



USAID
FROM THE AMERICAN PEOPLE

2016 PROGRESS REPORT

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

9 January 2017

This publication was produced for review by the United States Agency for International Development. It was prepared by the International Potato Center.

Advancing Achievements in Breeding for Early, Resilient, and Nutritious Potato and Sweetpotato

2016 Progress Report

International Potato Center (CIP)

Director: Barbara Wells
Address: Apartado 1558, Lima 12, Peru
Phone: (51)(1)349-6017/349 – 5783
Fax: (51)(1)349-5638
Website: <http://www.cipotato.org>

Responsible persons: Merideth Bonierbale m.bonierbale@cgiar.org
Wolfgang Grüneberg w.gruneberg@cgiar.org

Address: Apartado 1558, Lima 12, Peru
Phone: (51)(1)349-6017/349-5783
Fax: (51)(1)349-5638
Designation: Plant Breeder
Place and Role: CIP Headquarters

Duration: 2 years: October 2015–September 2017

TABLE OF CONTENTS

Acronyms	ii
I. Project Goals	I
1.1 PROJECT PURPOSE.....	I
1.2 OVERVIEW OF BREEDING OBJECTIVES AND OUTPUTS AT CIP TO BE SUPPORTED BY THE PROJECT	I
1.2.1 Breeding objectives.....	I
1.2.2 Breeding outputs	2
2. 2016 PROGRESS REPORT	2
2.1 MONITORING AND EVALUATION FRAMEWORK (REPORT BY MILESTONE ACCOMPLISHMENT—ANNEX) ...	2
2.2 SUMMARY OF ACHIEVEMENTS BY OUTPUT.....	2
2.2.1 Potato.....	2
2.2.2 Sweetpotato	10

ACRONYMS

ABS	Accelerated breeding scheme
CIP	International Potato Center
DArT	Diversity arrays technology
GCA	General combining ability
GTDMS	Global trial data management system
HIDAP	Highly interactive data analysis and productivity
LB	Late blight
LTVR	Lowland tropic virus-resistant potato population
NARS	National agriculture research system
OFSP	Orange-fleshed sweetpotato
PLRV	Potato leaf roll virus
SI	Self-incompatible
SolCap	Solanaceae Coordinated Agricultural Project
SPVD	Sweet potato virus disease
SSA	Sub-Saharan Africa

I. PROJECT GOALS

The International Potato Center (CIP) dedicates much of its scientific research to global food and nutrition security, and to enhancing smallholder's ability to adapt to climate change through the development of more resilient potato and sweetpotato varieties. Potato and sweetpotato are important food crops for addressing issues of global concern, including hunger, poverty, public health, and threats to the environment. CIP's breeding programs develop and disseminate improved potato and sweetpotato populations and build capacity locally for the selection of varieties that will enhance productivity; reduce farmers' dependence on external inputs; and help improve incomes and nutrition in target regions, cropping systems, and value chains. The use of innovative breeding approaches targeting population improvement and variety selection will effectively ensure higher yields, yield stability, and harness diversity toward dynamic sets of specific objective traits in new potato and sweetpotato varieties.

I.1 PROJECT PURPOSE

In the medium term, smallholder farmers in Asia, Africa, and Latin America will have access to new stable and high-yielding potato and sweetpotato varieties that are resilient to disease and climate change, enabling 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 the resilience of food security and farming and food systems. CIP follows a comprehensive scheme for breeding, comprising variety development and population improvement (Gallais 2003). 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 relevant for end-users around an improved population mean. Variety development is relatively straightforward and done in cooperation with national agricultural research systems (NARS). Population improvement is complex. It has to be carried out for a given agro-ecological zone or set of traits—for example, potato for subtropical lowlands or tropical highlands, and/or orange-fleshed sweetpotato (OFSP) with short growing season requirements. CIP's global potato and sweetpotato crop improvement programs emphasize genetic improvement and dissemination of populations. Variety selection and releases from improved populations are carried out in cooperation with partners in target countries.

I.2 OVERVIEW OF BREEDING OBJECTIVES AND OUTPUTS AT CIP TO BE SUPPORTED BY THE PROJECT

1.2.1 Breeding objectives

CIP's potato and sweetpotato breeding programs contribute to the center's overall goals through three main objectives:

1. Develop nutritious and biodiverse potato and sweetpotato populations with recognized added value and high variety ability.
2. Develop resilient potato and sweetpotato varieties by strengthening regional and local networks.
3. Improve selection accuracy and intensity, and shorten the breeding cycle in order to accelerate genetic gains.

1.2.2 Breeding outputs

CIP's breeding programs work toward five broad outputs. Each output consists of deliverables, activities, and milestones contributing to CIP's Strategic and Corporate Plan (see logframe in the annex). Outputs include:

1. Dynamic and 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.
2. Alignment of research with farmers' and end-users' preferences through participatory selection from initial selection stages.
3. Accelerated breeding methods (ABMs) and tools to help breeders select genotypes and parental lines in fewer years than with traditional clone-breeding schemes.
4. Improved and shared breeding databases and knowledge management, including databases of accurate phenotypic and breeding values of selected breeding lines and specific protocols and catalogs to support the orientation of breeding products and facilitate decision-making and outcomes from breeding research.
5. New capacities for applying knowledge, tools, and modern breeding approaches developed for more efficient progress in variety-oriented breeding programs of NARS.

2. 2016 PROGRESS REPORT

2.1 MONITORING AND EVALUATION FRAMEWORK (REPORT BY MILESTONE ACCOMPLISHMENT—ANNEX)

2.2 SUMMARY OF ACHIEVEMENTS BY OUTPUT

2.2.1 Potato

Potato—Output 1: Dynamic and 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

Accomplishment rate for the 2-year work plan = 65%. Significant attention is needed to the evaluation of the new cycle of recurrent selection of lowland tropic virus-resistant (LTVR) potato population and the implementation of mixed models for parental assessment for Deliverable 1; dissemination of best true seed families to NARS for Deliverable 2; and propagation of new stocks for phenotyping in Deliverable 3 in 2017.

Deliverable: Advanced cycle of recurrent selection of main breeding populations developed and true seed families generated for variety selection in target countries

CIP's recurrent selection programs lead to improved progenies and clones by intercrossing selected parents within and between its highland tropics adapted, late blight (LB)-resistant population (Population B) and its lowland subtropics virus-resistant population (Population LTVR) to recombine and increase allele frequencies and levels of traits needed for adaptation to major disease and environmental constraints of targeted tropical and continental environments. Emphasis is on improving earliness, processing and table quality, and drought and heat tolerance, while maintaining or enhancing past gains for resistance to LB, potato virus Y, and potato leaf roll virus (PLRV). Biofortification breeding for higher micronutrient

density—namely, iron (Fe) and zinc (Zn) concentrations—in potato tubers is a relatively new breeding objective, resulting in first sets of candidate varieties from 2017 and for the coming 5 years.

In Population B, heritability and correlations among yield and quality trait components were determined to inform the breeding program on the dual objectives of improving earliness and adaptation for climate change. Progeny tests and clonal assessment across locations in Peru revealed high heritability for yield components under warm conditions and enough genetic variability for further gains in breeding. Broad-sense heritability for glycoalkaloid concentrations on fresh weight basis was high, and correlation between glycoalkaloid concentrations and tuber yield under high temperatures was low. High heritability and low correlation between yield and glycoalkaloid concentrations will allow the selection of clones with high yield and low glycoalkaloid content under heat stress (see annex for details). Eight LB-resistant clones that showed good tuber yield and low glycoalkaloid concentrations under heat can serve as candidate varieties, and may be valuable parents in breeding programs aimed at improving heat tolerance along with LB resistance.

Plans to acquire and incorporate global advances in breeding for LB resistance and potato quality were advanced by contacting four foreign breeding programs to request material transfers of five LB-resistant varieties to CIP. Institutional inquiries have been made, terms of access discussed, and procedures for importation have been initiated. Because Peru requires risk assessment for germplasm exchange, authorities have been engaged to develop the necessary permissions for international exchange of these genetic materials. Risk analyses have been initiated by Peruvian authorities for importation from Holland, Mexico, and Chile.

In LTVR, a crossing plan combining the best 40 elite clones resulted in more than 400 crosses to comprise a new cycle in the recurrent selection scheme. A subset of 200 families with at least 300 seed each will comprise a North Carolina Design I (two 5 x 5 sets) for use in determining parental value with start in 2017. In parallel to the development of this genetic design, and in the interest of fully exploiting breeding data for genetic analysis, data sets from selection trials of 80 advanced clones from the last cycle of open recurrent selection of the LTVR population grown in more than 10 different environments since 2012 have been assembled in the highly interactive data analysis and productivity (HIDAP) data management system. This has been done to enable analysis using mixed models for the determination of breeding values that will complement—and may eventually be substituted for—expensive genetic designs once fully implemented by the breeding program.

Deliverable: First recurrent potato hybrid selection pool for heterosis exploitation developed

Interpopulation hybridization seeks to capitalize on CIP's advanced and genetically divergent populations B and LTVR to achieve additional genetic gains and harness heterosis by an overarching scheme of reciprocal recurrent selection. Selected parents from CIP's LTVR population and LB-resistant (B3) population were intercrossed in the interest of exploiting heterosis for yield in hybrid families varying for earliness, tolerance to abiotic stress, and combined resistances to LB and virus.

Fifty-eight families and more than 47,000 seeds were generated. Standard heterosis of the interpopulation families was determined using the variety 'Unica' as control in a series of experiments in multiple locations of Peru; additional evaluations were conducted in Kenya and Ethiopia. **In Peru, this analysis identified progenies with significant heterosis increments for yield and its components (tuber number and weight) as well as dry matter content in the range of 18–53% heterosis.**

Interpopulation crosses made in the direction LBHTxLTVR tended to show heterosis more frequently than the reciprocal cross type, whereas LTVRxLBHT crosses were generally later maturing than intrapopulation crosses of LTVR.

Progeny testing and genetic analysis of interpopulation combinations were also conducted to identify parents for improving abiotic stress tolerance and earliness, while maintaining and combining disease resistances. In Peru, this enabled identification of the best parents for ensuring genetic advance in population breeding and the recommendation of parents for transferring gains from CIP's improved populations to NARS's breeding programs. For example, 6 LBHT and 2 LTVR progenitors were identified with general combining ability (GCA) for resistance to LB. Four LBHT and 5 LTVR progenitors showed GCA for yield components under warm conditions, and 5 LBHT and 5 LTVR progenitors with GCA for yield under water-deficit and heat conditions were identified.

Deliverable: Populations comprising new sources of needed traits: micronutrient density and drought tolerance characterized and promising clones identified

Crosses of advanced tetraploid, disease-resistant progenitors with selected diploid clones with high micronutrient concentrations and high frequency of 2n pollen from cycle II biofortification breeding were evaluated for micronutrient contents and LB and virus resistance in a series of multilocal trials conducted over 4 years. At present, 30 tetraploid genotypes showing resistance to LB, good yield (0.8–1.5 kg/plant), and micronutrient concentration ranging 22–45 ppm of Fe and 15–35 ppm of Zn were identified. A clean (i.e., virus- and disease-free) copy of selected genotypes is maintained under quarantine screenhouse conditions for efficient in-vitro introduction and dispatch to NARS.

A small population of diploid, pigmented flesh potatoes was selected as a by-product of breeding for increased Fe and Zn contents in a landrace-derived gene pool. This population shows great morphological variability and diverse flesh colors—ranging from white to deep yellow—combined with the presence of blue and red pigments in different intensities and distributions. A group of 25 clones characterized by deep purple and red tuber flesh with high concentration of anthocyanins and high dry matter content (24–33%) has been selected. Additionally, these clones show high value for processing with low reducing sugars (< 0.2%) and excellent chipping quality. Three of these improved novelty-type diploid clones (304183-606, 303984-607, and 304183-601) showed high and stable yield across three locations of Peru: Aymara (central highland, 3,800 masl); Cajamarca (north highland, 2,500 masl); and Ayacucho (central-south highlands, 2,800 masl). They outperformed the diploid check varieties 'Amarilla', 'Maria Cruz', 'Cceccorani', and 'Chingos' and the tetraploid varieties 'Canchan' and 'Perricholi'.

Five tetraploid, drought-tolerant advanced CIP-bred clones were haploidized to generate a diploid population of progenies and clones for genetic studies on morphological and physiological components of drought tolerance. Ten families totaling 245 dihaploids were identified from among 3,528 seeds, and seedling tubers were produced. These will be multiplied to generate sufficient number of tubers per genotype in 2017.

Potato—Output 2: Alignment of research with farmers' and end users' preferences

The accomplishment rate for the 2-year project is 54%. Significant attention is needed to data collection and development of training and data management tools for accelerated breeding with regional hubs and to recruitment and orientation of new staff in 2017.

Deliverable: Regional breeding hubs strengthened

Design of tools for systematization of germplasm exchange (tracking) has advanced toward improved communication on breeding materials exchanged and evaluated in and across regions, by CIP and with partners. An employment offer has been made to fill CIP's vacancy in sub-Saharan Africa's (SSA) potato breeding program. Unfortunately, CIP closed its office in Uzbekistan, which has set back capacity development and delivery as well as strategy for breeding for temperate-continental agro-ecologies, long-day adaptation, and abiotic stress tolerance. A new office was opened in Georgia to partly compensate for this.

The development of new breeding platforms in Africa (Ethiopia and Kenya) and Asia (Vietnam) is key to achieving timely feedback on the performance of CIP's global populations and improving these for local adaptation, while reducing the time required for the identification of varieties suited for local needs. Until these will be fully functional and contribute to regional capacity for potato breeding, procedures for germplasm evaluation are inefficient and product advancement in variety release is slow, delaying impact of new genetics. An accelerated breeding scheme (ABS) has been initiated with 24 true seed families provided for selection in Vietnam, with the aim of identifying candidate varieties in just five years. In the Red River Delta in late 2016, 190 first generation cycle selections were planted. Linking of standard protocols in CIP's HIDAP was advanced in 2016 in preparation for training on streamlined selection and analytical procedures in 2017. Individual training in the use of HIDAP to support all aspects of a potato breeding program were provided for collaborators in Vietnam, Kenya, Ethiopia, and Rwanda. Promising, advanced, and elite clones were identified from recent introductions of true seed families and clones as in-vitro plants to Bangladesh, Rwanda, Kenya, Ethiopia, and Uzbekistan.

Deliverable: Candidate varieties adapted to cropping systems and local needs identified by regional hubs

Six sets of improved potato materials were advanced in Ethiopia during 2016: (1) advanced inter-cross (LBHTxLTVR) population introduced as true seed families in LxT design from HQ in 2013; (2) SAP (SSA Population) from crosses made in Nairobi in 2013 and 2014; (3) OSU-processing type; (4) trait observation network diversity panel; (5) diploid Fe and Zn clones from cycle II and cycle III biofortification breeding; and (6) a CWR (crop wild relative) population from INIA-Uruguay is under multiplication for assessment of adaptation and resistance to bacterial wilt. Sets '1', '2', '3', and '5' are supported with USAID's contribution, whereas '4' is supported by BMZ and '6' is supported by the Global Crop Diversity Trust; '5' has joint support from HarvestPlus (Consortium Research Program on Agriculture for Nutrition and Health). Evaluation and selection in '1' LBHTxLTVR Group has continued under field conditions for LB resistance, and 16 promising clones were selected for yield and tuber characteristics. Evaluation and selection for heat tolerance has continued with 176 clones selected in Worer in the Afar region for trialing under conditions of heat and saline soils. Harvest will take place at end of November 2016. The most promising clones from LBHTxLTVR Group will be transferred to NARS in 2018. Data on selection percentages by family will be used to infer parental value for improvement of SSA populations. Family evaluation and clonal selection are continuing in Adet from '2' in SAP-2013 crosses and '3' 22 OSU-processing type families. Harvest is in progress. Evaluation of SAP-2014 crosses continues in 2016, with 1,270 clones selected and replanted in the greenhouse; evaluation is ongoing. Multi-locational testing and farmer exposure trials of '5' 19 Andean diploid landrace and advanced tetraploid clones selected for high Fe and Zn continued in 2016, for additional results

regarding the mineral contents, in order to provide a variety release recommendation. Evaluation of advanced diploid Fe or Zn clones from cycle III biofortification breeding has been continuing, with 98 clones selected for their agronomic potential and/or their Fe and Zn concentration. These clones have been bulked in 2016, and were sent to Nairobi for virus elimination. CIP research staff and national program collaborators in Ethiopia were trained in the use of HIDAP for managing breeding information.

Forty-two advanced CIP clones with traits such as LB and virus resistance, in combination with acceptable processing qualities, were introduced into Rwanda in 2013. They have since been down-selected to 9 promising clones, which are being assessed in multi-locational trials in five locations. The 9 clones are CIP393280.64, CIP393371.58, CIP396018.241, CIP398190.615, CIP393371.164, CIP393077.159, CIP395112.6, CIP392617.54, and CIP399075.22. Three farmers' varieties are being used as checks, and release of up to 5 varieties is planned for 2017. The varieties currently used for processing in Rwanda were released more than 20 years ago without processing qualities in mind. Following a request from the government of Rwanda in March 2016, an additional 6 clones selected for processing quality in CIP trials were sent from CIP-Nairobi to the Rwanda Agriculture Bureau. Trialing began in October 2016. Multi-locational evaluation and selection with nutrient profiling of diploid Fe and Zn clones are being carried out in Rwanda with HarvestPlus. Nineteen clones from cycle II biofortification breeding are being evaluated in two locations, and 100 clones from cycle III are being evaluated in two locations.

In Kenya two sets of bred potato germplasm are being evaluated in the field: (1) advanced inter-cross (LTVRxLBHT) population introduced as true seed families in LxT design from HQ in 2013, and (2) SAP from crosses made in Nairobi in 2013 and 2014. From LTVRxLBHT, 11 clones were trialed and 5 promising clones identified at harvest. In SAP 2013, 44 clones were field selected by 2016. SAP 2014 was split into batches, 16A and 16B, to better handle the numbers in the available greenhouse space. Some 2,324 clones of 16A were trialed in the field in 2016, and 271 were selected. SAP 2015 crosses have been planted in the greenhouse. CIP research support staff based in Nairobi were trained in the use of HIDAP for managing breeding information.

CIP and the Tuber Crops Research Center, Bangladesh Agricultural Research Institute, conducted six experiments on potato evaluation at different research stations and farmers' fields during the 2015–2016 cropping season. Thirty-two CIP-bred clones in four categories (processing quality, abiotic stress tolerance, virus resistant, and candidate varieties) were multiplied. A total of 21,306 kg of seed tubers were produced, of which 19,970 kg were stored in the specialized cold store at BSPC, Debiganj, for use in FY 2016–2017.

Ten elite CIP-bred clones with processing qualities were evaluated in the research stations (Bogra, Jessore, and Barisal) and farmers' fields (Jessore and Barisal) following participatory Mother& Baby trial approach to select suitable clones for yield, taste, and storability. Considering participant choice at vegetative stage evaluation, organoleptic test, yield performance, and storability evaluation, 4 CIP clones—CIP-218 (304351.109), CIP-224 (304371.58), CIP-225 (304371.67), and CIP-235 (304405.47)—were selected for advanced yield trials from 2017.

Fourteen CIP-bred potato clones were evaluated with two check varieties in the research station of Bogra for heat tolerance and yield. From this trial, 5 clones—CIP-218 (304351.109), CIP-118 (388615.22), CIP-235 (304405.47), and CIP-112 (380606.6)—were selected as heat-tolerant, high-yielding potato clones.

CIP-10 (397029.21) and CIP-13 (397073.7) were evaluated in advanced yield trials along with two check varieties in the research stations of Bogra, Debiganj, Joydebpur, Jamalpur, Jessore, and Munshiganj. They have been recommended for inclusion in regional yield trials that start in 2017.

Two promising clones, CIP-112 (380606.6) and CIP-126 (392797.22), were evaluated in farmers' fields and research stations of Bogra, Debiganj, Joydebpur, Jamalpur, Jessore, and Munshiganj; both were found promising and will be proposed for release as table/processing potato varieties in Bangladesh. The National Seed Board of Bangladesh approved and released CIP-139 (396311.1) as a salt- and heat-tolerant variety, and CIP-127 (392820.1) as a heat-tolerant variety. The Board named these clones BARI Alu-72 and BARI Alu-73, respectively, at their 90th meeting on 9 October 2016.

In the newly released variety promotion and dissemination trials, two LB-resistant potato varieties BARI Alu-46 (CIP-395193.6) and BARI Alu-53 (CIP-393280.64) were demonstrated on 250 farmers' fields in 15 locations during 2015–2016. The two varieties gave average yields of 29.46 t/ha and 26.81 t/ha, respectively. Both of these varieties can be cultivated with no or only minimum frequency (1–2 times per season) of fungicide application, which significantly reduces the cost of production.

Potato—Output 3: Accelerated breeding methods and tools to help breeder's select potato genotypes and parental lines

Accomplishment level for the 2-year work plan is 58%. Significant attention is needed to the identification of candidate genes for adaptive and nutritional traits, production and propagation of research genetic stocks, and the comprehensive evaluation of tetraploid biofortified population data sets for decision-making on top selections for distribution to NARS. Publication in peer-reviewed journals will also be emphasized in 2017.

Deliverable: Strategies and tools to enhance selection and trait transfer in and among gene pools

Incorporating new traits into potato by traditional breeding methods is time consuming and the rate of success is low. CIP uses molecular and genomic technologies to test new approaches that could accelerate breeding by increasing selection accuracy and effective population size. Opportunities to reduce the duration of selection cycles and expedite variety identification are also explored at pilot levels and scaled up when successful. New breeding methods for more effective trait transfer, gene identification, and fixation center on alteration of breeding habit, specifically to enable and exploit inbreeding at the diploid level.

Validation and first application of a molecular marker assay to assist the introgression of the highly effective *R_{ldg}* gene for PLRV resistance to Population LTVR while maintaining and increasing frequencies of *R_{yadg}* have found the latter marker to be 80% accurate in a prebreeding population segregating for both genes. Molecular characterization of 340 out of 2,134 clones selected for agronomical attributes is complete; third-season assessment of PLRV resistance phenotype is pending for assessment of the efficiency of *R_{ldg}*.

Toward marker-assisted selection for LB resistance, SolCap_SNP_c2-56148 was converted to a high-resolution melting marker, which was validated using 87 clones from B3 population and confirmed the SolCap marker results with 97% agreement. To validate the marker-trait association, a population of 11 controlled cross families was developed using B3 and LTVR population clones; tuber families were harvested for planting in the field during 2017.

A genome-wide association study was carried out in a diploid landrace-derived population to identify markers linked to Fe and Zn concentration in potato tubers. Four and 6 genotyping by sequencing markers were significantly associated with Fe and Zn concentration, respectively. One of these 10 markers was associated with both Fe and Zn content in one location and mapped to 1 Mbp from a gene encoding a ZIP metal transporter protein on chromosome 8. A second marker associated with Zn content was from chromosome 1 in the proximity of another ZIP metal transporter. Further efforts to study these loci and validate their usefulness as candidates for marker-assisted selection will be performed during 2017.

Our concept, that rendering self-incompatible (SI) diploid potato accessions self-compatible by introgressing the S-locus inhibitor gene from *S. chacoense* will overcome interspecific reproductive barriers, was first demonstrated in 2015. A crossing block comprising two types of crosses (i.e., SI diploid cultivated plants x SI diploid wild plants, diploid cultivated derived self-compatible hybrid plants x SI diploid wild plants) and both crossing types using mentor pollen to prevent premature fruit drop, were set up in October 2016. This crossing block will provide complementary information to confirm this novel trait transfer method and hybrid progenies capturing LB resistance from underutilized diploid wild potato species.

Self-compatible diploid germplasm provides several advantages in breeding. Although diploid potato species are usually SI, preventing selfing that is needed to generate inbred lines, we identified five rare self-compatible diploid landrace genotypes from Groups Phureja and Stenotomum. Two-hundred SI plants from each of two of these self-compatible landraces were planted in November 2016, to test models for the inheritance of self-compatibility. Resulting knowledge will be used to systematize the use of this reproductive trait in diploid/hybrid potato breeding, genetic mapping using recombinant inbred lines, and trait transfer strategies.

To initiate a diploid breeding program, a set of 738 dihaploid genotypes was developed this year by haploidization of 23 4x elite clones with variation for yield, quality traits, resistances, and heat tolerance from CIP's LTVR population and LB resistance B3 population. Most dihaploids (85%) produced 3–5 tubers, whereas the remaining (15%) produced up to 8 tubers. Tubers will be propagated to get enough to carry out a field assessment for agronomic attributes from 2017.

We began to test and develop the potential of crop models to help characterize and predict the performance of our potato breeding populations and clones in and across environments and scenarios in about 2013. Two potato growth models (DSSAT-SUBSTOR and SOLANUM) were calibrated, and genetic parameters adjusted according to development of test clones representing CIPs advanced populations. Many sequential crop and postharvest measurements were taken in seven experiments carried out in three locations in Peru using two sets of germplasm with contrasting adaptation patterns (tropical highland and subtropical lowlands). The genetic coefficients that defined growth and development of each genotype/set were determined under each model. Statistics show that SUBSTOR model has a slightly better fit to field performance than the SOLANUM model. For the clones adapted to lowland tropics, we noticed a negative bias, indicating that both models tend to underestimate yields, whereas in genotypes adapted to tropical highlands, the models tend to overestimate yields. Improvement of the parameters for fit to tropical germplasm and environments may thus still be required before applications can be developed.

Output 4: Improved and shared breeding databases available for knowledge management, including trait-specific protocols and catalogs to support the orientation of breeding products and facilitate decision-making with data sets for monitoring progress toward objectives

Accomplishment level for the 2-year project is 55%. Specific attention is needed to the development and systematization, including data collection facility for protocols for rapid assays to assess breeding materials for quality traits and for each and all stages of the accelerated breeding scheme.

Deliverable: Standardized methodologies and protocols to assess adaptive traits and communicate intrinsic qualities and add value to breeding materials developed and available in the global trial data management system (GTDMS) of CIP

Breeding management systems and interactive web access to information on breeding populations, clones, progenitors, and true seed with associated phenotypic information have been improved through 2016. Accomplishments include new modules for standard evaluation procedures, expanded trait dictionaries, and analytical and visualization facilities connected to reporting options. New data types encountered in phenotyping and genotyping are incorporated into data dictionaries using ontology approach and experience. CIP has available online the GTDMS (<https://research.cip.cgiar.org/gtdms/>). This includes direct access to potato and sweetpotato knowledge portals and better support of shared protocols, catalogues, and novel breeding management tools. Four of these tools are described here. (1) CIPCROSS is a botanical seed inventory tracking system for clonal crop breeding that provides support for tracking germplasm from crossing blocks and botanical seed inventories to cross-country movement. (2) HIDAP is an institutional effort to unify best practices for data collection, data quality, and data analysis for clonal crop breeders. One of the main new characteristics of the current software platform is the web-based interface that provides a highly interactive environment. It can be used both online and offline. Key features include support for data capture, creation of field books, data access from breeding databases (e.g., CIP-Biomart and Sweetpotatobase), data quality checks, single and multi-environmental data analysis, index selection, and reproducible reports. Novel features include material management of breeding materials, including families and clones, and connection to the institutional pedigree and corporate database at CIP. (3) The Field Book Registry tool is a system for management and registration of the field books for the different experiments at CIP. The field books are updated in the database in real time. It facilitates viewing the status of field books in the database and sending reports to the user. (4) The visual interface “Biomart” was built using the plant ontology as a structured vocabulary and database resource (MySQL) that links phenotypic and laboratory data as well as trial metadata, pedigree, geographic, soil, and climate data.

A key advance in breeding management systems in 2016 has been the development of data management structures to connect breeding material lists of families and clones with the institutional pedigree and corporate database at CIP. This permits on- and offline verification and maintaining the identity of clones across the different selection stages for their management in HIDAP.

Database of accurate phenotypic values for main constraints, quality, and adaptation traits available for promising materials

Improvements to three modules of CIP's International Cooperators Guide for the Standard Evaluation of Potato Clones were made through 2016. Module 9, "Assessment of Dormancy and Sprouting Behavior of Elite and Advanced Potato Clones," was completed with respective trait dictionary and data collection and analysis facilities in HIDAP.

Module 8, "Assessing Potato Clones for Drought Tolerance under Field Conditions," has been drafted to establish standard procedures for the conduct and documentation of (1) drought tolerance phenotyping and (2) standard evaluation trials. For drought tolerance phenotyping (1), 26 morphological and physiological traits and means for assessing them at five stages of plant development have been defined in CIP's trait dictionary. Fourteen morphological and physiological traits are measured two times before drought initiation and two times after drought initiation; another 12 traits are evaluated at harvest. A related protocol (2) for the practical evaluation of potato clones for drought tolerance remains to be derived from the phenotyping protocol. This is based on accumulated knowledge of the most informative subset of measurements and traits, in light of phenotyping a diversity panel in well-watered and water-limiting conditions in several locations.

Module 10, "Participatory Varietal Selection of Potato Clones Using the Mother & Baby Trial Design," has been uploaded in the GTDMS portal (<https://research.cip.cgiar.org/potatoknowledge/pvs.html>). It includes an electronic field book and analytical software with graphics capacity. The electronic field book was distributed and used by researchers of CIP-HQ and partners from Latin America and the Caribbean (Peru and Colombia) and Southwest and Central Asia (India, Nepal, Bhutan, and Bangladesh), with minimal training and follow-up by Skype.

New data types are being collected to identify plant growth features (particularly root architecture) that influence tolerance to drought. A phenotyping experiment was conducted using 65 genotypes from DMDD population. Sprouts were kept over water for 14 days and root traits such as root break, root volume, root surface area, root projected area, root length, number of roots, and root depth were evaluated at 3, 6, 9, and 14 days after placing shoots over water. Fresh and dry weights of shoots and roots were also evaluated; quantitative trait loci analysis was done using MapQTL6 software. No consistent quantitative trait loci were found, but shoot-related traits appeared related to chromosome 11. Improved methodologies for root trait measurement and image analysis are under development in order to identify genetic characteristics that contribute to drought tolerance.

Comprehensive analysis of data for a 10-year period of conduct of standard evaluation trials of CIP's advanced bred clones was conducted as a means to assess progress toward multiple breeding objectives. The analysis quantified and documented the achievement of elite clones carrying one, two or three key traits, among them disease resistances and quality parameters.

2.2.2 Sweetpotato

Sweetpotato—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

Accomplishment level for the 2-year project is 60%.

Deliverable: Global OFSP breeding population for wide adaptation and earliness

The global hybrid population was developed by controlled crossing between different gene pools (PZ08 x PJ07; PZ06 x PJ07; and PJ05 x PZ08). In total, 990 families were developed with a number of seeds from 5 to. Seeds of 800 hybrid families were scarified (5–15 seeds/family). A total of 7,580 genotypes were evaluated in two locations: Satipo (humid tropic environment) and Ica (dry arid environment). The experiment was conducted with three plants for each genotype planted per plot. The clones ‘Daga’ and ‘Cemsa’ were planted as check clones; the 103 parents were included in the experiment. The parents were planted in two replications within each experimental site. The harvest was conducted 100 days after planting. The agronomic traits recorded were storage root shape, dry matter of storage roots, and beta-carotene content. We note here that we have one additional data set of harvest of Satipo (2015); however, their parents were not included and dry matter was not determined. The best cross combination is currently repeated, and 15 parents in each pool PZ and PJ (2 x 15) are undergoing intra-gene pool recombination.

Deliverable: Pre-breeding population for sweet potato virus disease (SPVD)

The clones with best performance for virus resistance from the SPVD-resistant-2 population were selected for development of the SPVD-resistant-3 population. In this crossing block we also included the best clones from the SPVD-resistant-1 population. The crossing block was a factorial design to combine the different parents. The parents were the clones VJ11.042 (CIP110025.1), VJ11.045 (CIP110025.2), VJ11.047 (CIP110025.4), VJ11.048 (CIP110025.5), VJ11.050 (CIP110025.7), VJ11.051 (CIP110025.8), VJ11.043 (CIP110025.10), VJ11.044 (CIP110025.11), VJ11.028 (CIP110019.16), VJ11.031 (CIP110019.17), PZ06.085 (CIP105086.1), PJ05.064 (CIP189151.34), VJ08.330 (CIP107729.9), VJ08.390 (CIP107734.5), and VJ08.476 (CIP107701.5). We obtained 617 seeds and germinated them directly in vitro, which is our fast-track approach to moving the material into the genebank and dissemination. The SPVD-resistant-3 population is maintained in vitro; additionally the material is multiplied in the greenhouse for the next field evaluation (i.e., evaluation of agronomic traits) and to carry out an enzyme-linked immunosorbent assay for SPVD in the greenhouse. The best material from this population can be sent quickly to the regions because the material was germinated from true seed in vitro.

Between 1 and 19 seeds were obtained for each of the following crosses:

VJ11.046 x VJ11.050, VJ11.050 x VJ11.046, VJ11.050 x VJ11.050, VJ11.050 x VJ11.047, VJ11.050 x VJ11.042, VJ11.050 x VJ11.390, VJ11.050 x VJ11.330, VJ11.047 x VJ11.046, VJ11.047 x VJ11.050, VJ11.047 x VJ11.047, VJ11.047 x VJ11.042, VJ11.047 x VJ11.390, VJ11.047 x VJ08.330, VJ11.042 x VJ11.046, VJ11.042 x VJ11.050, VJ11.042 x VJ11.047, VJ08.390 x VJ11.046, VJ08.390 x VJ11.050, VJ08.390 x VJ11.047, VJ08.390 x VJ11.042, VJ08.390 x VJ08.390, VJ08.390 x VJ08.330, VJ08.330 x VJ11.046, VJ08.330 x VJ11.050, VJ08.330 x VJ11.047, VJ08.330 x VJ11.042, VJ08.330 x VJ08.330, VJ08.476 x VJ08.330, VJ08.476 x VJ08.390, VJ08.476 x VJ11.046, VJ08.476 x VJ11.047, VJ08.476 x VJ11.042, VJ08.476 x VJ11.030, VJ08.476 x VJ08.476, PJ05.064 x PJ05.064, PJ05.064 x VJ08.390, PJ05.064 x VJ08.330, VJ11.029 x VJ08.330, VJ11.029 x VJ11.050, VJ11.029 x VJ11.047, VJ11.029 x VJ11.046, VJ11.029 x VJ11.042, VJ11.029 x VJ11.029, VJ11.028 x VJ11.050, VJ11.028 x VJ11.028, VJ11.028 x VJ08.390, VJ11.028 x VJ11.046, VJ11.028 x VJ11.047, VJ11.028 x VJ08.330, VJ11.028 x VJ11.042, VJ11.034 x VJ11.046, VJ11.034 x VJ11.047, VJ11.034 x VJ08.390, VJ11.034 x VJ11.050, VJ11.031 x VJ11.031, VJ11.033 x VJ08.330, VJ11.033 x VJ08.390, VJ11.033 x VJ11.033, VJ11.033 x VJ11.046, VJ11.033 x VJ11.047, VJ11.033 x VJ11.050, VJ11.001 x VJ08.330, VJ11.001 x VJ11.050, VJ11.001 x VJ11.046, VJ11.001 x VJ11.047, VJ11.001 x VJ11.042, VJ11.001 x VJ08.390, PZ06.085 x VJ11.047, PZ06.085 x VJ11.042, PZ06.085 x

VJ11.046, PZ06.085 × VJ11.050, PZ06.085 × VJ08.330, PZ06.085 × PZ06.085, PZ06.085 × VJ08.390, VJ11.036 × VJ08.390, and VJ11.036 × VJ11.047.

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

Accomplishment level for the 2-year project is 50%.

Deliverable: Varieties as well as farmers' and end users' priorities and preferences documented and integrated into varietal breeding

True seed from 650 families was sent to the Central Tuber Crops Research Institute of India and material under multiplication. True seed from 650 families was sent to the Indonesian Legumes and Tuber Crops Research Institute, where the material was multiplied and is currently undergoing ABS field trials.

Sweetpotato—Output 3: Accelerated breeding methods and tools to help breeders select genotypes and parental lines in fewer years than with traditional clone-breeding schemes

Accomplishment level for the 2-year project is 50%.

Deliverable: Accelerated breeding method developed by improved strategies for selection and trait transfer in early breeding stages after applying field surface/nearest neighbor models

There are several methods to deal with field heterogeneity in big trials. Options that we already have implemented to use are (1) the alpha lattice designs (Patterson and Williams 1976) that can be analyzed using the package *Agricolae* (De Mendiburu 2016), or general purpose packages for linear mixed models like *nlme* (Pinheiro et al. 2016) or *lme4* (Bates et al. 2015); or (2) methods for spatial analysis using splines. For this second option we can use the R package *mgcv* (Wood 2006)—a package to fit generalized additive models—or the more specific package *SpATS* (Rodriguez-Alvarez et al. 2016), a package for spatial analysis of field trials with splines, among others. In addition, we will get a license for the package *ASReml* (Butler 2009). With this package we can fit models for $ARI \times ARI$ -correlated errors and fit polynomial models or smoothing splines for error trends in the field. Another option is the more traditional nearest neighbor adjustment, which is implemented in the *AGROBASE* (www.agronomix.com) software. We are evaluating the option to buy this software for next year.

References

- Bates, D., M. Maechler, B. Bolker, and S. Walker. 2015. Fitting Linear Mixed-Effects Models Using *lme4*. *Journal of Statistical Software* 67(1): 1–48. doi:10.18637/jss.v067.i01
- Butler, D. 2009. *asreml: asreml() fits the linear mixed model*. R package version 3.0. (www.vsni.co.uk)
- De Mendiburu, F. 2016. *agricolae: Statistical Procedures for Agricultural Research*. R package version 1.2-4. (<https://CRAN.R-project.org/package=agricolae>)
- Patterson, H.D., and E.R. Williams. 1976. A new class of resolvable incomplete block designs. *Biometrika* 63: 83–92.
- Pinheiro, J., D. Bates, S. DebRoy, D. Sarkar, and R Core Team. 2016. *nlme: Linear and Nonlinear Mixed Effects Models*. R package version 3.1-128. (<http://CRAN.R-project.org/package=nlme>)

Rodriguez-Alvarez, M.X., M. Boer, and P. Eilers. 2016. SpATS: Spatial Analysis of Field Trials with Splines. R package version 1.0-4. (<https://CRAN.R-project.org/package=SpATS>)

Wood, S.N. 2006. *Generalized Additive Models: An Introduction with R*. Boca Raton, FL: Taylor & Francis Group, LLC.

Deliverable: Deliverable: Accelerated breeding method developed by using diversity arrays technology (DArT) markers

We have screened 482 genotypes for sweet potato chlorotic stunt virus and sweet potato feathery mottle virus resistance in the screenhouses in San Ramon. We included susceptible and resistant group previously used to identify simple sequence repeat, amplified fragment length polymorphism, and DArT markers for SPVD resistance, as three parents of the resistant group and one for the susceptible group. The experiment took place from July to October 2016, and the virus evaluation was performed twice (2 and 3 months after grafting). The complete set of genotypes is being propagated for field evaluations in March 2017, with 10 plants/plot and two repetitions in three environments: Cañete, Huaral, and San Ramon.

Plants from VZ08 population (455 genotypes), resistant (14), and susceptible (12) groups are being propagated in San Ramon screenhouses for DNA extraction. Plants will be sent to Lima for DNA extraction on January. **By March 2017, simple sequence repeat and amplified fragment length polymorphism primers previously suggested as SPVD resistance markers will start being tested on VZ08 population. DNA will be stored for future molecular tests at CIP-HQ.**

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

Accomplishment level for the 2-year project is 60%.

Deliverable: Regional breeding hubs strengthened

With respect to the ABS, we published Andrade M.I., J. Ricardo, A. Naico, A. Alvaro, G. Makunde, J. Low, R. Ortiz, and W. J. Grüneberg. 2016. Release of orange-fleshed sweetpotato (*Ipomoea batatas* [L.] Lam.) bred cultivars in Mozambique through an accelerated breeding scheme. *Scientia Horticulturae*¹ in which ABS has been described. Twenty-five breeders contribute to this paper. We are working on another manuscript using variance component estimations and model calculations to quantify the advantages of ABS.

From 31 May to 3 June, the 2nd Annual Meeting of the Asia Sweetpotato Breeders Network was carried out in Malang, Indonesia; participants from 7 Asian countries attended. The next Asian Sweetpotato Breeders meeting will be in Odisha, India, around August 2017.

Sweetpotato—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

Accomplishment level for the 2-year project is 50%.

¹ This publication complements Grüneberg et al. 2015. Advances in sweetpotato breeding from 1993 to 2012. CABI International. (Available from <http://www.cabi.org/Uploads/CABI/OpenResources/44202/Chapter%201%209781780644202%20Epdf.pdf>)

Deliverable: Database for early bulking (the <100-day sweetpotato)

Early bulking: Information was collected on early bulking clones (33 varieties) from a new publication and 53 new sources and clones, respectively. The 33 varieties are CRI-Apomuden (CIP-440254) from Ghana; 2000-038, 2000-040, and RW97-062 from Rwanda; Sowola (CIP-441744), Dimbuka-Bukulula (CIP-443752), and NASPOT-12-O from Uganda; Riba (CIP-420027), Rangita (CIP-420009), Mendrika (CIP-199004), and Bora (CIP-199062.2) from Madagascar; Ndou, Monate, and Letlhabula from South Africa; SreeRethna, COCIP-I (IB-90-10-20), Rajendra Sakarkhand, Sree Arun (CIP-490056), Sree Kanaka, and Indira Naveen from India; and Yanshu-5, Sushu-8, Xushu-23, Guangshu-87, and Xingxiang from China (Grüneberg et al. forthcoming). For the new source, 128 promising clones were evaluated in Peru. Harvest was conducted after 100 days at five locations: Huaral, Piura, San Ramon, Pucallpa, and Satipo (storage root yields were 8.4, 23.0, 19.6, 13.4, and 14.9 t/ha). In the group “moist and sweet,” root yields greater than 20 t/ha were observed for 31 clones. In the group “dry and starchy,” root yields greater than 12 t/ha were observed for 22 clones. **New early bulking clones with the attribute moist and sweet are** Z06.077, PZ06.085, 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. **New early bulking clones with the attribute dry and starchy are** 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. However, we note that heritability calculations for early bulking are pending.

Deliverable: Database for non-sweet sweetpotato

Non-sweetpotato: The established data set of non-sweet sweetpotato currently comprises 114 clones. All clones were selected after a test for non-sweetness after cooking (taste panel). These clones deserve to be tested for zero or low amylase activity. The clones are PJ14.11970, PJ14.11972, PJ14.11983, PJ14.11984, PJ14.11994, PJ14.12020, PJ14.12054, PJ14.12057, PJ14.12066, PJ14.12095, PJ14.12110, PJ14.12111, PJ14.12114, PJ14.12120, PJ14.12205, PJ14.12228, PJ14.12239, PJ14.12244, PJ14.12260, PJ14.12271, PJ14.12277, PJ14.12278, PJ14.12306, PJ14.12311, PJ14.12315, PJ14.12319, PJ14.12320, PJ14.12337, PJ14.12339, PJ14.12340, PJ14.12353, PJ14.12383, PJ14.12384, PJ14.12389, PJ14.12393, PJ14.12395, PJ14.12419, PJ14.12423, PJ14.12427, PJ14.12428, PJ14.12435, PJ14.12445, PJ14.12446, PJ14.12447, PJ14.12449, PJ14.12470, PJ14.12512, PJ14.12517, PJ14.12525, PJ14.12538, PJ14.12539, PJ14.12540, PJ14.12545, PJ14.12549, PJ14.12552, PJ14.12557, PJ14.12565, PJ14.12571, PJ14.12575, PJ14.12586, PJ14.12595, PJ14.12597, PJ14.12607, PJ14.12609, PJ14.12620, PJ14.12638, PJ14.12653, PZ12.12983, PZ14.12069, PZ14.12079, PZ14.12669, PZ14.12702, PZ14.12704, PZ14.12725, PZ14.12752, PZ14.12753, PZ14.12762, PZ14.12777, PZ14.12790, PZ14.12791, PZ14.12796, PZ14.12851, PZ14.12856, PZ14.12920, PZ14.12930, PZ14.12931, PZ14.12934, PZ14.12940, PZ14.12944, PZ14.12962, PZ14.12968, PZ14.12969, PZ14.12971, PZ14.12975, PZ14.12977, PZ14.12981, PZ14.12983, PZ14.12992, PZ14.12994, PZ14.13011, PZ14.13013, PZ14.13014, PZ14.13015, PZ14.13016, PZ14.13023, PZ14.13026, PZ14.13051, PZ14.13060, PZ14.13069, PZ14.13079, PZ14.13080, PZ14.13082, PZ14.13977, and PZ14.19326.

Deliverable: Database for genetic gains by modified demonstration trials

Genetic gain trials are conducted in Mozambique (five locations) and Peru (six locations—three in humid tropics and three in semi-arid locations). These trials are supported by the Sweetpotato Action for Security and Health in Africa project. First harvests will be completed in Peru in December 2016. All genetic gain trials in Peru are carried out under two treatments, early harvest and normal harvest. By mid-2017 we expect to have a database for genetic gains established.

U.S. Agency for International Development
1300 Pennsylvania Avenue, NW
Washington, DC 20523
Tel: (202) 712-0000
Fax: (202) 216-3524
www.usaid.gov