP312927.048	Cr	Cr	Ob	S	13.01	29.40	39.19	35.25	8.11	175	0.61			NT	T	21.89			120
39	CIP312928.013	Cr	Cr	Ob	S	22.69	25.90	13.00			1610	5.63	ER	ER	T	NT	21.47	Good	11.20	120
	Amarillis					4.27	26.50	12.39	31.32	4.19	1423	4.98			NT	NT	20.31		5.85	120
	Desiree					12.95	22.60		27.09	0.84					T	NT				120
	Yungay						26.00	2.39			1645	6.00			NT	NT	22.50		8.63	120
	Kory							13.00			435	2.00			NT	NT				120
	Canchan								28.96	1.83						NT	22.04			120
	CIP397077.16 SARNAV									4.32						T				

TABLE A2_ POTATO. ADVANCED CLONES B3C3

#	Clone	Skin color	Flesh color	Tuber shape	Eyes deep	Marketable tuber yield th^{-1}				Majes RI 2018-2019	LB Average 2015-2018		Virus Resistance		Tolerance		Dry Matter % Huancayo 2018-2019	Chips color	TGA mg/100gr FW SRA 2016-2017		Maturity days	Parental value TY	Phenotypic Stability	
						HYO 2015-2018	SRA 2017	OXA 2015-2018	Majes NI 2018-2019		AUDPC	Scale	PVX	PVY	Heat	Drought			SRA 2016	HYO 2016			MTY	Late Bligh resistance
1	CIP308427.194	Pi	Cr	Ob	S	35.78	22.22	7.89	25.90	5.97	17.50	0.07	ER		T	T	19.92		19.55	3.80	90-110		Stable	Stable
2	CIP308445.142	Red	Cr	Ob	S	34.06		20.15	21.85	1.91	110.83	0.42					21.82	Good	8.25		120			
3	CIP308452.167	Cr	Cr	El	S	48.13	8.98	23.40	20.99	1.06	180.83	0.68	ER	ER	NT		21.86	Good	19.48		120		Stable	Stable
4	CIP308452.253	Pi	Cr	Ov	S	30.17	10.43	22.95	20.54	0.61	58.33	0.22			NT		19.43	Good			120			
5	CIP308474.153	Rd/Cr	Cr	Ov	S	30.37	24.49	13.63	21.29	1.36	490.00	1.85			T		19.34	Good	2.99	3.17	90-110			Stable
6	CIP308476.16	Rd	Cr	Ov	S	30.76		19.14			145.83	0.55	ER	ER			24.77		4.97		120	Good		
7	CIP308478.59	Cr	Cr	Ob	S	43.24	33.71	21.70	21.70	1.77	320.83	1.21			T		19.41		3.16	7.90	90-110			Stable
8	CIP308479.56	Cr	Cr	Ro	S	47.53	24.90	20.14	23.93	4.00	285.83	1.08		ER	T	T	23.80	Good	9.44	3.63	90-110	Good		Stable
9	CIP308480.287	Cr	Cr	El	S	25.26	12.59	13.02	21.07	1.13	105.00	0.40	ER		NT		21.31	Good	14.51		120		Stable	Stable
10	CIP308480.334	Cr	Cr	Ob	S	35.00	22.64	49.01			105.00	0.40	ER		T		20.99	Good	7.34	5.01	90-110	Good		
11	CIP308480.376	Cr	Cr	Ob	S	34.39		21.38			175.00	0.66					23.69	Good	5.14	3.10	120			
12	CIP308481.302	Cr	Cr	El	S	39.26		24.07	21.77	1.83	501.67	1.90					20.79				120			
13	CIP308482.163	Pi	Cr	Ob	S	44.32	20.63	42.72	22.74	2.81	180.83	0.68	ER	ER	T		18.28		12.97	5.55	90-110		Stable	Stable
14	CIP308482.318	Rd	Cr	Ob	S	31.65		23.70			140.00	0.53					20.00		6.52	28.60	120			
15	CIP308486.187	Cr	Cr	Ro	S	41.55	11.84	34.52	21.90	1.97	227.50	0.86	ER		NT		21.75	Good			120	Good	Stable	Stable
16	CIP308486.220	Cr	Cr	Ob	S	30.00	21.38	27.55			262.50	0.99			T		20.96	Good	2.70		90-110	Good		
17	CIP308486.314	Pr	Cr	Ov	S	27.49		53.15	22.57	2.64	192.50	0.73	ER				18.07	Good			120	Good		
18	CIP308486.328	Cr	Cr	Ob	S	20.67		11.51			169.17	0.64	ER	ER			21.41	Good		2.51	120	Good		
19	CIP308486.355	Pr	Cr	Ro	S	52.64	11.73	32.90	24.88	4.94	291.67	1.10	ER	ER	NT	T	24.44	Good	7.73		120	Good	Stable	Stable
20	CIP308487.157	Rd	Cr	Ov	S	33.63	4.43	12.74	20.93	1.00	210.00	0.79	ER		NT		23.44	Good		5.16	120			Stable
21	CIP308487.163	Rd	Cr	Ob	S	54.54		16.71			303.33	1.15	ER	ER			21.01	Good		9.97	120	Good		
22	CIP308487.197	Rd	Cr	Ob	S	44.08	8.89	46.59	26.82	6.89	315.00	1.19	ER	ER	NT	T	20.38			7.89	120			Stable
23	CIP308487.390	Rd	Cr	Ob	S	28.00	21.20	27.33	21.79	1.86	285.83	1.08	ER		T		21.89	Good	7.98	7.84	90-110			
24	CIP308488.198	Rd	Cr	Ob	S	15.00	25.07	23.21	25.43	5.49	186.67	0.71	ER		T	T	23.05	Good	4.89	9.58	90-110	Good		
25	CIP308489.367	Cr	Cr	Ob	S	16.00	23.62	44.05	21.28	1.35	140.00	0.53			T		20.99	Good			90-110			
26	CIP308493.22	Cr	Cr	Ov	S	31.74	14.67	24.51	21.23	1.29	408.33	1.54	ER		NT		21.07		7.32		120		Stable	Stable
27	CIP308494.368	Cr	Cr	El	S	36.57		15.33	22.34	2.41	175.00	0.66	ER				23.79	Good	19.83		120	Good		
28	CIP308495.227	Cr	Cr	Ob	S	35.60		27.85	21.94	2.01	64.17	0.24	ER				22.86		16.88	10.04	120			
29	CIP308495.329	Rd	Wh	Ob	S	27.11		18.74	22.36	2.42	285.83	1.08	ER				23.70				120			
30	CIP308497.212	Rd	Ye	Ov	S	27.52	21.06	7.45			676.67	2.56	ER		T		24.11		15.11		90-110		Stable	
31	CIP308498.280	Cr	Cr	Ov	S	20.70	23.72	31.63	20.97	1.04	303.33	1.15	ER		T		22.95	Good	19.74		90-110		Stable	Stable
32	CIP308498.326	Cr	Cr	Ov	S	27.33		26.07	23.61	3.67	87.50	0.33					21.82	Good	2.86	6.91	120			
33	CIP308499.112	Rd	Cr	Ov	S	28.00		11.92			198.33	0.75					23.81	Good	7.47		120			
34	CIP308499.143	Rd	Cr	Ob	S	22.98	13.06	10.37			227.50	0.86			NT		22.82		7.28		120			
35	CIP308499.334	Pi	Cr	Ov	S	38.27		15.36	23.74	3.80	140.00	0.53		ER			19.33	Good	10.60		120	Good		
36	CIP308499.76	Rd	Ye	Ro	S	35.67		16.44	22.40	2.56	163.33	0.62					22.88	Good	7.31	5.17	120	Good		
37	CIP308501.211	Cr	Ye	Ob	S	14.89		23.85	22.28	2.35	291.67	1.10					20.02	Good			120	Good		
38	CIP308502.95	Pr	Cr	Ob	S	21.00		10.22			75.83	0.29	ER	ER			23.26		1.50		120			
39	CIP308503.312	Cr	Cr	Ob	S	35.82		50.37	25.59	5.56	256.67	0.97	ER	ER		T	19.12	Good	18.95	19.73	120			
40	CIP308510.80	Pi	Ye	Ov	S	31.80	16.32	28.52	22.78	2.84	221.67	0.84	ER	ER	T		20.65		20.52		90-110		Stable	Stable
41	CIP308513.318	Pr	Cr	Ov	S	41.11	17.47	16.13	22.56	2.62	204.17	0.77	ER		T		18.43	Good	3.62	6.35	90-110	Good	Stable	Stable
42	CIP308513.404	Pr	Cr	Ob	S	28.28	12.30	10.37	20.98	1.05	303.33	1.15			NT		24.40	Good	10.16		120		Stable	Stable
43	CIP308518.201	Pi	Cr	Ob	S	42.69	16.45	32.12	20.91	0.97	87.50	0.33			T		21.96		2.10	14.30	90-110		Stable	
44	CIP308518.256	Cr	Cr	Ob	S	30.22		11.85			105.00	0.40					18.82				120			
45	CIP308518.7	Rd	Cr	Ob	S	43.67	12.96	42.55	22.82	2.88	140.00	0.53			NT		20.93	Good	15.64		120		Stable	Stable
46	CIP308519.110	Cr	Ye	El	S	35.41		36.44	22.32	1.38	705.83	2.67	ER	ER			20.57	Good	1.11	2.75	120			
47	CIP308519.359	Cr	Cr	Ov	S	35.07		18.89	23.59	3.65	379.17	1.43		ER			24.13	Good	9.58		120			
48	CIP308519.433	Cr	Cr	Ob	S	30.35	16.32	27.41	20.91	0.98	390.83	1.48		ER	T		26.22	Good	13.98		90-110		Stable	Stable
49	CIP308519.59	Cr	Ye	El	S	56.41		20.07	21.13	1.20	390.83	1.48	ER	ER			24.37	Good	10.57		120			
50	CIP308520.290	Cr	Cr	El	S	36.80		11.63	21.69	1.75	134.17	0.51	ER	ER			20.47			10.17	120			
51	CIP308520.348	Cr	Cr	Ob	S	33.39		44.07	23.78	3.85	151.67	0.57					17.94		18.53		120			
	Amarilis					35.66	5.24	7.64	22.22	2.28	1534.17	5.80			NT		21.12	Good			120			
	Yungay					26.19		1.50	24.85	4.91	1586.67	6.00					21.27			4.98	120			
	Desiree					15.28	13.39	6.34	22.95	3.01	2053.00	7.76			T						90-110			
	Kory							4.17													120			
	Canchan							0.00	21.83	1.89							24.59	Good			120			
	Capiro																23.18	Good			120			

NI = Normal Irrigation, ER= Extreme resistance, TGA= Total Glycoalkaloids, RI= restricted Irrigation, T= Tolerant, SRA= San Ramon, LB= Late Blight, NT=non-tolerant, OXA= Oxapampa, Cr= Cream, Ro = Round, S= Superficial, Pi= Pink, Wh = White, Ob = Oblong, Rd = Red, El = Elliptic, Ov = Oval

TABLE A3_POTATO. TOP 56 DIHAPLOIDS ACCORDING TO REPRODUCTIVE CHARACTERISTICS

Item	CIPN	Breeder Code	Flowering degree	Pollen Quantity	Pollen Viability (%)	2n pollen (%)	Flowering peak (days)	Plant vigor	Parent
Population: B3									
Family: CIP393228.67 x HI									
1	CIP515521.006	PL-HT13.006	5.6 + 0.3	4 + 1.4	19.7 + 1.6	ne	75 + 0	3 + 0	Female
2	CIP515521.007	PL-HT13.007	4.9 + 0.7	2 + 1.4	16.7 + 12.2	ne	75 + 0	3 + 0	Female
3	CIP515521.001	PL-HT13.001	4.4 + 0.3	1.4 + 1.6	10.4 + 6.6	ne	105 + 0	ne	Female
4	CIP515521.002	PL-HT13.002	3.9 + 0.7	1.6 + 0.9	26.5 + 13.5	ne	83 + 29	ne	Female
5	CIP515521.008	PL-HT13.008	3.9 + 1	2 + 1.4	35.2 + 2.7	0.0	68 + 11	ne	Female
6	CIP515521.005	PL-HT13.005	3.9 + 0.4	1.3 + 0.4	25 + 14.9	0.7	83 + 32	ne	Female
7	CIP515521.013	PL-HT13.013	2.3 + 0.7	3 + 1.4	52.7 + 10.3	2.4	68 + 32	ne	Male
Family: CIP395017.242 x HI									
8	CIP312727.006	BIOT-727.006	4 + 0.8	0 + 0	ne	ne	75 + 21	3 + 0	Female
9	CIP312727.005	BIOT-727.005	4 + 0.8	1 + 0	17.2 + 5.6	ne	45 + 0	5 + 0	Female
Population: BW									
Family: CIP391931.1 / 458 x HI									
10	CIP518002.008	DHP-042.008	4.8 + 1.1	5 + 2.8	25.5 + 15	ne	75 + 0	3 + 0	Female
11	CIP518002.011	DHP-042.011	4.5 + 0.7	3 + 0	48.4 + 1.2	ne	53 + 11	3 + 0	Female
12	CIP518002.007	DHP-042.007	4.5 + 0.7	2 + 1.4	35.2 + 6.5	ne	75 + 21	5 + 0	Female
13	CIP518002.012	DHP-042.012	4 + 2.8	4 + 1.4	83 + 0.8	0.0	53 + 11	2 + 1.4	Male
14	CIP315040.005	PL-DT5.005	2.8 + 0	6 + 0.7	87.1 + 2.5	0.5 + 0.6	60 + 0	ne	Male
15	CIP315040.004	PL-DT5.004	1 + 1.2	4.5 + 3	87 + 1	0.0	71 + 31	ne	Male
Population: LBHT-1									
Family: CIP398190.89 x HI									
16	CIP515525.003	PL-HT18.003	4.5 + 0.1	3 + 0	22.9 + 4.2	ne	75 + 0	3 + 0	Female
17	CIP515525.009	PL-HT18.009	3.8 + 1.1	2.5 + 0.7	27.3 + 13.2	ne	83 + 32	ne	Female
Population LTVR									
Family: CIP300048.12 / LR00.006 x HI									
18	CIP316613.009	PL-HT1.009	2.3 + 0.1	5 + 0	71.2 + 6.6	ne	105 + 0	ne	Male
19	CIP316613.020	PL-HT1.020	1.6 + 0.6	5 + 0	65.8 + 2.6	0.0	98 + 11	ne	Male
20	CIP316620.002	35-HT1.002	1 + 0.6	2 + 1.4	81.4 + 6.2	ne	83 + 32	ne	Male
Family: CIP300056.33 / LR00.014 x HI									
21	CIP518009.038	DHP-109.038	4.5 + 0.1	0 + 0	ne	ne	90 + 0	6 + 0.3	Female
22	CIP518003.015	DHP-031.015	3.3 + 0.7	0	ne	ne	98 + 11	5.2 + 1.4	Female
23	CIP315029.020	35-DT1.020	3.2 + 1.4	0 + 0	ne	ne	75 + 21	ne	Female
24	CIP516006.225	DHP-006.225	3.2 + 0.3	0	ne	ne	83 + 11	5 + 0	Female
25	CIP518003.012	DHP-031.012	2.6 + 0.6	0	ne	ne	83 + 11	4.8 + 1.4	Female
26	CIP518003.013	DHP-031.013	2.5 + 0.4	0	ne	ne	75 + 21	4 + 1.4	Female
27	CIP518009.040	DHP-109.040	2.5 + 1	0	ne	ne	105 + 0	5.6 + 0.8	Female
28	CIP516006.227	DHP-006.227	2.4 + 0.8	0	ne	ne	90 + 21	6 + 0.3	Female
Family: CIP300072.1 / LR00.022 x HI									
29	CIP316618.010	35-HT2.010	3.8 + 0.3	3 + 2.8	29.1 + 31.9	ne	60 + 0	ne	Female
30	CIP515505.014	DHP-505.014	2.2 + 0.6	2 + 1.4	68.1 + 22.8	ne	105 + 0	ne	Male
Family: CIP300093.14 / LR00.026 x HI									
31	CIP516016.024	DHP-016.024	5 + 0	1 + 0	0 + 0	ne	75 + 21	3 + 0	Female
32	CIP516016.017	DHP-016.017	4.3 + 1.1	0.5 + 0.7	ne	ne	75 + 21	3 + 0	Female
Family: CIP388615.22 / C91.640 x HI									
33	CIP515504.027	DHP-504.027	4.2 + 1.1	3 + 0	2.5 + 3.5	ne	75 + 0	5 + 0	Female
Family: CIP390637.1 / 93.003 x HI									

Item	CIPN	Breeder Code	Flowering degree	Pollen Quantity	Pollen Viability (%)	2n pollen (%)	Flowering peak (days)	Plant vigor	Parent
34	CIP316336.111	DHP-336.111	5.3 + 0.4	0 + 0	ne	ne	75 + 0	3 + 0	Female
Family: CIP392740.4 / 92.065 x HI									
35	CIP312544.005	BIOT-544.005	4.6 + 0.8	5 + 0	46.9 + 4.7	ne	75 + 0	5 + 0	Female
Family: CIP392820.1 / C93.154 x HI									
36	CIP316601.058	PL-HT10.058	4.6 + 0	0.3 + 0.4	ne	ne	75 + 0	5 + 0	Female
37	CIP316601.049	PL-HT10.049	4.1 + 0.7	0 + 0	ne	ne	83 + 11	4 + 1.4	Female
38	CIP316603.017	DHP-603.017	3.8 + 1.4	1.8 + 1.8	0 + 0	ne	65 + 9	5 + 0	Female
39	CIP316601.047	PL-HT10.047	3.7 + 1.8	3.3 + 2.5	63.2 + 21.2	ne	83 + 11	3 + 0	Male
40	CIP316601.036	PL-HT10.036	3.4 + 0.6	0.2 + 0.2	ne	ne	90 + 21	ne	Female
41	CIP316601.065	PL-HT10.065	2.8 + 0.3	0 + 0	ne	ne	75 + 21	4 + 1.4	Female
42	CIP312558.002	BIOT-558.002	5.4 + 0.6	2 + 1.4	2.2 + 0.8	ne	68 + 11	3 + 0	Female
43	CIP312575.001	BIOT-575.001	3.8 + 0.3	0 + 0	ne	ne	90 + 21	3 + 0	Female
44	CIP312554.003	BIOT-554.003	3	0	58.1	ne	75	5	Male
Family: CIP397067.2 / 346.2 x HI									
45	CIP312807.005	BIOT-807.005	4.7 + 1	0 + 0	ne	ne	83 + 11	5 + 0	Female
Family: CIP397077.16 / WA.077 x HI									
46	CIP518006.016	DHP-030.016	6.3 + 0.4	5 + 2.8	55.1 + 34.4	0.0	68 + 11	5 + 0	Female
47	CIP315048.036	35-DT8.036	4.2 + 0.6	2 + 1.4	9.9 + 8.3	ne	90 + 21	ne	Female
48	CIP518005.724	DHP-033.724	3.6 + 1.4	0.5 + 0.7	ne	ne	45 + 0	3.6 + 0.8	Female
49	CIP518005.093	DHP-033.093	3.5 + 0.7	1 + 0	5.1 + 1.5	ne	75 + 0	5 + 0	Female
50	CIP315048.004	35-DT8.004	3.4 + 0.6	0 + 0	ne	ne	53 + 11	ne	Female
51	CIP518005.091	DHP-033.091	3 + 0	0	ne	ne	60 + 0	5 + 0	Female
52	CIP315048.048	35-DT8.048	3 + 0	1 + 0	2.6 + 3.7	ne	98 + 11	ne	Female
53	CIP516004.176	DHP-004.176	2.3 + 1	0	ne	ne	90 + 0	6.2 + 0	Female
54	CIP315047.053	PL-DT8.053	1.2 + 1.1	3 + 0	74.2 + 3.2	ne	53 + 11	ne	Male
Family: CIP397099.4 / WA.073 x HI									
55	CIP515509.001	PL-HT16.001	3.4 + 0.8	0.8 + 1.1	ne	ne	75 + 0	3 + 0	Female
Population: Tuberosum									
Family: CIP800827 / Atlantic x HI									
56	CIP315052.002	PL-DT10.002	3.1 + 1.4	1.4 + 0.3	70.9 + 6.1	0.2 + 0.4	83 + 15	4 + 1.4	Male

TABLE A4_ SWEETPOTATO. OFSP HYBRID POPULATION I PARENTS (90-DAYS HARVEST) TRANSFER TO CIP'S GENEBANK FOR GLOBAL DISSEMINATION

Clone Breeding Code	Clone CIP No.	Female CIP No.	Female Breeding Code	Male CIP No.	Male Breeding Code	Family CIP No.
PJ14.00031	CIP113001.31	189129.12	PJ05.012	189129.12	PJ05.012	CIP113001
PJ14.00044	CIP113002.8	189129.12	PJ05.012	189151.34	PJ05.064	CIP113002
PJ14.00084	CIP113003.10	189129.12	PJ05.012	190089.6	PJ05.114	CIP113003
PJ14.00197	CIP113008.1	189129.12	PJ05.012	194568.12	PJ05.210	CIP113008
PJ14.01502	CIP113063.8	190094.29	PJ05.120	190094.91	PJ05.124	CIP113063
PJ14.01518	CIP113063.24	190094.29	PJ05.120	190094.91	PJ05.124	CIP113063
PJ14.01935	CIP113078.27	190094.29	PJ05.120	189134.1	PJ05.255	CIP113078
PJ14.02153	CIP113090.7	190094.91	PJ05.124	189151.32	PJ05.220	CIP113090
PJ14.02303	CIP113099.27	190094.91	PJ05.130	190089.6	PJ05.114	CIP113099
PJ14.02629	CIP113111.5	190094.91	PJ05.130	189153.7	PJ05.235	CIP113111
PJ14.02666	CIP113112.6	190094.91	PJ05.130	189153.18	PJ05.236	CIP113112
PJ14.02677	CIP113113.3	190094.91	PJ05.130	194544.2	PJ05.248	CIP113113
PJ14.02826	CIP113118.6	190094.91	PJ05.130	189152.31	PJ05.306	CIP113118
PJ14.03230	CIP113137.1	194581.4	PJ05.171	189134.1	PJ05.255	CIP113137
PJ14.03297	CIP113139.21	194581.4	PJ05.171	189145.21	PJ05.303	CIP113139
PJ14.03621	CIP113150.3	194568.12	PJ05.210	189151.8	PJ05.212	CIP113150
PJ14.03815	CIP113155.17	194568.12	PJ05.210	189165.9	PJ05.233	CIP113155
PJ14.03821	CIP113155.23	194568.12	PJ05.210	189165.9	PJ05.233	CIP113155
PJ14.04069	CIP113162.13	194568.12	PJ05.210	189145.21	PJ05.303	CIP113162
PJ14.04503	CIP113184.9	189151.8	PJ05.212	190094.36	PJ05.257	CIP113184
PJ14.05584	CIP113226.11	189153.29	PJ05.216	189134.1	PJ05.255	CIP113226
PJ14.05634	CIP113227.30	189153.3	PJ05.216	190094.36	PJ05.257	CIP113227
PJ14.05846	CIP113241.12	189151.32	PJ05.219	190094.36	PJ05.257	CIP113241
PJ14.06163	CIP113264.1	189165.9	PJ05.233	190089.6	PJ05.114	CIP113264
PJ14.06186	CIP113265.2	189165.9	PJ05.233	190094.29	PJ05.120	CIP113265
PJ14.06198	CIP113265.14	189165.9	PJ05.233	190094.29	PJ05.120	CIP113265
PJ14.06199	CIP113265.15	189165.9	PJ05.233	190094.29	PJ05.120	CIP113265
PJ14.06227	CIP113268.13	189165.9	PJ05.233	194581.4	PJ05.171	CIP113268
PJ14.06822	CIP113300.22	189153.18	PJ05.236	190094.29	PJ05.120	CIP113300
PJ14.06914	CIP113302.57	189153.18	PJ05.236	194581.4	PJ05.171	CIP113302
PJ14.07107	CIP113313.16	189153.18	PJ05.236	190094.36	PJ05.257	CIP113313
PJ14.07404	CIP113329.36	194544.2	PJ05.248	189151.32	PJ05.220	CIP113329
PJ14.07502	CIP113332.25	194544.2	PJ05.248	189134.1	PJ05.255	CIP113332
PJ14.07654	CIP113347.4	194541.55	PJ05.253	189151.32	PJ05.220	CIP113347
PJ14.08437	CIP113397.2	190094.36	PJ05.257	189145.21	PJ05.303	CIP113397
PJ14.08556	CIP113400.15	189145.21	PJ05.303	189129.3	PJ05.012	CIP113400
PJ14.08711	CIP113406.16	189145.21	PJ05.303	194568.12	PJ05.210	CIP113406
PJ14.08780	CIP113412.7	189145.21	PJ05.303	189165.9	PJ05.233	CIP113412
PJ14.08844	CIP113414.13	189145.21	PJ05.303	189153.18	PJ05.236	CIP113414
PJ14.08857	CIP113414.26	189145.21	PJ05.303	189153.18	PJ05.236	CIP113414

Clone Breeding Code	Clone CIP No.	Female CIP No.	Female Breeding Code	Male CIP No.	Male Breeding Code	Family CIP No.
PJ14.08879	CIP113415.11	189145.21	PJ05.303	194544.2	PJ05.248	CIP113415
PJ14.08891	CIP113415.23	189145.21	PJ05.303	194544.2	PJ05.248	CIP113415
PJ14.09323	CIP113435.27	189152.31	PJ05.306	189134.1	PJ05.255	CIP113435
PJ14.09482	CIP113444.17	194556.56	PJ05.324	189151.32	PJ05.220	CIP113444
PZ14.09654	CIP113452.9	105083.1	PZ06.042	105083.1	PZ06.042	CIP113452
PZ14.09689	CIP113454.2	105083.1	PZ06.042	105229.1	PZ06.072	CIP113454
PZ14.09697	CIP113454.10	105083.1	PZ06.042	105229.1	PZ06.072	CIP113454
PZ14.09698	CIP113454.11	105083.1	PZ06.042	105229.1	PZ06.072	CIP113454
PZ14.09717	CIP113456.4	105083.1	PZ06.042	105058.2	PZ06.120	CIP113456
PZ14.09762	CIP113458.3	105083.1	PZ06.042	105212.1	PZ06.196	CIP113458
PZ14.09781	CIP113458.22	105083.1	PZ06.042	105212.1	PZ06.196	CIP113458
PZ14.09799	CIP113458.40	105083.1	PZ06.042	105212.1	PZ06.196	CIP113458
PZ14.09882	CIP113460.33	105083.1	PZ06.042	105495.1	PZ06.304	CIP113460
PZ14.09909	CIP113461.7	105083.1	PZ06.042	189151.32	PZ06.349	CIP113461
PZ14.09911	CIP113461.9	105083.1	PZ06.042	189151.32	PZ06.349	CIP113461
PZ14.09966	CIP113466.2	105080.1	PZ06.048	105269.1	PZ06.235	CIP113466
PZ14.09979	CIP113467.11	105080.1	PZ06.048	105495.1	PZ06.304	CIP113467
PZ14.09984	CIP113467.16	105080.1	PZ06.048	105495.1	PZ06.304	CIP113467
PZ14.10005	CIP113471.5	105080.1	PZ06.048	105511.1	PZ06.359	CIP113471
PZ14.10013	CIP113472.6	105080.1	PZ06.048	105175.1	PZ06.441	CIP113472
PZ14.10017	CIP113473.2	105229.1	PZ06.072	105083.1	PZ06.042	CIP113473
PZ14.10020	CIP113473.5	105229.1	PZ06.072	105083.1	PZ06.042	CIP113473
PZ14.10203	CIP113480.11	105229.1	PZ06.072	105269.1	PZ06.235	CIP113480
PZ14.10213	CIP113481.1	105229.1	PZ06.072	105495.1	PZ06.304	CIP113481
PZ14.10265	CIP113482.15	105229.1	PZ06.072	105071.1	PZ06.307	CIP113482
PZ14.10448	CIP113492.22	105100.1	PZ06.114	105058.2	PZ06.120	CIP113492
PZ14.10473	CIP113493.20	105100.1	PZ06.114	105030.1	PZ06.124	CIP113493
PZ14.10478	CIP113493.25	105100.1	PZ06.114	105030.1	PZ06.124	CIP113493
PZ14.10491	CIP113493.38	105100.1	PZ06.114	105030.1	PZ06.124	CIP113493
PZ14.10564	CIP113494.55	105100.1	PZ06.114	105212.1	PZ06.196	CIP113494
PZ14.10610	CIP113495.45	105100.1	PZ06.114	105269.1	PZ06.235	CIP113495
PZ14.10683	CIP113498.5	105100.1	PZ06.114	189151.32	PZ06.349	CIP113498
PZ14.10763	CIP113502.14	105100.2	PZ06.115	105229.1	PZ06.072	CIP113502
PZ14.11004	CIP113516.4	105058.2	PZ06.120	105212.1	PZ06.196	CIP113516
PZ14.11152	CIP113529.4	105030.1	PZ06.124	105175.1	PZ06.441	CIP113529
PZ14.11182	CIP113531.19	105212.1	PZ06.196	105229.1	PZ06.072	CIP113531
PZ14.11280	CIP113537.24	105212.1	PZ06.196	189151.32	PZ06.349	CIP113537
PZ14.11317	CIP113542.2	105269.1	PZ06.235	105030.1	PZ06.124	CIP113542
PZ14.11380	CIP113548.5	105269.1	PZ06.235	105511.1	PZ06.359	CIP113548
PZ14.11407	CIP113550.14	105495.1	PZ06.304	105229.1	PZ06.072	CIP113550
PZ14.11826	CIP113587.23	105175.1	PZ06.441	105030.1	PZ06.124	CIP113587
PZ14.11854	CIP113588.20	105175.1	PZ06.441	105212.1	PZ06.196	CIP113588

Clone Breeding Code	Clone CIP No.	Female CIP No.	Female Breeding Code	Male CIP No.	Male Breeding Code	Family CIP No.
PZ14.11883	CIP113590.1	105175.1	PZ06.441	105495.1	PZ06.304	CIP113590
PZ14.11887	CIP113590.5	105175.1	PZ06.441	105495.1	PZ06.304	CIP113590
PZ14.11898	CIP113590.16	105175.1	PZ06.441	105495.1	PZ06.304	CIP113590
PZ14.11904	CIP113590.22	105175.1	PZ06.441	105495.1	PZ06.304	CIP113590
PZ14.11929	CIP113590.47	105175.1	PZ06.441	105495.1	PZ06.304	CIP113590
PZ14.11937	CIP113591.4	105175.1	PZ06.441	189151.32	PZ06.349	CIP113591

TABLE A5_ SWEETPOTATO. ELITE TS IN CIP'S SEED STOCKS FROM H0 HYBRID POPULATION (100-DAY GROWING PERIODS)

Female Breeding Code	Female CIP Code	Male Breeding Code	Male CIP Code	CIP Family Code	TS Available for Distribution
Low DM elite OFSP cross-combinations (DM <28%)					
PJ05.124	CIP190094.91	PZ08.038	CIP107160.1	CIP114637	6,975
PJ05.120	CIP190094.29	PZ08.011	CIP107215.2	CIP114621	8,778
PJ05.130	CIP194513.23	PZ08.038	CIP107160.1	CIP114645	10,415
PJ05.213	CIP194575.8	PZ08.038	CIP107160.1	CIP114706	7,992
PJ05.213	CIP194575.8	PZ08.090	CIP107154.1	CIP114710	448
PJ07.265	CIP106311.2	PZ08.011	CIP107215.2	CIP114724	1,512
Low DM elite OFSP cross-combinations (DM ≥28%)					
PJ07.061	CIP106373.1	PZ08.038	CIP107160.1	CIP114410	16,788
PJ07.061	CIP106373.1	PZ06.085	CIP105886.1	CIP113665	8,853
PJ07.690	CIP106806.2	PZ06.304	CIP105495.1	CIP114922	14,265
PJ07.079	CIP106082.1	PZ06.304	CIP105495.1	CIP118017	13
PJ05.213	CIP194575.8	PZ08.153	CIP107095.1	CIP114712	8,121
PJ05.064	CIP109151.34	PZ08.153	CIP107095.1	CIP114613	16,967
Total					**101,127**

TABLE A6_SWEETPOTATO: ESTIMATED OFF-SPRING PERFORMANCE OF OFSP ELITE CROSSING FROM H0 HYBRID POPULATION (BASED ON TWO LOCATIONS, PERU/CAÑETE AND SATIPO)

Cross Combination PJ X PZ	No. of Commercial Root/Plant	Storage Root Yield (t/ha)	Foliage Yield (t/ha)	Root DM (%)
Low DM elite OFSP cross-combinations				
PJ05.124-PZ08.038	3.50	27.4	30.0	25.7
PJ05.120-PZ08.011	3.31	31.0	16.1	25.8
PJ05.130-PZ08.038	2.83	27.9	25.2	26.2
PJ05.213-PZ08.038	2.78	24.3	40.3	27.4
PJ05.213-PZ08.090	2.70	25.7	42.3	27.3
PJ07.265-PZ08.011	2.68	20.1	30.7	28.0
High DM elite OFSP cross-combinations				
PJ07.061-PZ08.038	2.67	27.8	31.3	29.8
PJ07.061-PZ06.085	2.62	19.5	30.0	28.7
PJ07.690-PZ06.304	2.17	16.3	29.8	29.7
PJ07.079-PZ06.304	2.17	20.5	40.4	28.3
PJ05.213-PZ08.153	2.15	25.8	23.8	32.3
PJ05.064-PZ08.153	2.00	17.4	14.7	31.6

TABLE A7_SWEETPOTATO: TS GENERATED FROM SPVD PRE-BREEDING POPULATION PV19

	Male Parent	105086.1	194540.5	110019.21	112240.7	107548.5	107729.9	107734.5	107577.23	107581.1	107582.3
Female Parent	Breeding Code	PZ06.085	PJ05.052	VJ11.034	112240.7	VZ08.124	VJ08.330	VJ08.390	VZ08.263	VZ08.312	VZ08.340
CIP105086.1	PZ06.085	650	2,246	1,679	292	314	1,829	281	364	1,673	290
CIP194540.5	PJ05.052	958	131	607	142	1,030	727	25	95	833	201
CIP110019.21	VJ11.034	658	515	89	5	263	21	518	221	219	189
CIP112240.7	CIP112240.7	184	146			39		66	128	6	17
CIP107548.5	VZ08.124		272	87	97	34	148	139	151	234	47
CIP107729.9	VJ08.330	168	298	22	9	196	52	328	301	256	87
CIP107734.5	VJ08.390	78	1	82	72	44	90	16	155	30	25
CIP107577.23	VZ08.263	3	53	9	4	2	22	20	4		
CIP107581.1	VZ08.312	44	92	64	60	29	151	149	3	11	1
CIP107582.3	VZ08.340	2	1	15			1	3			

NOTE: Rows include the female parents, while columns represent male parents for the crossings. Each cell represents a family (female x male) and the number inside is the amount of seeds obtained.

TABLE A8_SWEETPOTATO. DART MARKERS FOUND IN ASSOCIATION WITH SPVD RESISTANCE IN PV08 WITH VALIDATION IN PZ08 AND NEW DART MARKERS OBSERVED IN

Marker ID	Discovery Population PV08		Validation Population PZ08	
	R^2	p-value	R^2	p-value
7548044	0.48	0.002	0.00649	0.93921
7574925	0.37	0.006	NA	NA
7573123	0.36	0.008	0.02342	0.69402
7572542	0.35	0.009	0.00751	0.92581
7563062	0.34	0.01	0.00876	0.90864

Marker ID	SNP	p-value	R^2	*I. trifida* *		*I. triloba* *	
				Chromosome	Position	Chromosome	Position
7548840	0-45:G>T	8.55×10^{-4}	0.30571	Chr07	18698051	Chr 07	25385600
9841480	0-53:T>C	1.86×10^{-3}	0.27135	Chr01	265857	Chr01	265227
9840935	0-49:C>A	1.95×10^{-3}	0.26941	Chr14	1166311	Chr14	1187019
7541065	0-20:A>T	2.54×10^{-3}	0.25783	Chr11	6912748	Chr11	9090385
7574783	0-57:G>T	2.55×10^{-3}	0.25773	Chr02	15604927		0
7571182	0-59:A>T	8.88×10^{-4}	0.25495	Chr09	22875164	Chr09	31155137

TABLE A9_SWEETPOTATO: GG BY REGIONS ESTIMATED BASED ON VARIETY RELEASES ACROSS TWO DECADES (UPDATED JULY 2019; EXPERIMENTS FUNDED BY GATES FOUNDATION THROUGH THE SASHA PROJECT)

Agro-ecological Zone	GG Parameters and Year Period Considered	Storage Root Yield (90 days harvest) t/ha	Storage Root Yield (120 days harvest) t/ha	Foliage Yield (90 days harvest) t/ha	Foliage Yield (120 days harvest) t/ha	β-carotene (120 days harvest) mg/ 100 g root FW
Arid Pacific coast	Release period	1992-2014	1992-2014	1992-2014	1992-2014	1992-2014
	Baseline	5.1	10.1	43.1	52.4	0.83
	Annual gain	0.29	0.47	-0.31	-0.34	0.30
	Predicted 2019	11.5	20.5	36.3	44.9	7.43
	Est. current gain %	2.5%	2.3%	-0.1%	-0.1%	4.0%
Amazon basin‡	Release period	1992-2014	1992-2014	1992-2014	a.	1992-2014
	Baseline	5.7	9.2	34.5	n.p.	0.87
	Annual gain	0.30	0.49	0.05	n.p.	0.36
	Predicted 2019	12.3	20.0	35.6	n.p.	8.79
	Est. current gain %	2.4%	2.5%	0.1%	n.p.	4.1%
Southern Africa	Release period	n.a	2000-2016	n.a	2000-2016	a.
	Baseline	n.a	7.2	n.a	14.7	n.p.
	Annual gain	n.a	0.16	n.a	0.20	n.p.
	Predicted 2019	n.a.	9.8	n.a.	17.9	n.p.
	Est. current gain %	n.a.	1.6%	n.a.	1.1%	n.p.
east Africa (Uganda)	Release period	n.a.	1995-2013	n.a.	1995-2013	1995-2013
	Baseline	n.a.	10.3	n.a	22.6	0.0
	Annual gain	n.a.	0.38	n.a	-0.07	0.35
	Predicted 2019	n.a.	17.1	n.a.	21.3	5.4
	Est. current gain %	n.a.	2.2%	n.a.	-0.3%	6.5%
west Africa (Ghana)	Release period	n.a.	1999-2015	n.a.	1999-2015	1999-2015
	Baseline	n.a.	7.4	n.a	15.9	0.0
	Annual gain	n.a.	0.07	n.a	-0.23	0.19
	Predicted 2019	n.a.	8.5	n.a.	12.2	3.0
	Est. current gain %	n.a.	0.8%	n.a.	-1.9%	6.3%

*Assume to be transferable to other humid topical zones with high rainfall. n.a. = not available; n.p. = so far not predicted.

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