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Andean Potato Diversity Helps Agricultural Development in Uganda: *Victoria* and the Contribution of the CIP Genebank

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Abstract

The genebank of the International Potato Center (CIP) conserves and facilitates access to highly diverse germplasm of potato, sweetpotato, and Andean roots and tubers (ARTCs) as a global public good toward food security. While it is generally understood that the CIP genebank has played an important role in the release of many CIP-related varieties grown by smallholder farmers in lower income countries, the contribution has not been evaluated in quantitative terms. This study assessed the contributions of the CIP genebank to two potato varieties: Pallas poncho (CIP 399085.23, Peru) and Victoria (CIP 381381.20, Uganda). We measured the share of economic benefits from adoption of the improved variety Victoria in Uganda derived from germplasm supplied by the CIP genebank. Relative contribution of Provenance (RCP), a measurement based on pedigree analysis, was used to apportion the CIP genebank contribution in the studied varieties. Victoria's economic benefits in Uganda were measured through attributing and valuing productivity gains based on an economic surplus analysis. The estimated contribution of the CIP genebank to Pallas poncho and Victoria is 35 and 72 percent, respectively. The gross benefit of Victoria in Uganda is estimated at \$1.04 billion dollars (2016 \$USD), which exceeds the annual operational cost of the entire genebank many times over. Breeding and extension costs were not considered. Seventy-two percent of the portion of the economic benefits corresponding to germplasm are due to the CIP genebank contribution. Findings demonstrate the magnitude of economic benefits generated by the use of conserved germplasm, which is only one of the components of the total economic value. They remind us that the availability of germplasm and its diversity is perhaps the most important element in varietal development.

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1. Introduction

One of the most important and consumed crops around the world is potato. Potato is a major crop for food security due to its high nutritional value (FAO 2008) and is the fourth most important food crop with respect to the gross value of production and the fifth most relevant food crop for low-income food deficit countries (FAOSTAT 2016).

Potatoes have played a major role in human history. The tuber was a protagonist of one of the most well-known and massive human migrations caused by the Irish potato famine in 1845. Mass starvation in Ireland resulted from the almost complete dependence of a poor population on a potato crop that collapsed due to wide-spread infection with the plant pathogen *Phytophthora infestans*, the causal agent of the potato late blight (Yoshida et al. 2013). This devastating outbreak occurred as a consequence of genetic uniformity in the varieties cultivated at that time in Europe. Virtually none of potato plants grown in farmers' fields had genetic resistance to the pathogen. The crisis that ensued highlights the crucial importance of genetic diversity for not only plant and crop health but human well-being.

Today, many of the 163 countries growing potatoes use a limited number of varieties. Most cultivated commercial varieties worldwide belong to the species *Solanum tuberosum* subspecies *tuberosum*. Large crop fields usually contain only a few cultivars or even few clones with the same genetic composition during a crop cycle (Lin 2011). This can be contrasted to practices of small farmers in Andean and African regions, who typically prefer to have a highly diverse portfolio with several varieties or cultivated species of potato planted at the same time to minimize risks associated with heterogeneous environments (Kolech et al. 2017; Brush, Taylor, and Bellon 1992; FAO 2008).

Key to agricultural sustainability and to resilient crops is the ability of plants to tolerate or resist challenging environmental biotic and abiotic factors (such as pests and inclement weather) that can cause stress and yield loss. The genetic combinations of each plant determine how they interact with the environment. In general, if one plant in a monoculture farming system is susceptible, then the rest of them are susceptible as well. Conversely, the more diverse the available plant germplasm, the more efficient resiliency is, because this diversity can be used for the generation of new plant varieties that respond to the upcoming challenges and human needs (Sarr, Goeschl, and Swanson 2008). This requires a dynamism in varietal change. If successful, varietal change not only contributes to food security and agricultural development, but also represents an opportunity to reduce poverty in rural and urban areas (Walker and Alwang 2015).

The CGIAR genebanks collaborate with global partners to build a diverse bank of plant germplasm by conserving plant accessions from different origins and with varied traits (Crop Trust 2016). Their main activities include acquisition, conservation under optimal conditions, identification, characterization, and utilization, with conservation being the main priority. These activities make the germplasm available on behalf of the global community under the International Treaty on Plant Genetic Resources for Food and Agriculture [ITPGRFA] (FAO 2009) and support the CGIAR Centers in order to fulfil their mission.

The genebank at the International Potato Center (CIP) in Lima, Peru is one member of this consortium. It safeguards an *ex situ* genetic resource collection comprised of improved varieties, advanced clones, landraces, and wild relatives of potato, sweetpotato, and nine other Andean roots and tubers (CIP Genebank 2019). The CIP genebank holds one of the largest *in vitro* genebanks in the world (CIP Genebank 2019). CIP genebank houses two collections. The first is the CIP genebank collection composed of landraces, wild relatives and some advanced lines, which are held “*in trust*” under the Food and Agriculture Organization (FAO). The second collection is the *in vitro* collection of CIP-derived breeding materials that contains advanced breeding lines and are maintained and distributed with the support of the genebank thanks to its *know-how* of germplasm management and legal issues of germplasm movement. The CIP genebank distributes germplasm from both types of collections for research, training and breeding, using the Standard Material Transfer Agreement (SMTA), and under the guidelines of the ITPGRFA and legal framework (CIP Genebank 2019).

This study measures the share of the CIP genebank in the economic benefits generated by the adoption of improved potato varieties. The following section provides contextual background. Section 3 summarizes data and methods. Estimating economic benefits consists of three steps: i) apportionment of contribution of the provenance to the improved variety, involving pedigree analysis and evaluation of the Relative Contribution of Provenance (RCP), ii) estimation of the productivity gain or attribution, and iii) valuation of the productivity gain. We carry out an apportionment analysis for two improved potato varieties Pallas poncho (CIP 399085.23, INIA 2007), and Victoria (CIP 381381.20). We calculate attribution and value in the case of Victoria (CIP 381381.20). Results are presented in Section 4, followed by a discussion and concluding section.

2. Context

Agricultural gains related to varietal improvement in potato production in developing countries have led to productivity growth, increased returns on investment, positive experiences in technology transfer, and improved north-south and south-south cooperation (Walker et al. 2003).

However, potato varietal change is slow and a large portion of potato producers in developing countries do not invest or do not have the resources to implement a full-scale breeding program. As a consequence, potato breeding programs in developing countries are typically restricted to the evaluation of introduced materials (Walker et al. 2003). The selection of materials from CIP-related varieties played a key role in expanding the diversity of germplasm available to these programs, including breeding programs in large countries such as India, which have used the material as parents for new varieties (Walker et al. 2003). The contribution of CIP germplasm to Indian potato varieties has been established through pedigree analysis of the genetic base of Indian potatoes (Gopal and Oyama 2005). Four CIP accessions in the CIP genebank collections, two in the genebank collection and two in the collection of CIP-derived breeding materials, were found as ancestors of 77 Indian potato selections.

Potato germplasm, safeguarded by the CIP genebank, has been used to accomplish diverse research projects and varietal development. Release, adoption, and use for several years of improved varieties demonstrates that these varieties are having an impact (Walker et al. 2003). Varietal success relies on different stages of development and implementation, including germplasm used, breeding program, seed production and distribution strategy, extension services, adoption rate and consumer preferences. The complete process from finding adequate germplasm until the use of the variety by farmers and consumers can take several decades and substantial resources. Although assessing each one of these elements separately represents a challenge, it is necessary given the importance of evaluating their performance in order to improve and adjust their process and strategies, to allocate resources where they are required, or to achieve a better connection and synchrony between the elements in the value chain.

Plant genetic resources are natural resources and physical assets that produce different types of benefits associated with a total value derived from use and non-use value (Smale 2019 This is Working Paper 1 in this series). Use value includes current and future direct or indirect values, and option value. Direct use value results from the use of plant genetic resources to obtain food, fibers, or medicines that directly benefiting humans. Indirect use value results from contributions made by plant genetic resources to other resources such as ecosystems or habitats. Option value is related to the uncertain capacity to respond to unpredicted future challenges. Use values are thought to be the largest component of the total value of plant genetic resources. The non-use value, including existence and bequest values, is difficult to quantify given its dependence on society's valuation (Tyack et al. 2018). Most of the values associated with genetic resources are not measured in market prices. Additionally, it is particularly challenging to attempt to distinguish the contribution of the genebank from the breeding program, and of the breeding program from the other environmental factors that affect the economic impact of improved varieties in farmers' fields since these are interlinked (Smale 2019 working paper 1).

Past analyses of economic benefits have focused on evaluating the returns to the CIP potato breeding program but not to the CIP genebank independently. Walker et al. (2003) and Thiele et al. (2008) estimated a rate of return to CIP's investment in potato breeding of about 15 and 20 percent, using 1997 and 2007 data, respectively. Both studies included germplasm conservation as one component of the CIP potato breeding rather than as a distinct activity.

Robinson and Srinivasan (2013) analyzed the economic impact of an improved potato variety, Cooperation-88 (C-88), considering the pedigree to demonstrate CIP germplasm use. C-88 is a variety of major importance in China, and widely adopted by farmers after its release in 1996. The variety exhibits late blight resistance and is high yielding in sub-tropical highlands. C-88 is a product of a collaboration between CIP and the Chinese national agricultural research system (NARS). The main contribution from the CIP genebank was the provision of the male parent. Robinson and Srinivasan (2013) estimated economic benefits of this variety and reported pedigree information that confirms a CIP germplasm contribution. However, a detailed CIP genebank contribution analysis or quantification of the contribution based on pedigree was not made and the pedigree was not fully detailed.

3. Data and Methods

Methods applied in the two sections of this study are described separately below.

3.1. Estimation of Economic value

An estimation of the commercial value of progenitors used for the improvement of crop varieties has been discussed by Smale (2004). Three components for assessing the value of the progenitors' contribution are considered. First, "apportion" the genetic contribution of a progenitor. Second, "attribute" the productivity gain resulting from the varietal change by farmers. Third, "value" the productivity gain. The product of these terms, valued, represents the estimated benefits share of the progenitor.

3.2. Apportionment of contribution of provenance to improved variety

Apportioning has been applied previously to find the contribution of breeding programs by using general conventions such as 1 or 0 as in the "any ancestor" rule, or other methods that use conventions that contain a biological and inheritance logic such as the "geometric rule", which assigns geometrically declining weights to the crosses in the pedigree depending on the generation. These methods have been applied by Pardey et al. (1996) and other studies to evaluate the genetic contribution of CIMMYT wheat varieties (Lantican, Dubin, and Morris 2005). However, Smale (2004) notes that these algorithms do not apportion the benefits of a single ancestor and they are not based on genetic contribution. Additionally,

some skepticism concerning the use of Mendelian inheritance has arisen based on the assumptions of real genetic composition of progenitors and progeny, how these are transmitted from one generation to another, and the effects of selection, backcrossing or mutation. Therefore, we are proposing to use the Relative Contribution of Provenance (RCP).

In order to quantify the contribution of the source of material or provenance, we use the RCP, a simplified measurement that evaluates the proportion of the contribution of the source to the studied variety. The *provenance* is considered a divisible attribute. Provenance can correspond to the relationship with a geographic area, a country, or an affiliation, in our case the proportion of provenance from the CIP genebank or, for example, the contribution of landraces.

In our study, a pedigree analysis was completed with the goal of apportioning the contribution of the CIP genebank based on the evaluation of the relationship between the individuals in the pedigree of a variety and the material housed in the genebank. A pedigree represents a genealogy that corresponds to the complete set of ancestors contributing to a present specific variety. Pedigrees for the varieties Pallay poncho (CIP 399085.23) and Victoria (CIP 381381.20) were reconstructed in order to identify their ancestors. Pallay poncho was selected because all the ancestors used for its development were provided by the CIP genebank collection. This variety was used to validate and test the stringency of the RCP measurement. Victoria was selected due to the availability of pedigree information and data on the adoption rates and other economic parameters in Uganda.

Identities of pedigree genotypes and other associated information were detailed with the assistance of the breeders from CIP Genetics and Crop Improvement Program, especially senior breeders Manuel Gastelo, Walter Amoros, and Elisa Salas through personal communications. The pedigree for the variety Pallay poncho was provided by M. Gastelo, who participated in its development. The pedigree for Victoria was constructed by collecting and cross-checking information about its ancestors from physical and digital pedigree books and personal communications with breeders.

Pedigrees were built under the convention of biparental offspring. This assumes that an offspring has two parents, each one contributing 50 percent of its genetic material. In other words, a descendant is the product of sexual reproduction between a plant that provided an egg, “mother”, and a plant that provided a grain of pollen, “father”. Only genotypes related to the CIP genebank, holding a CIP number, or material directly related to CIP developed accessions were considered for the pedigree construction, that means that material before the CIP’s creation was not included.

Bulk pollination is a breeding strategy that facilitates success rate of crosses. A bulk of pollen is a mixture of pollen from different plants, with different genotypes, that is used to pollinate one mother plant.

Although several pollen grains from different plants are applied at the same time, in the end, only one grain of pollen fertilizes each egg. When bulks were present in the pedigrees, special effort was made to obtain the complete composition of the bulk in order to assign potential contribution. The number of bulk members or genotypes was considered in the calculation.

Additional information on the pedigree genotypes that had a CIP number (accessions) was obtained after comparing their CIP number against the CIP genebank database. Then, independent categories were assigned to each known member in the pedigree according to the relationship with the CIP genebank and the origin of each material. Categories consisted of: i) CIP bred germplasm in CIP genebank collection, ii) CIP bred germplasm in the collection of CIP-derived breeding materials supported by CIP genebank, iii) Wild relative germplasm in CIP genebank collection, iv) Landrace germplasm in CIP genebank collection, v) externally bred germplasm in CIP genebank collection, vi) externally bred germplasm in the collection of CIP-derived breeding materials supported by CIP genebank, vii) CIP bred germplasm, but not included in the genebank collection, viii) non-CIP related or not in CIP genebank germplasm, or material with no information. Categories were used as criteria to assign a contribution value using the RCP quantitative analysis.

Using the relationships observed between descendants and ancestors shown in the pedigree (parents, grandparents, great-grandparents, etc.), the RCP was calculated for every progenitor and used for the analysis. This measurement is calculated in a similar way to the relative genetic contribution (RGC) as described by Gopal and Oyama (2005). The RGC is a strategy that allows the quantification of the theoretical genetic material distribution coming from each of two parents. It assumes that 50 percent of the genetic material comes from each parent every time a cross takes place (Delannay, Rodgers, and Palmer 1983; Gopal and Oyama 2005; Barton and Etheridge 2011). According to this scheme, the total genetic material of the studied variety comes from its two parents who contributed with 0.5 each one. The contribution of the previous progenitors depends on the parentage grade. Parents in the first generation back from the studied variety provide half their genetics to an offspring, grandparents contribute a quarter, and in this way successively. However, since the studied varieties and some of their ancestors were artificially selected during the breeding process, in practice, some ancestors made a greater genetic contribution to the final production than others. An accurate quantification of genetic contribution requires more information about specific traits or DNA sequence information for every member of the pedigree, which was not available.

Consequently, we used the Relative Contribution of Provenance (RCP) in our quantitative analysis. RCP follows the path of the pedigree and the Mendelian strategy of genetic contribution. However, instead of genetic material, the inherited attribute is the provenance. Thus, RCP would represent a theoretical genetic contribution in the absence of selection, and the contribution of the provenance. This is possible given that two plants are crossed to obtain a descendant. If we consider the provenance as an attribute (e.g. nationality), each parent will contribute half of the final product.

The genebank contribution considered in this case is based on the pedigree analysis, its composition and the categories associated with each genotype. We considered that a genotype has a relationship with the CIP genebank when its germplasm is in the CIP genebank collection or in the collection of CIP-derived breeding materials supported by the CIP genebank. The total genebank contribution was calculated by adding the values of the RCP of the materials found in the pedigree that were related to CIP genebank accessions. An accession provides a complete genebank contribution when it is part of the CIP genebank. As a condition, only genotypes with supporting information of a direct relationship with the genebank, in its collection or maintained by the genebank, were considered for contribution analysis, even if they came from other breeding material at CIP. Accessions produced by CIP breeders or other sources that were not in the genebank collection were not included in the contribution analysis, although some of them might have had a previous genebank contribution.

Contributions of provenance by category or category subsets of genebank related accessions in the pedigrees were analyzed using the RCP. Contribution of provenance by country of origin also was evaluated for Pallas poncho and was considered in a separate analysis. For each accession, only the most recent progenitor from the maternal and the paternal branches that fulfill the studied condition (category or country of origin) were considered. For this reason, the RCP value may vary from one category to another or when compared to total genebank contribution value. Every category of RCP should be analyzed separately; for example, the 100 percent of contribution for the variety when studying category A corresponds to the RCP value of category A plus the RCP value of everything that does not belong to category A as a whole. It was considered that some of the pedigree branches present genotypes with different categories located in different generations. Depending on the studied category, some of the genotypes might be disregarded for contribution to avoid double contribution. The category analysis considers the most recent ancestor that meets the category requirement, in contrast to the total contribution analysis, which considers the most recent ancestor that is linked to the CIP genebank.

In order to calculate the contribution of a bulk, the bulk was considered to be a unit formed by a certain number of members or genotypes which correspond to the several individuals that are sources of pollen.

Contribution for every bulk member was estimated following the rules described previously in which each progenitor provides 50 percent of the contribution, then each value was added into a partial contribution. Then, because only one pollen donor in the bulk is the true parent of the descendant plant, the partial contribution according to the generation was penalized by dividing by the number of genotypes used in the bulk. A whole bulk contribution value corresponds to the 50 percent of its descendant, which is the value normally provided by one of the parents in a cross; however, this has a lower value than a conventional parental contribution due to the penalization. This results in some varieties with total contribution values of less than one hundred percent.

3.3. Attribution of the productivity gain of Victoria (CIP 381381.20)

Attribution relies on the estimation of productivity gain derived from the use of a new variety, with new genetic composition, compared to other varieties previously grown on farm (Smale 2004). Productivity gain estimation is influenced by genetic composition of the new variety and other management and environmental factors in the field. Data collected from farmer's fields may provide more accurate information due to actual field conditions as compared to data collected under experimental controlled conditions. A simple way to express productivity gain is in terms of yield per unit land area, as is used in this study. However, other benefits from a new variety also could include early maturity, enhanced product quality, improved quantity or quality of fodder, or improved tolerance of biotic or abiotic stresses, which could increase the geographical and temporal range in which the crop is cultivated (Evenson and Gollin 2003).

The variety Victoria was obtained by CIP as the product of a cross made in 1981 and was released in Uganda in 1991. The same germplasm has been distributed, released and cultivated under different names in several other African countries including Kenya, Congo, Rwanda, Madagascar, Burundi, and Malawi (Walker and Alwang 2015). Victoria was selected based on the availability of related information, including its pedigree (previous sections), agronomic, and market-related data. Attribution was estimated based on yield gain in comparison to other potato varieties used in Uganda.

The yield gain of Victoria compared to other varieties in Uganda was calculated based on farm-level data collected from a 2005 CIP Survey (Kaguongo et al. 2008) (Table 1). Kanguongo et al. (2008) conducted a farm survey in two major potato producing areas that were selected as representative of the potato sector of Uganda. Interviewees were chosen with a stratified sampling frame using sub-locations and villages randomly designated within potato growing areas, and farmers randomly selected in each village. Yield gain was estimated using yield data for the most commonly grown potato varieties in Uganda that represent the 94.6 percent of the potato-growing area in 2004-5 according to Kaguongo et al. (2008)

(Table 1). The yield gain between Victoria and other commonly grown varieties was calculated and weighted by their corresponding total area under the variety (Formula 1).

Formula (1)

$$\text{Yield gain} = \sum [(1 - (Y_i / Y_v)) * A_i],$$

where

Y_i is the average yield of the other variety that would be grown in the absence of Victoria;

Y_v is the yield of Victoria; and

A is the total area under the variety that would be grown in the absence of Victoria.

3.4. Valuation of the productivity gain of Victoria (CIP 381381.20)

Economic benefits of the productivity gain can be evaluated through different methods using econometric approaches or economic surplus analysis (Alston, Norton, and Pardey 1995). Economic surplus analysis is one of the most commonly used methods to assess the benefits of a variety considering agronomic and market-related information to measure the benefits that the variety has contributed to an economy (Formula 2). To value the productivity gain, an *ex post* economic surplus analysis was completed using methods applied by Alston, Norton, and Pardey (1995) and Norton, Ganoza, and Pomareda (1987). A closed economy model was assumed for this study, which means that the effects of trade were not considered. Under this assumption, an increase in potato production can have a substantial price-reducing effect in the market.

Formula (2)

$$B_t = P_0 Q_0 K (1 + 0.5Ken/(e+n)),$$

Where:

B_t = gross annual benefits (total surplus is in blue);

$K = (a-c)/a$ reflects yield and cost changes, adoption of variety; and e and n = supply and demand elasticities

Some assumptions were used to estimate the economic benefits of Victoria. The yield gain due to the use of Victoria was estimated at 8% (see above). This yield gain could be underestimated given the possibility that 5.4 percent correspond to local varieties with no data associated but presumably with lower yields than Victoria. The cost change per hectare was considered at 5%. We assume that production practices would not change drastically by adopting Victoria, so the cost for farmers would not increase in a large proportion. Possibly one of the factors that contribute to the cost change is the higher cost of seeds compared to local varieties.

The adoption of a new technology, such as an improved variety, can cause a shift in the supply curve (Figure 4). A new improved variety with higher disease resistance, earlier maturity, or higher and stable yield leads to an increase in production, reducing the cost of production per unit compared to other varieties, which would result in an increase in total potato supply in the market. This supply increment will lead to a decrease in the price of potato for the consumers (and producers), all other things equal. Consumers might also increase their demand for potatoes over time due to growth in per capita income and population. Technology, income, and population changes would create new equilibriums in demand and supply over time. Economic surplus analysis allows us to quantify benefits based on changes in the parameters involved in these market interactions.

The analysis included a period of 25 years, from the time it was released in 1991 until 2016. There is no available market data after 2016. Required data related to the variety, such as release year and adoption rate, were obtained from previous CIP publications and other literature (Kaguongo et al. 2008; Thiele et al. 2008; Walker and Alwang 2015). Considering the data from CIP surveys and from the DIIVA Project (Diffusion and Impact of Improved Varieties in Africa), the adoption rate measured as percentage of area under Victoria in Uganda was 34 percent in 2005 and 53.6 percent in 2010. An adoption curve was constructed following a piece-wise linear model, taking as starting point the year of release 1991, Victoria adoption in 2005 and 2010, and an estimated average decrease of 5 percent during 2015 and 2016.

Information about market- and Uganda-related parameters, such as potato yields, agricultural gross production value, quantity of production, harvested area, and Uganda population changes, were collected from the FAO statistical database (FAOSTAT 2016, <http://faostat.fao.org>) and The World Bank (2018, <http://www.worldbank.org>). Potato prices for Uganda were calculated based on the value of agricultural gross production and production quantity data. Potato elasticities of supply (ϵ) and demand (η) needed for assessing price responsiveness to supply and demand changes were assumed to be 0.8 and -0.3, respectively based on Fuglie (2007). Two scenarios were used to calculate the benefits of Victoria in Uganda depending on whether there is an impact of the exogenous factor “change in population”.

Uganda's average annual population change for the studied period was 3.32 percent. Because benefits occurred over time, their present value (PV) was calculated. For this PV calculation a discount rate of 3% percent was used. Inflation adjustment was done at the end of the economic surplus analysis, converting data from 2010 (base year) to 2016 USD.

4. Results

4.1. Estimation of Economic value

Apportionment of contribution of provenance from genebank

Pallay poncho (CIP 399085.23, Peru)

Pallay poncho is a variety released in response to a food security threat in the rural community of Chacllabamba, a traditional Andean community located at 4100 meters above sea level (masl) in the Cuzco area of Peru. Farmers in this community experienced a loss of 90% of their native varieties due to late blight in 2003. The reduction in potato production was a serious constraint for this community considering that native potatoes are the base of their food security (Landeo et al. 2007). Thanks to breeders' testimonies (M. Gastelo, personal communication) and internal reports we identified, it was confirmed that the initial germplasm used for developing this improved variety was 100 percent derived from the CIP landrace germplasm collection.

The pedigree of *Pallay poncho* shows the germplasm and breeding strategy used for varietal development (Figure 1). The starting material was obtained by CIP between 1970 and 1974 and belongs to the genebank collection. The advanced clone that became the variety was obtained after the 7th generation of crosses made over 13 years by CIP breeders. The variety's germplasm was included in the CIP genebank collection as *in vitro* material. Currently it has the highest health status, and is ready for national (Peru) and international distribution under the requirements of the SMTA.

In the pedigree, the use of three different groups of bulk employed to provide pollen (the male parent) was evident (Bulk ADG, Bulk – B, and Bulk B1C2). The detailed composition of Bulk ADG and B is completely known, unlike the Bulk B1C2, whose composition is not detailed due to lack of information. The bulk ADG consists of 20 individual genotypes all of which belonged to the CIP genebank collection. The Bulk-B is formed by 21 genotypes ("n?" in Figure 1), which were obtained using other landrace accessions from the CIP genebank collection and Bulk-ADG.

At least 29 different landraces provided genetic contributions to Pally poncho. These landraces were collected in Peru and Bolivia, mostly in communities located at high elevations, ranging 2,017 and 3,965 masl (Figure 2).

A contribution analysis of provenance considering the genebank as the source of material was made based on Pally poncho's pedigree. Out of the theoretical genebank contribution of 100 percent, 35 percent was demonstrated as the genebank-derived contribution through the RCP analysis, 50 percent was contribution from unknown genotypes (Bulk B1C2), and 15 percent was the product of the penalty given to the known bulks, which is the total bulk contribution divided by the number of its genotypes.

Victoria (CIP 381381.20)

Victoria comes from the LB population developed by CIP breeders in Peru, with the objective of obtaining late blight resistant clones with good yields. Victoria's pedigree was built based on information obtained from CIP breeders' pedigree books (Figure 3). Victoria was the product of the 5th generations of crossing. According to Victoria's pedigree and its known genotypes, the variety was obtained using materials derived from the CIP genebank collection and the collection of CIP-derived breeding materials, which included one wild relative, one landrace, ten externally bred accessions, and eight CIP bred accessions.

The pedigree shows the use of three different bulks of pollen along the varietal development process. More detailed information about bulk composition is only available for "Precoz bulk", which is formed by 16 genotypes. Detailed information about "PVX+PVY bulk", which contributed resistance to potato viruses PVX and PVY, and "YUR bulk", was not available.

In the case of Victoria's breeding process, some intermediate clones with special features for breeders were obtained through breeding at CIP, included in the breeding or genebank collection and used in the next generation towards the varietal development. Additionally, the germplasm corresponding to Victoria is in the CIP genebank collection as *in vitro* material, in good health status and therefore available for distribution in Peru and internationally.

Similarly, contribution analysis of provenance, considering the genebank as the source of material, was made based on the pedigree of Victoria. The CIP genebank holds two potato collections, (i) the CIP genebank collection, which includes the materials under the ITPGRFA, and (ii) the collection of CIP-derived breeding materials, which is housed, maintained and distributed by CIP genebank. As the product of the total contribution analysis, considering the genotypes belonging to the two collections, the CIP

genebank total contribution to Victoria (CIP 381381.20) is 72 percent, in contrast to 28 percent corresponding to non-CIP-genebank-related material.

Considering the same analyzed pedigree path, taking the most recent ancestor with CIP genebank affiliation for the RCP analysis, we determine that the 72 percent of contribution is distributed among categories as follows (Figure 3): i) CIP bred germplasm in CIP genebank collection, 8.6%; ii) CIP bred germplasm in the collection of CIP-derived breeding materials supported by the CIP genebank, 14.1%; iii) Wild relative germplasm in the CIP genebank collection, 6.3%; iv) Landrace germplasm in the CIP genebank collection, 6.3%; v) externally bred germplasm in the CIP genebank collection, 8.6%; vi) externally bred germplasm in the collection of CIP-derived breeding materials supported by the CIP genebank, 28.1%; vii) CIP bred germplasm, but not included in the genebank collection, 9.4%; viii) non-CIP related or not in the CIP genebank germplasm, or material with no information, 18%; and bulk with not identified composition, 0.8%. Under this analysis, the CIP genebank collection contributed 30% to Victoria germplasm, and the collection of CIP-derived breeding materials supported by the CIP genebank contributed 42%.

Attribution and value of the productivity gain in the case of the Victoria (CIP 381381.20)

Victoria (CIP 381381.20) was selected for further analysis due to the availability of information including its pedigree, agronomic, and market-related data. The adoption path of Victoria (CIP 381381.20) in Uganda was built based on percentage of area under variety, and displayed an upward trend from its official release in 1991 up to 2010 (Figure 5). The adoption rate may have begun to decline at some point after 2010, but precise information is not available. However, knowing that the variety is still being used, a constant adoption rate was assumed from 2010 to 2014, and then a 5 percent decrease per year was considered until 2016.

Although Victoria (CIP 381381.20) was initially developed as a resistant variety against late blight, it has lost part of its resistance in Uganda because the pathogen that causes the disease has been able to partially overcome it (Kaguongo et al. 2008). Nevertheless, Victoria (CIP 381381.20) still has useful resistance, which allows farmers to control the disease using fungicides to maintain yield levels. Victoria (CIP 381381.20) is still being used by Ugandan farmers due to its high yield, early maturity, and highly desired red skin and cream flesh. The market demand is the most important criterion for variety selection in Uganda.

Yield change was determined using data from the farm-level study by Kaguongo et al. (2008) (Table 1). On average and after normalizing for adoption, Victoria's yield is 7.55 percent higher than the yield attained by the other seven commonly grown varieties in Uganda.

Applying a closed economy model for an ex-post economic surplus analysis, the benefits of the adoption of the variety Victoria (CIP 381381.20) in Uganda were calculated for the period 1991 – 2016. Results indicate that the estimated present value (PV) of the gross benefits due to Victoria (CIP 381381.20) adoption, from 1991 to 2016 are \$859 million (2016\$USD, 3% DR) when human population growth is not considered. In contrast, when the change in increased population growth for the period and hence increased demand is considered, and assuming the ceiling adoption rate holds, the PV of the benefits increases to \$1.04 billion dollars (2016\$USD, 3% DR). This value is derived from aspects of varietal development and adoption, such as used germplasm, breeding efforts, seed multiplication, distribution programs and extension, besides the use of the germplasm and its associated traits. Based on relative contribution of provenance (RCP) and the pedigree analysis of Victoria, it is possible to say that 72 percent of the economic benefits corresponding to germplasm are due to the CIP genebank contribution.

The total annual cost of the CIP genebank in 2016 (Table 2) is estimated at \$3.5 million (not including the one-time non-recurring costs) of cryobanking potato and sweetpotato accessions of about \$2.5 million (spread over about five years). Including these cryobanking expenses, the total annual cost of the genebank is \$4 million. These cost estimates are based on cost per accession and other associated costs (Consortium Board of Trustees 2011), inflated to 2016. Other costs associated with to breeding, extension and other programs supporting the adoption of the variety are not described here.

The gross economic benefit of Victoria in Uganda is estimated at \$1.04 billion (2016 \$USD) for a 25-year period (1991 to 2016), about \$42 million per year. The total cost of running the genebank to conserve 16,718 accessions of potato, sweet potato, and Andean roots and tubers is estimated at \$4 million per year, less than a tenth of the economic benefits derived from a single variety in one country.

5. Discussion

A study by Walker et al. (2003) reports that about 23% of the varieties released in 30 countries are related to CIP, indicating that CIP genebank may have contributed to a large portion of these successful varieties. However, the specific role of the genebank as a germplasm holder and provider, or its role as an important supporter to conserve and clean breeder's materials has not been analyzed.

The relative contribution of provenance method (RCP) was used to estimate the apportioning of the contribution of the CIP genebank. Although RCP quantification is similar to the method adopted by Pardey et al. (1996) known as the “geometric rule”, RCP is focused on the germplasm of the progenitors rather than on the cross itself between two progenitors. The RCP is based on the biological principle of sexual reproduction where an organism is the product of the union of two sets of genetic materials formed by a large number of genes coming from a female and a male, 50 percent from each one. In general, the product of the interaction between these two sets of genetic materials among themselves and with the environment will determine the traits that the descendant will exhibit. This approach is based on a simplified way to track the inheritance of genetic material from one generation to another. Although, the RCP does not track the exact genetic composition of a descendant, it quantifies the contribution of the provenance of the progenitors following the path of genetic Mendelian inheritance through the pedigree and give clues about the relative genetic composition.

Mendelian laws work on a gene scale. Genetic population’s modifiers (like genetic drift, natural selection, small population sizes, and non-random mating) work additionally on large timescales affecting the frequencies of the forms of a gene (alleles) found in a population. Such factors do not have a large effect on the pedigrees due to the small timescale in which pedigrees take place [~10 generations] (Barton and Etheridge 2011). Artificial selection, due to the breeding process, and other specific biological factors, like differences between the plant species used for varietal development may add a modifying effect on the real genetic composition of the variety. However, RCP is not affected because it is not a measure of real genetic composition.

Pedigrees are useful for identifying the ancestors of an individual and the relationships among them, also to track inheritance of a trait that depends only on one gene and is exhibited among the genotypes in the genealogy. For example, a trait depending on a single gene under simple Mendelian patterns of inheritance, e.g. a sex-linked trait such as color blindness in humans. However, this is not the case for many traits seen in agriculture, for instance yield. Yield is a complex trait that depends on many genes (quantitative trait), and the epistatic interaction between them, which means that one gene modifies the function of other. Additionally, if the variety have other traits of interest besides a good yield, like resistance to a disease, a color, early maturity, etc. the complexity to track the origin of the trait combination will increase.

A way to refine apportioning based on genetic contribution considering the real genetic composition of the genotypes in the pedigree would be to take advantage of the latest sequencing technologies and other methods that involve a high number of molecular markers to determine which specific portions of genetic

material are coming from one parent or another. Specific DNA sequences can be linked to specific traits which can be useful to track traits of interest for example in haplotype blocks. However, this would require a substantial amount of resources, especially for polyploids (containing several copies of a set of chromosomes with more than one form of each gene or allele) in which this is still not fully understood. Other type of resources are time and information necessary for experimental implementation, given the need of material acquisition, DNA extraction and sequencing, bioinformatic analysis, identification of relationships between genotype and phenotype under determined environmental conditions, among others. Having the DNA of at least a minimum number of ancestors that allow to run the analysis would be required. This could represent a challenge considering the different origins of the germplasm and the spatial and temporal distances when these materials were used. Spatial and temporal distances could place barriers in getting the correct samples for analysis, especially for varieties that were developed several decades ago.

Pedigrees of two CIP genebank related varieties were systematically studied. As the pedigrees show (Figure 1 and 3), the CIP genebank contribution is variable in the same way that was observed by Robinson and Srinivasan (2013). Some varieties like Pallas poncho (CIP 399085.23), a staple variety released in Peru in 2007 (Landeo et al. 2007), have been developed entirely using starting germplasms from the CIP genebank collection, while others, like Victoria (CIP 381381.20), released in Uganda in 1991, originated from the use of different germplasm from CIP genebank collection, the collection of CIP-derived breeding materials maintained and distributed with the support of CIP genebank and other various sources.

The RCP analysis allowed the estimation of the CIP genebank contribution for Pallas poncho (CIP 399085.23) at 35.16 percent, out of a theoretical 100 percent. This shows that the analysis made in this study is highly conservative due to the use of the relationships evidenced in the pedigree and the penalties applied to bulks considered for the RCP estimation.

The economic surplus analysis allowed us to estimate the economic benefits derived from the adoption of the variety Victoria (CIP 381381.20) by Ugandan farmers. The PV of the gross benefits from 1991 to 2016 is estimated at \$1.04 billion dollars (2016 \$USD), considering population growth at 3.3% in Uganda. The value of the gross benefits of one accession in one country, obtained over a 25 years period, is many times larger than the 2016 CIP genebank total annual cost of \$3.5 million. The total annual cost supports not only potato accessions but also sweetpotato and other Andean roots and tubers (not including the one-time non-recurring costs). The reported benefit is not a net benefit, which would be the total benefits minus the total discounted. The latter would include the genebank costs, breeding costs, costs of varietal

development, extension and adoption. Some of these costs occurred before the variety was released as the cross that gave origin to the variety was made in 1981. Some of these costs are shared among several varieties that were developed under the same breeding process and have been released and adopted in several countries. This part of the benefit analysis needs a further examination.

The CIP genebank contribution for Victoria (CIP 381381.20) was used to apportion the economic benefits of Victoria (CIP 381381.20) in Uganda. Based on relative contribution of provenance (RCP) and the pedigree analysis, it is possible to say that 72 percent of the benefits derived from the use of germplasm correspond to CIP genebank contribution. CIP genebank collection contributed 30 percent, and the collection of CIP-derived breeding materials supported by CIP genebank contributed 42 percent.

6. Conclusion

The pedigrees of two varieties reported as CIP genebank derived varieties were built and complemented with information about the origin and availability of the pedigree members in the CIP genebank, allowing analyses of the composition and contribution of the CIP genebank based on the relative contribution of provenance (RCP) of the members. This analysis demonstrated a CIP genebank contribution of 35 percent for the variety Pally poncho (CIP 399085.23), based on the use of germplasm in the CIP genebank collection; and 72 percent for the variety Victoria (CIP 381381.20) based on the use of germplasm in the CIP genebank collection and the collection of CIP-derived breeding materials supported by CIP genebank. Additionally, 30 percent of this 72 percent contribution for the variety Victoria (CIP 381381.20) is due to the use of only germplasm in the CIP genebank collection. These values correspond to the apportioning component and can be used to support benefits due to the genebank.

Adoption of Victoria (CIP 381381.20) in Uganda led to farm-level productivity gains (Kaguongo et al. 2008). Yield gain, estimated at about 8% higher than other varieties used in Uganda, corresponds to the attribution component. The valuation of the productivity gain and other market related information were used for an economic surplus analysis that allows the estimation of the gross benefits of the adoption of Victoria (CIP 381381.20) by Ugandan farmers at \$1.04 billion 2016\$USD.

We estimate that the relative genetic contribution of the CIP genebank represents 72 percent of the gross economic benefits earned on farms in Uganda from growing the improved variety Victoria. Excluding genebank, breeding, extension costs, the estimated benefit from adopting Victoria in Uganda is \$1.04 billion (2016 \$USD) for a 25-year period, about \$42 million per year. Considering that Victoria's germplasm has also been widely adopted in other countries, under other names, the total Victoria's benefits and related CIP genebank contribution may be greater. The total cost of running the genebank to

conserve 16,718 accessions of potato, sweetpotato, and Andean roots and tubers is estimated at \$4 million per year, less than a tenth of the economic benefits derived from a single variety in one country.

This example highlights how conserving genetic resources in the CIP genebank plays a key role in the agricultural development of lower-income, potato-producing countries such as Uganda. There are numerous improved varieties like Victoria and Cooperation-88 that include important genetic contributions from the CIP collection.

Complementary and more exhaustive studies could be conducted by making available more detailed information about a new improved variety of interest. Further historical information about the breeding process together with detailed biological information, such as the absolute genetic composition of the germplasm used -preferably associated with a trait description- would help to calculate a more precise ancestral contribution with more robust biological significance. Additional information about adoption, including the attributes that the variety presents in the field in addition to yield would provide insights into other types of benefits. More complete data about applied strategies, such as extension or seed program, and associated costs of the related processes, would help to estimate net economic benefits more accurately.

The economic benefits described in this study correspond to a current direct *use value*. However, the economic value of plant genetic resources comprises different types of value as described by Smale (2019). Direct use value, related to derived food, fiber and medicinal products, is only one component of the total value. Total value additionally considers indirect use value, option use value, non-use value based on existence, and non-use value based on bequest. The total economic value of Victoria and the CIP genebank contribution is larger than the economic benefits showed in this study. Other studies are needed to assess other types of economic values related to Victoria germplasm.

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8. Tables

Table 1. Yield gain of Victoria (CIP 381381.20) compared to other potato varieties in Uganda

Variety	Yield (kg/ha)	Yield Change (%) [*]	Total area under variety (%)	Yield gain (%) [*]
Victoria	6,847	0	34	
Kinigi	8,719	-27.34	14	-3.83
Rwangume	7,877	-15.04	12	-1.81
Rutuku	7,367	-7.59	4	-0.30
Rwashakye	5,723	16.42	2	0.33
Cruza	4,895	28.51	13	3.71
Kasaza	3,981	41.86	0.6	0.25
Bumbamagara	2,648	61.33	15	9.20
Other varieties	No reported		5.4	
Total			100	7.55

Most commonly grown varieties in 2004-5 (kg/ha). Source: modified from 2005 CIP Survey (Kaguongo et al., 2008). * calculated values in this study. Yield gain = $\sum [(1 - (Y_i / Y_v)) * A_i]$, where Y_i is the average yield of the other variety that would be grown in the absence of Victoria; Y_v is the yield of Victoria; and A is the total area under the variety that would be grown in the absence of Victoria.

Table 2. Estimated Annual cost of the CIP Genebank in 2016 (US\$)

Costs	Crop		
	Potato	Sweetpotato	Andean Roots and Tubers
Number of Accessions	6747	7643	2328
Annual recurring cost per accession	\$188.60	\$166.90	\$161.20
Total annual cost of maintaining accessions	\$1,272,484	\$1,275,617	\$375,274
Annual cost of acquiring new accessions	\$94,951	\$175,593	\$10,097
Annual capital costs	\$164,212	\$118,686	\$17,918
Total annual cost	\$1,531,647	\$1,569,896	\$403,289

Source: Consortium Board of Trustees (2011)

9. Figures

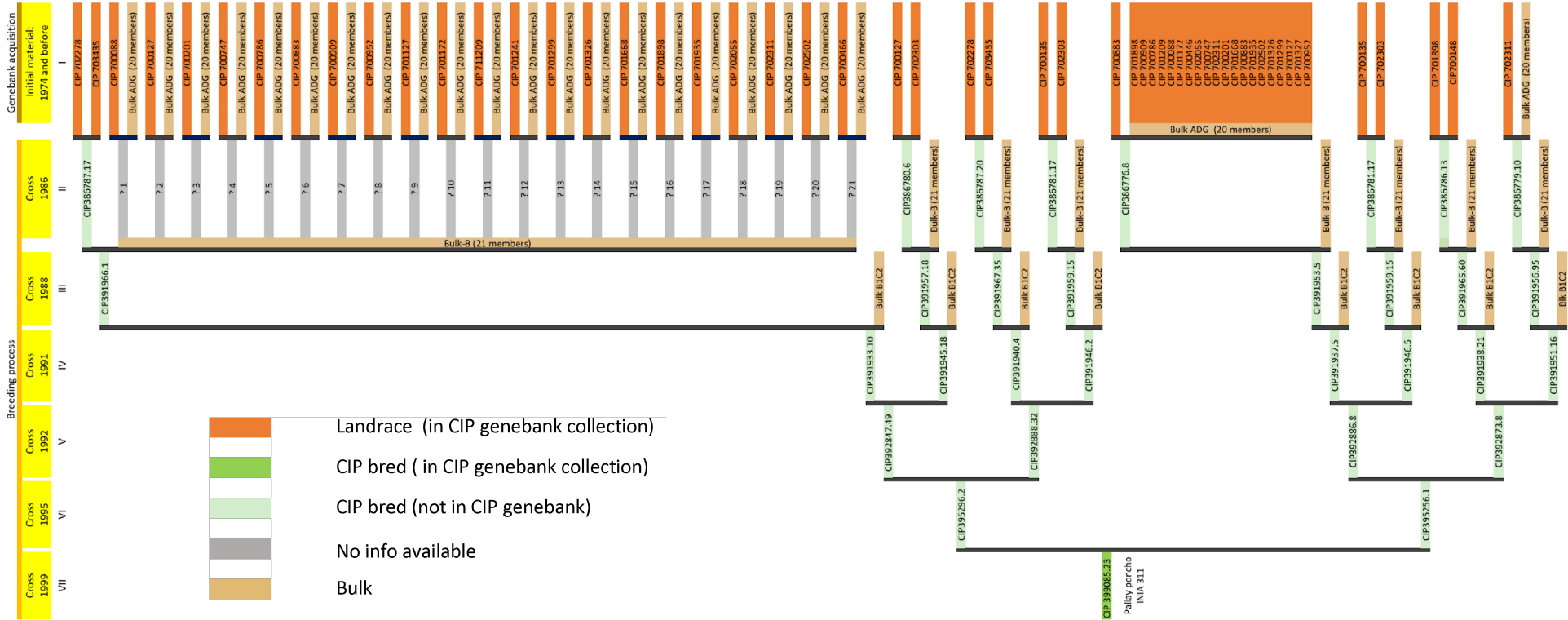


Figure 1. Pedigree of Pally poncho (CIP 399085.23). Source: Modified from M. Gastelo, personal communication.

Geographic localization of Pally poncho ancestors and Pally poncho recipient community in Peru

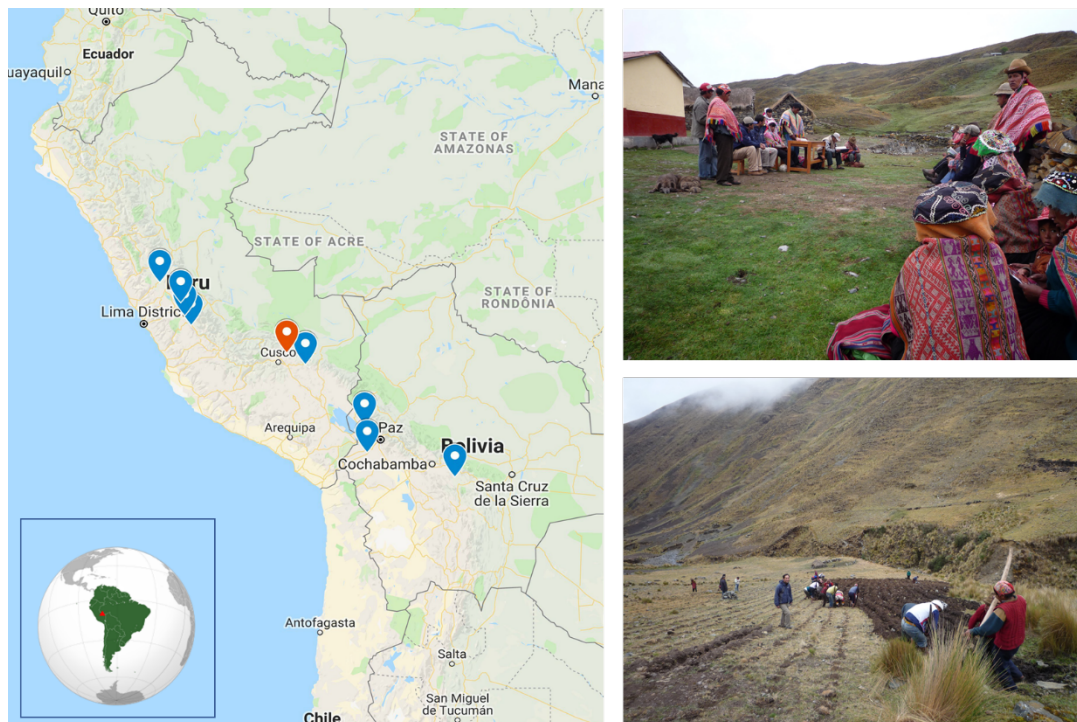


Figure 2. Map of South America showing the places where landraces used for the Pally poncho (CIP 399085.23) breeding were obtained (blue) and the location of the community of Chaclabamba in Peru. This community was included in the participatory breeding process and it was also the place where improved variety was first released (red). Pictures correspond to the community of Chaclabamba Source: Authors, Pictures by W. Pradel.

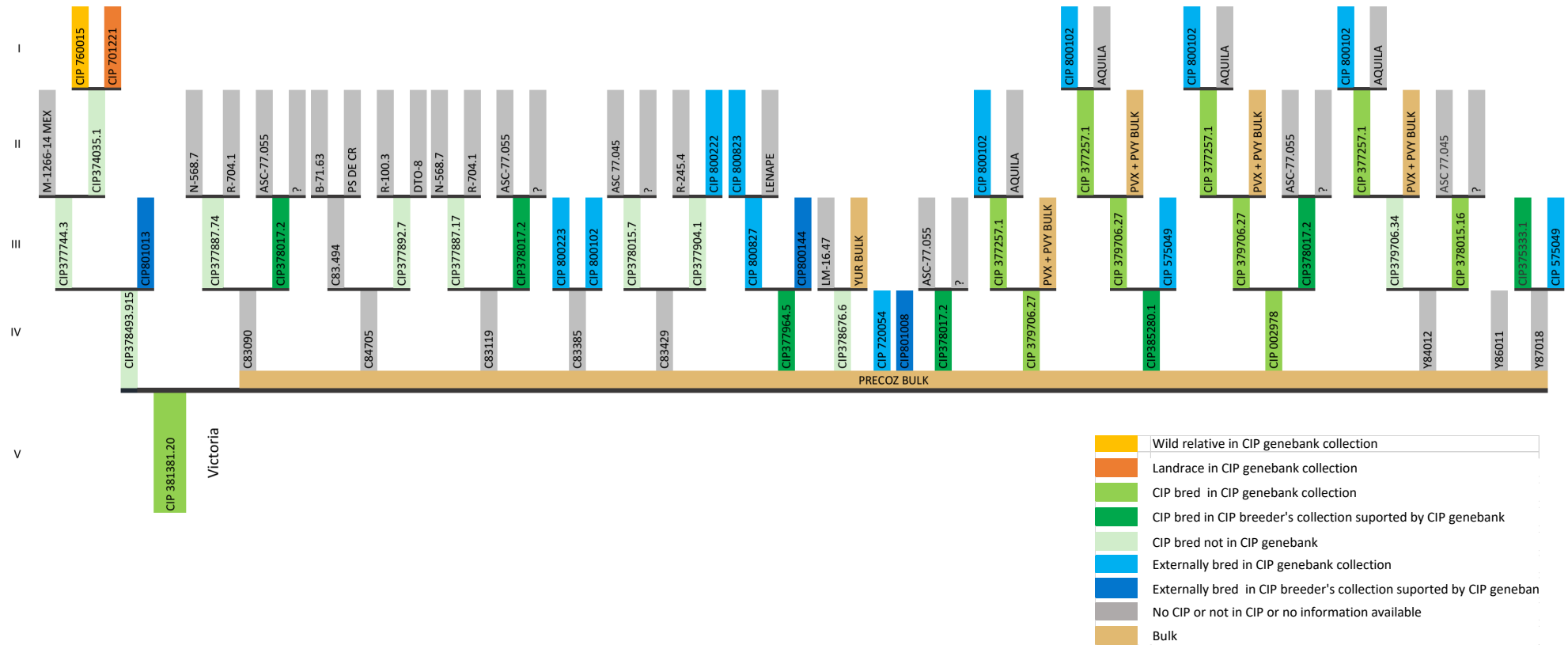


Figure 3. Pedigree of Victoria (CIP 381381.20). Source: Authors, based on CIP’s pedigree book database.

Economic surplus analysis

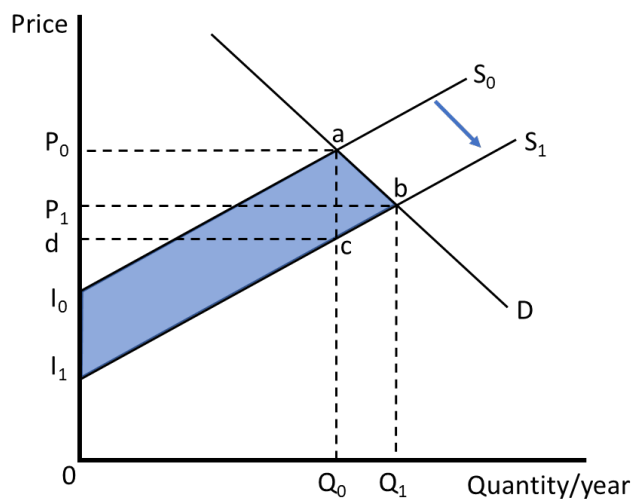


Figure 4. Economic surplus analysis. Source: (Alston, Norton, and Pardey 1995).

$B_t = P_0 Q_0 K (1 + 0.5 K e n / (e + n))$, where: (1) B_t = gross annual benefits (total surplus is in blue); (2) $K = (a - c) / a$ reflects yield and cost changes, adoption of variety, and (3) e and n = supply and demand elasticities.

Adoption path of Victoria (CIP 381381.20) in Uganda (1991-2016)

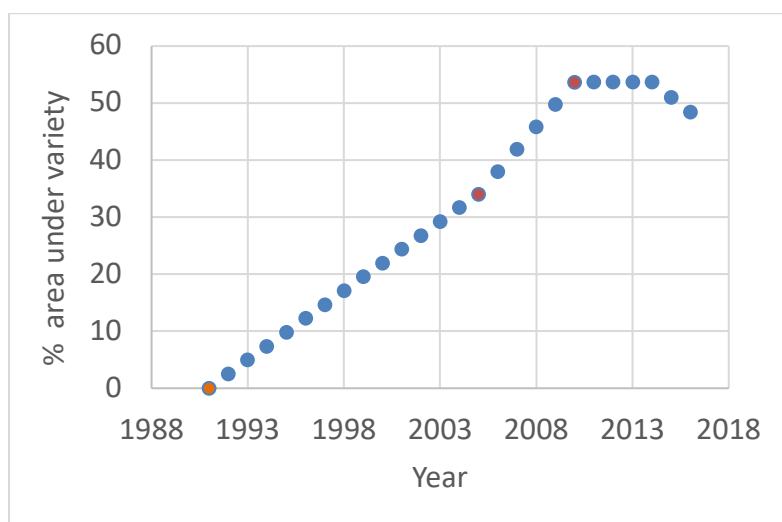


Figure 5. Adoption curve of Victoria (CIP 381381.20) in Uganda. Source: Authors