



# Andean potato diversity conserved in the International Potato Center genebank helps develop agriculture in Uganda: the example of the variety 'Victoria'

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## Abstract

The International Potato Center (CIP) genebank conserves and facilitates access to highly diverse germplasm of potato, sweetpotato, and Andean roots and tubers as a global public good for food security. While it is generally understood that material from 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. By applying the relative contribution of provenance based on pedigree data, we apportion the CIP genebank contribution of two released potato varieties: Pallas Poncho and Victoria. The estimated contribution of the CIP genebank to Pallas Poncho and Victoria is 35% and 72%, respectively. We then used an economic surplus approach to measure Victoria's benefits in Uganda by attributing and valuing productivity gains. The gross benefit of Victoria in Uganda is estimated at USD \$1.04 billion (2016 value), which exceeds the annual operating cost of the entire genebank over its lifetime. Seventy-two percent of the economic benefits corresponding to germplasm of Victoria are due to the CIP genebank contribution. Our findings demonstrate the magnitude of economic benefits generated by the use of conserved germplasm provided by the CIP genebank in crop improvement, which is only one of the several components of its total economic value. These results show that the availability of diverse germplasm is perhaps one of the most important elements in varietal development.

**Keywords** Genebank · Genetic resources · Genetic diversity · Improved potato adoption · Economic benefits

## 1 Introduction

One of the most important and consumed crops around the world is potato (*Solanum tuberosum* and other *Solanum* spp.). Potato is a major crop for food security due to its high nutritional value (FAO 2008). It 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 (FAO 2019).

Potatoes have played a major role in human history. The tuber was a protagonist of one of the most renowned and massive human migrations caused by the Irish potato famine in 1845, where 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 of the plant pathogen *Phytophthora infestans*: the causal agent of the potato late blight [LB] (Yoshida et al. 2013). This devastating outbreak occurred as a consequence of a low diversity in the varieties cultivated at that time in Europe. Virtually none of potato plants grown in farmers' fields had genetic resistance to the pathogen (Fraser 2003). This crisis highlights the crucial importance of genetic diversity for not only plant and crop health but human wellbeing.

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*

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subspecies *tuberosum*, and large-scale crop cultivations usually contain only a few cultivars or even a few clones with the same genetic composition during a crop cycle (Lin 2011). This can be contrasted to the common practices of smallholder farmers in Andean and African regions with limited agricultural inputs, who typically prefer to have a highly diverse planting portfolio with several varieties or cultivated species of potato planted at the same time to minimize risks associated with heterogeneous and changing environments (FAO 2008; Brush et al. 1992; Kolech et al. 2017).

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

The genebank at the International Potato Center (CIP) in Lima, Peru, is a member center of the CGIAR and started its operations in 1971. 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 [ARTCs] (CIP 2019). CIP holds one of the largest in vitro genebank collections in the world composed mainly of landraces, wild relatives, and some advanced lines and improved varieties, which are held *in trust* under the Food and Agriculture Organization (FAO) (CIP 2019). Additionally, the CIP genebank houses a second collection, also held under the auspices of the ITPGRFA, comprised of an in vitro collection of CIP-derived breeding materials that contains only advanced breeding lines, which are maintained and distributed with the support of the genebank thanks to its knowledge of germplasm conservation, management, and controlled movement. The CIP genebank distributes germplasm from both collections for research, training, and breeding, using the Standard Material Transfer Agreement (SMTA), under the guidelines and legal framework of the ITPGRFA (CIP 2019).

Agricultural gains related to varietal improvement in potato production in developing countries have led to productivity growth, substantial returns on investment, positive experiences in technology transfer, and improved north–south and south–south cooperation (Walker et al. 2003). Diverse potato germplasm, safeguarded by the CIP genebank, has contributed to numerous research projects and varietal development. Past analyses of economic benefits of CIP have primarily focused on evaluating returns to the CIP potato breeding program without considering the specific role of the CIP

genebank. 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% 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 Cooperation-88 (C-88), another CIP-related improved potato variety. C-88 is a variety of major importance in China and has been widely adopted by farmers since its release in 1996. The variety exhibits LB resistance and is high yielding in sub-tropical highlands. C-88 is the product of a collaboration between CIP, the Chinese National Agricultural Research System, and the Benguet State University (Philippines). The main contribution from CIP was the provision of the male parent. Robinson and Srinivasan (2013) estimated economic benefits of this variety and reported pedigree information that confirms the CIP germplasm contribution. However, Robinson and Srinivasan did not fully detail the C-88 pedigree and did not conduct a contribution analysis or quantification of the contribution based on pedigree.

Our analysis addresses this gap. We measure the share of the CIP genebank in economic benefits derived from improved varieties through 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 the improved potato variety Pallas Poncho, to evaluate the feasibility of conducting an RCP analysis. Next, we perform a full analysis comprising apportionment, attribution, and valuation of the productivity gain for the improved variety Victoria as an example to quantify the portion of the CIP genebank contribution in economic benefits derived from the adoption of Victoria in Uganda.

## 2 Data and methods

### 2.1 Data

We consider biological, economic, and agricultural data for this study. We studied two improved potato varieties: Pallas Poncho, identified in the CIP genebank collection with the number CIP 399085.23 and in the Global Information System (GLIS) of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) with the code GLIS DOI: <https://doi.org/10.18730/P5PDG>; and Victoria, identified with the number CIP 381381.20 and GLIS DOI: <https://doi.org/10.18730/P5MW4>. Senior breeders from the CIP Genetics and Crop Improvement

Program assisted us in detailing biological information of the two varieties (Manuel Gastelo, Walter Amoros, and Elisa Salas through personal communications).

We selected the variety Pally Poncho because all the initial material used for its development was provided by the CIP genebank collection (Gastelo, M. personal communication). The pedigree for the Pally Poncho was provided by M. Gastelo, who participated in its development.

The variety Victoria was selected as an example for further analysis given the availability of detailed information about its pedigree, agronomic, and market-related data. The agronomic and market-related data allowed us to conduct an economic impact assessment of the variety. Victoria was obtained by CIP breeders as the product of a cross made in 1981 and later 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). We reconstructed the pedigree for the variety Victoria by collecting and cross-checking information about its ancestors from physical and digital pedigree books and personal communications with breeders.

We calculate the yield gain of Victoria compared to other varieties grown in Uganda based on farm-level data collected from a 2005 CIP farm survey conducted in the two major potato-producing areas of Uganda (Kaguongo et al. 2008) (Table 1). Interviewees were chosen using a stratified sampling frame and include all four counties and the 25 potato-producing sub-counties in the Kabale and Kisoro districts. From each sub-county, one sub-location was randomly selected, and from each sub-location, one village was randomly selected. We randomly sampled six farmers in each village, and interviewed 144 farmers in total.

We obtained variety-related data, such as release year and adoption rate, from previous CIP publications and the Diffusion and Impact of Improved Varieties in Africa (DIIVA) Project (<https://www.asti.cgiar.org/diiva>) (Kaguongo et al. 2008; Thiele et al. 2008; Walker and Alwang 2015).

We collected information about market- and Uganda-related parameters, such as potato yields, agricultural gross production value, quantity of production, harvested area, and Uganda population changes from the FAO statistical database (FAO 2019) and the World Bank (2018). We calculated potato prices for Uganda based on the value of agricultural gross production and quantity of production data.

## 2.2 Estimation of economic value

The three steps involved in estimating the commercial value of progenitors used by plant breeders to improve varieties has been summarized by Smale (2004). The first step is to ‘apportion’ the genetic contribution of a progenitor. The second is to ‘attribute’ the productivity gain resulting from the varietal change by farmers. The third is to ‘value’ the productivity gain. The product of these terms represents the estimated benefits share of the progenitor.

### 2.2.1 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

**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	6847	0	34	
Kinigi	8719	−27.34	14	−3.83
Rwangume	7877	−15.04	12	−1.81
Rutuku	7367	−7.59	4	−0.30
Rwashakye	5723	16.42	2	0.33
Cruza	4895	28.51	13	3.71
Kasaza	3981	41.86	0.6	0.25
Bumbamagara	2648	61.33	15	9.20
Other varieties	Not reported		5.4	
Total			100	7.55

Most commonly grown varieties in 2004–2005 (kg/ha). \*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. Source: modified from 2005 CIP survey (Kaguongo et al. 2008)

depending on the generation. Pardey et al. (1996) and other studies have applied these methods to evaluate the genetic contribution of the International Maize and Wheat Improvement Center (CIMMYT) wheat varieties (e.g. Lantican et al. 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 scepticism concerning the strict 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.

We use the RCP to quantify the contribution of the source of material or provenance to the studied variety. The provenance is considered a divisible attribute. Provenance can be related to a geographic area, a country, or an affiliation; in this analysis, we studied the proportion of provenance corresponding to the affiliation to the CIP genebank. Unlike the 'geometric rule' applied by Pardey et al. (1996), RCP is focused on the germplasm of the progenitors rather than on the cross between two progenitors.

In this study, we used the pedigrees of the varieties Pally Poncho and Victoria to identify their ancestors and perform a pedigree analysis 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 specific variety.

We only consider genotypes related to the CIP genebank, holding a CIP number, or material directly bred by CIP for the pedigree construction. Pedigrees are built under the convention of biparental offspring. This assumes that an offspring has two parents, each one contributing 50% 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'). Some pedigrees may include bulks due to the bulk pollination strategy.

Bulk pollination is a frequently used breeding strategy that facilitates the success rate of crosses in potato. This strategy uses a bulk of pollen, which is a mixture of pollen from different plants, with different genotypes 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 pedigrees had bulks in their architecture, we made a special effort to obtain the complete composition of the bulk to calculate the RCP because it includes the number of bulk members or genotypes in its calculation.

We obtained additional information on the pedigree of genotypes that had a CIP number (accessions) after comparing their CIP number against the CIP genebank database. Based on this information, we define eight categories of germplasm according to the relationships of a pedigree member and its

provenance: i) CIP-bred germplasm in the CIP genebank *in trust* collection; ii) CIP-bred germplasm in the collection of CIP-derived breeding materials supported by CIP genebank; iii) wild relative germplasm in the CIP genebank *in trust* collection; iv) landrace germplasm in the CIP genebank *in trust* collection; v) externally bred germplasm in the CIP genebank *in trust* collection; vi) externally bred germplasm in the collection of CIP-derived breeding materials supported by the CIP genebank; vii) CIP-bred germplasm not included in the genebank *in trust* collection; and viii) non-CIP-related, or not in CIP genebank germplasm, or material with no information. We use categories as criteria to assign a contribution value using the RCP quantitative analysis.

We calculate the RCP using the relationships observed between descendants and ancestors shown in the pedigree (parents, grandparents, great-grandparents, etc.) for every progenitor. This measurement is calculated in a similar way to the relative genetic contribution (RGC), which quantifies the theoretical genetic material distribution coming from each of two parents (Gopal and Oyama 2005). Although, the RCP can track the inheritance of genetic material from one generation to another, it does not track the exact genetic composition of a descendant. Instead, it quantifies the contribution of the provenance of the progenitors following Mendelian inheritance through the pedigree and provides insight regarding the relative genetic composition.

Mendelian factors do not have a substantial effect on the pedigrees due to the small timescale in which pedigrees take place [~10 generations] (Barton and Etheridge 2011). Mendelian laws work on a gene scale. Modifiers of genetic populations (such as genetic drift, natural selection, small population sizes, and non-random mating) can additionally play a role in large timescales and affect the frequencies of gene forms (alleles) found in a population. Artificial selection that results from the breeding process and other specific biological factors, including differences between the plant species used for varietal development, may influence the real genetic composition of a variety. However, RCP is not affected because it is not a measure of real genetic composition.

RCP assumes that 50% of the total genetic material of the studied organism comes from each parent every time a cross takes place (Delannay et al. 1983; Gopal and Oyama 2005; Barton and Etheridge 2011). 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 each generation is successively reduced by half. Considering that since the studied varieties and some of their ancestors were selected during a breeding process driven by breeders' preferences, in practice, this artificial selection introduces bias to the theory, resulting in some ancestors making a greater genetic contribution to the variety 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 in our case.

We use the RCP for our quantitative analysis. RCP follows the path of the pedigree and the Mendelian model of genetic contribution. However, instead of genetic material, we consider ‘provenance’ as an inherited attribute that passes from ancestors to offspring. Besides the contribution of the provenance, RCP would represent a theoretical genetic contribution in the absence of selection. The use of RCP is possible given that two plants are crossed to obtain a descendant, and the attribute ‘provenance’ (e.g. nationality) in the final product will depend on the form of this attribute in the parental plants.

The genebank contribution is based on the pedigree analysis, its composition, and the categories associated with each genotype. The categories of the germplasm correspond to different forms of the attribute ‘provenance’. We considered that a genotype has a relationship with the CIP genebank when its germplasm is in the CIP genebank collection; this includes the *in trust* collection and the collection of CIP-derived breeding materials supported by the CIP genebank. The total genebank contribution corresponds to the addition of the values of the RCP of the materials found in the pedigree in categories related to the CIP genebank collection. 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 collection are considered for contribution calculation. Accessions produced by CIP breeders or other sources that are not found in the genebank collection are not included in the contribution analysis, although some of them might have had a previous genebank contribution.

In order to estimate the total RCP related to the CIP genebank in the case of Victoria, we scanned Victoria’s pedigree from the most recent ancestors to the oldest, identifying those members that belong to the categories i–vi (related to the CIP genebank). Only the most recent member or members in the paternal and maternal line, or pedigree branches, that fulfil the category requirement contribute to the total RCP. In the cases where there are no members of the categories i–vi in a determined branch of the pedigree, contribution is applied to the corresponding category that is not related to the genebank (vii or viii). In the event of having more than one member belonging to a genebank-related category but in different generations in a pedigree branch, only the most recent member(s) will contribute to the RCP. Parents of members that are already contributing to the RCP might be disregarded for contribution to avoid double contribution.

We applied bulk penalty when the bulk composition is known, otherwise it does not contribute to the genebank-related RCP. In the case of Victoria, we use bulk penalty for ‘Precoz bulk’, where the number of members is 16 (Fig. 4). A bulk is considered a unit formed by a certain number of

members or genotypes that are used as sources of pollen. To calculate the contribution of a bulk, we estimated the contribution of every bulk member following the rules described previously based on its progenitors’ category and generation; we then added each value into a provisional bulk contribution. Considering that only one pollen donor in the bulk is the true parent of the descendant plant, the provisional contribution is penalized by dividing by the number of genotypes used in the bulk. In theory, a whole bulk would contribute to the 50% passed on to its descendant, which is the value normally provided by one of the parents in a cross. However, when RCP is used to find a bulk contribution, this has a lower value than a conventional parental contribution due to the penalization applied. Varieties with bulks in their pedigrees show total contribution values of less than 100%.

RCP can also be used to calculate the contribution to a variety of a specific category. This would include all the members that fulfil the requirement across the whole pedigree following the rules previously described. This analysis is not shown in this study.

### 2.2.2 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 farmers’ fields may provide more accurate information thanks 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 used in this study. However, other benefits from a new variety 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).

We estimate attribution based on yield gain of Victoria in comparison to other potato varieties used in Uganda. We estimate yield gain using yield data for the most commonly grown potato varieties in Uganda that represent the 94.6% of the potato-growing area in 2004–2005 according to Kaguongo et al. (2008) (Table 1). We calculate the yield gain between Victoria and other commonly grown varieties and weight by their corresponding total area under the variety (Eq. 1).

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

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.

### 2.3 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 et al. 1995). Economic surplus analysis is commonly used to assess the benefits of a variety, considering its agronomic and market-related information, and its contribution to an economy (Eq. 2).

$$B_t = P_0 Q_0 K (1 + 0.5Ken / (e + n)), \tag{2}$$

where:

- $B_t$  gross annual benefits (total surplus is in blue),
- $K$   $(a-c)/a$  reflects yield and cost changes due to the adoption of variety; and
- $e$  and  $n$  supply and demand elasticities, respectively.

To value the productivity gain, we completed an *ex post* economic surplus analysis using methods applied by Alston et al. (1995) and Norton et al. (1987). This study assumed a closed economy model, which means that the effects of trade are not considered. Under this assumption, an increase in potato production can have a substantial price-reducing effect on the market.

We use some assumptions to estimate the economic benefits of Victoria. The yield gain due to the use of Victoria is estimated at 8% (in Eq. 2). This yield gain could be underestimated given the possibility that 5.4% of all varieties correspond to local ones with no associated data but presumably with lower yields than Victoria. The cost change (increase) per hectare is estimated at 5%. We assume that production practices do not change drastically when adopting Victoria, so the cost to farmers does not increase much. The main factor that contributes to the cost change is the higher cost of seeds for Victoria compared to local varieties.

The adoption of a new technology, such as an improved variety, can cause a shift in the supply curve (Fig. 1) for the commodity. 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 can lead to a decrease in the price of potato for the consumers (and

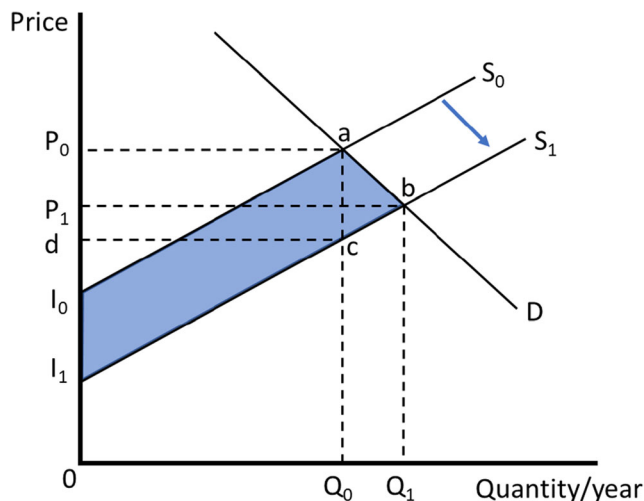


Fig. 1 Economic surplus analysis.  $B_t = P_0 Q_0 K (1 + 0.5Ken / (e + n))$ , where: (1)  $B_t$  = gross annual benefits (total surplus is in blue); (2)  $K = (a-c)/a$  reflects yield and cost changes, adoption of variety, and (3)  $e$  and  $n$  = supply and demand elasticities, respectively. Source: Alston et al. (1995)

producers), holding all other factors constant. Consumers might also increase their demand for potatoes over time due to growth in per capita income and population, causing the demand curve to shift to the right, partially offsetting the price effect of the supply shift. Thus, technology, income, and population changes create new equilibria 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.

Our analysis covers a period of 25 years, from the time Victoria was released in Uganda in 1991 up to 2016. There are no available market data after 2016. Using the data from CIP surveys and the DIIVA Project, the adoption rate, measured as a percentage of the area under Victoria in Uganda, was 34% in 2005 and 53.6% in 2010. We constructed an adoption curve following a piece-wise linear model, with the year of release, 1991, as a starting point, Victoria adoption in 2005 and 2010, and an estimated decrease in adoption of 5% in 2015 and 2016.

We assume potato elasticities of supply ( $e$ ) and demand ( $n$ ) needed for assessing price responsiveness to supply and demand changes to be 0.8 and  $-0.3$ , respectively, based on Fuglie (2007). Because benefits occurred over time, we calculated their present value (PV) using a discount rate of 3%. We conducted an inflation adjustment at the end of the economic surplus analysis in USD, converting data from 2010 (base year) to 2016. Additionally, our valuation of productivity considers two scenarios when assessing the benefits of Victoria in Uganda, one that considers the effects of population growth on the demand for potatoes in the country, and one that does not. Population grew at an average annual rate of 3.2% during the study period.

### 3 Results

#### 3.1 Apportionment of contribution of provenance from genebank

##### 3.1.1 Pally Poncho (CIP 399085.23, Peru)

Pally Poncho is a variety released in response to a food security threat in the rural community of Chacllabamba, a traditional Andean community located 4100 m 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 LB in 2003. The reduction in potato production caused a serious problem for them, considering that native potatoes are the base of their food security (INIA 2007). Based on the testimony of the breeder M. Gastelo (personal communication) and CIP internal reports, we confirmed that the initial germplasm used for developing this improved variety was 100% derived from the CIP genebank’s landrace germplasm collection. We used this knowledge to assess the feasibility of RCP measurement for estimating the apportionment of CIP genebank contribution.

The pedigree of Pally Poncho shows the germplasm and breeding strategy used for varietal development (Fig. 2). 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 seven generations 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, this material in the CIP genebank is disease free and available for national (Peru) and international distribution for research, training, and breeding upon acceptance of the SMTA.

In the pedigree, the use of three different bulks for pollination (the male parent contribution) 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. Bulk-B is formed by 21 genotypes (in Fig. 2), 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 between 2017 and 3965 masl (Fig. 3).

We carried out an RCP analysis using Pally Poncho’s pedigree as a point of reference. Out of the theoretical genebank contribution of 100% according to breeders’ confirmation, only 35% was apportioned as the genebank-derived contribution due to the lack of information on some of the bulks. Fifty percent was corresponded to the contribution from unknown genotypes (Bulk B1C2), and 15% was the product of the penalty given to the known bulks, which is the total bulk contribution divided by the number of its genotypes.

##### 3.1.2 Victoria (CIP 381381.20)

Victoria comes from the ‘B population’ developed by CIP breeders in Peru, with the objective of obtaining LB-resistant clones with good yields. Victoria’s pedigree was built based on information obtained from CIP breeders’ pedigree books (Fig. 4). Victoria was the product of five 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, 10 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

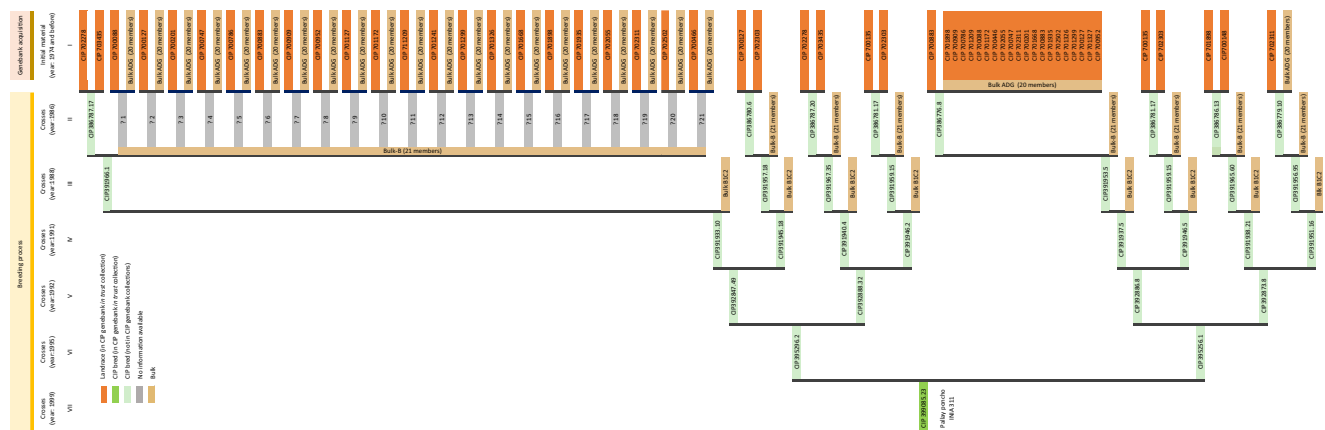
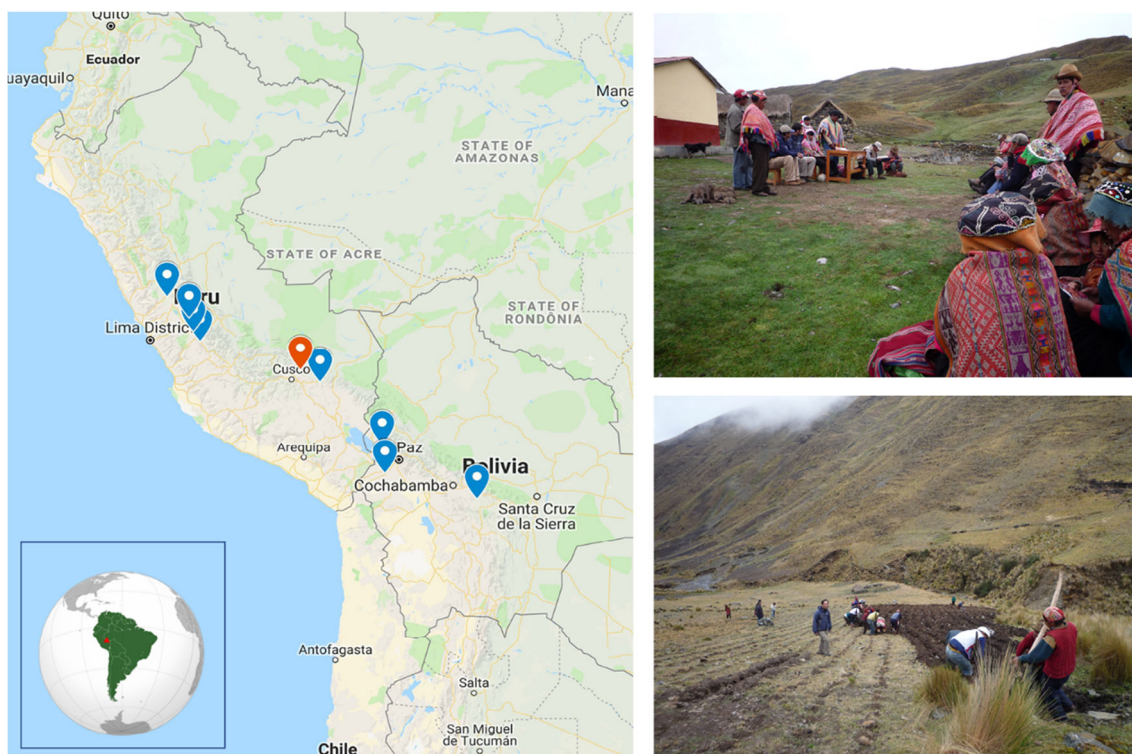


Fig. 2 Pedigree of Pally Poncho (CIP 399085.23). Source: modified from M. Gastelo, personal communication



**Fig. 3** Geographic localization of Pally Poncho ancestors and Pally Poncho recipient community in Peru. 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 (red). This community was included in the participatory breeding process and it was also where the improved variety was first released. Photos correspond to the community of Chaclabamba. Source: authors, photos by W. Pradel

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 key traits were obtained through breeding at CIP, included in the breeding or genebank collection, and used in the next generation towards the variety development. Additionally, the germplasm corresponding to Victoria is in the CIP genebank collection as phytosanitary-clean, *in vitro* material and is, therefore, available for distribution.

We carried out an RCP analysis using Victoria’s pedigree. As the product of the total contribution analysis, considering the genotypes belonging to the two collections, the CIP genebank base collection and CIP-derived breeding materials, we find that the CIP genebank total contribution to Victoria is 72% as compared to 28% for non-CIP-genebank-related material.

Considering the same analyzed pedigree path and taking the most recent ancestor with CIP genebank affiliation for the RCP analysis, 72% of the contribution is distributed among categories of germplasm as described in the Fig. 4. Under this analysis, we found that the CIP genebank base collection contributed 30% to Victoria germplasm, and the collection of CIP-derived breeding materials in the genebank supported 42%.

### 3.2 Attribution and value of the productivity gain of Victoria (CIP 381381.20)

We generated the adoption path of Victoria in Uganda using the percentage of potato area under this variety, which displayed an upward trend from its official release in 1991 up to 2010 (Fig. 5). The adoption rate may have begun to decline at some point after 2010, but precise information is not available. Knowing that the variety is still being used, we assumed a constant adoption rate from 2010 to 2014 and then a 5% decrease per year in 2015 and 2016.

Although Victoria was initially developed as a resistant variety against LB, it has lost part of its resistance in Uganda as the pathogen has evolved to partially overcome it (Kaguongo et al. 2008). Nevertheless, Victoria still has useful resistance, which allows farmers to control the disease using fungicides to maintain yield levels. Victoria is being used by Ugandan farmers due to its high yield, early maturity, and highly desired red skin and cream flesh. Market demand is the most important criterion for variety selection in Uganda (Kaguongo et al. 2008). On average, and after normalizing for adoption, Victoria’s yield is 7.55% higher than the yield attained by the other seven commonly grown potato varieties in Uganda.



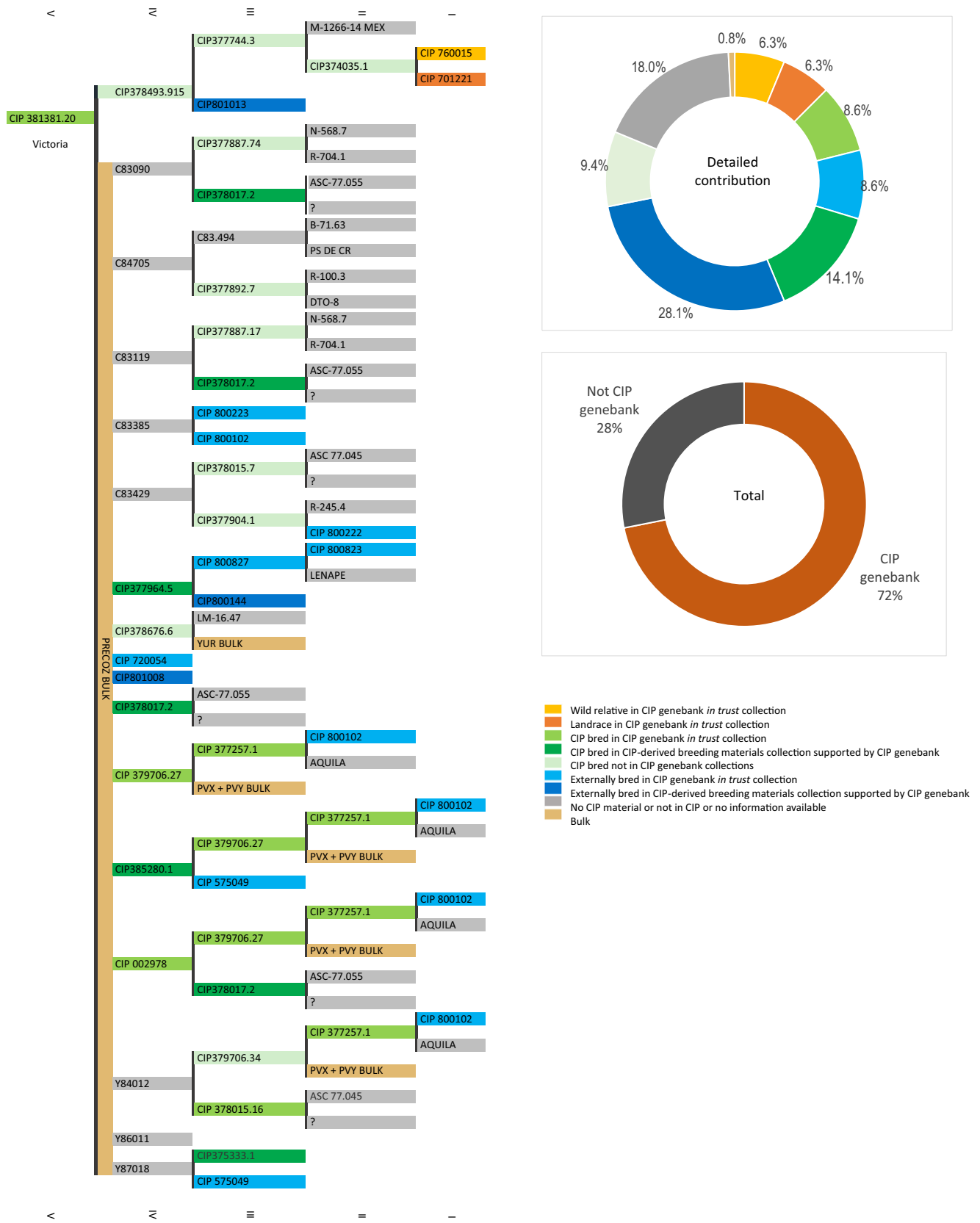
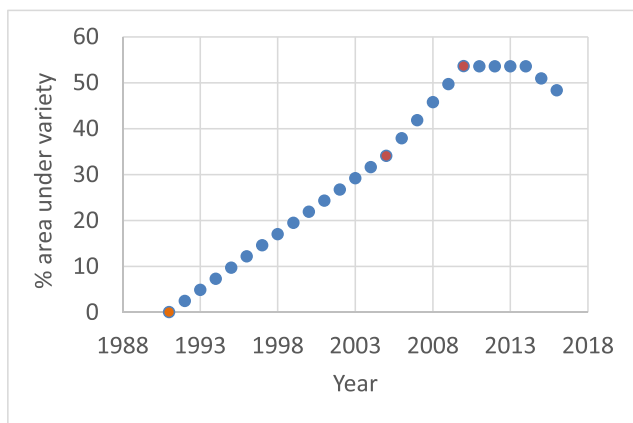


Fig. 4 Pedigree of Victoria (CIP 381381.20) and description of RCP proportions. Source: authors, based on CIP's pedigree book database



**Fig. 5** Adoption curve of Victoria (CIP 381381.20) in Uganda (1991–2016). Source: authors

Applying a closed economy model for an ex-post economic surplus analysis (few potatoes are traded internationally by Uganda), we calculated the benefits of the adoption of the variety Victoria in Uganda for the period 1991–2016. Our results indicate that the estimated PV of the gross benefits from Victoria adoption from 1991 to 2016 is USD \$859 million in 2016 dollars, when human population growth is not considered. In contrast, when the change in population growth for the period (3.32% annual increase), and hence increased demand, is considered, the PV of the benefits increases to USD \$1.04 billion in 2016 dollars.

The estimated benefits are derived from several aspects of varietal development and adoption, such as germplasm used and its associated traits, breeding efforts, seed multiplication, distribution programs, and extension. Based on RCP and the pedigree analysis of Victoria, we can say that 72% of the economic benefits corresponding to the germplasm are due to the CIP genebank contribution.

The reported benefit is not a net benefit, which would be the gross benefits minus total discounted costs. The latter would include the genebank costs, breeding costs, costs of varietal development, extension, and adoption. Some of these costs occurred in the crosses for variety development before the variety was released, and various were shared among other varieties developed under the same breeding process. Several

of these varieties have been released and adopted in different countries.

The total annual cost associated with running the CIP genebank, including safely maintaining and distributing accessions in 2016 (Table 2), was estimated at USD \$3.5 million, not including the one-time, non-recurring costs of cryobanking potato and sweetpotato accessions of about USD \$2.5 million (spread over about five years). Including these cryobanking expenses, the total annual cost of the genebank is approximately USD \$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 breeding, extension, and other programs supporting the adoption of the variety are not described here.

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

### 4 Discussion

Walker et al. (2003) reported that about 23% of the potato varieties released in 30 countries are related to CIP, indicating that the 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 phytosanitary clean breeder’s materials, has not been analyzed. Similarly, work by Robinson and Srinivasan (2013) analyzed the economic impact of the improved potato variety C-88 and proved CIP germplasm was incorporated in its development. However, the authors did not fully detail the biological information related to the pedigree nor perform apportion analysis to estimate the contribution.

**Table 2** Estimated annual cost of the CIP genebank in 2016 (USD \$)

Costs	Crop		
	Potato	Sweetpotato	ARTCs
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)

Therefore, we systematically studied the pedigrees of two CIP genebank-related varieties to determine the contribution of the genebank by tracking the affiliation of their ancestors. As the pedigrees show (Figs. 2 and 4), the CIP genebank contribution is variable, which was also observed by Robinson and Srinivasan (2013). Some varieties, such as Pallas Poncho, have been developed entirely using germplasm from the CIP genebank collection, and even in this case, only material included in the category ‘landrace’ original from a relatively small geographic area (Figs. 2 and 3). Others, such as Victoria, originated from the use of various categories of germplasm from the CIP genebank collection and other external germplasm sources.

The RCP analysis uses the available information to apportion the CIP genebank contribution to a variety. The estimated contribution for Pallas Poncho is 35% out of a theoretical 100%. This example shows that RCP is affected by the presence of bulks in the pedigree, and when part of the genotypes in the pedigrees do not have associated information. It demonstrates that the RCP estimation is highly conservative due to the strict use of the relationships evidenced in the pedigree, the use of the related information such as affiliation, and the penalties applied to bulks.

We were only able to conduct the apportionment analysis for Pallas Poncho, rather than the full benefit analysis, due to the lack of biological-, agronomic- and economic-related information. Absence of such data also occurs for other improved varieties that have been adopted by farmers. In these cases, it may be possible to use other means to evaluate other types of benefits. In the case of Victoria, the biological and agronomic data, together with survey data on the adoption of the variety in Uganda at the country level, allowed us to make a full economic benefits assessment.

Uganda has the third highest population growth rate in the world (United Nations Population Fund 2017). This lends support to the second scenario where population growth played a role in shifting the demand for potatoes, with USD \$1.04 billion in estimated benefits.

The estimated gross economic benefits correspond to one accession in one country over a 25-year period. The total cost of running the genebank to conserve 16,718 accessions of potato, sweetpotato, and ARTCs is estimated at USD \$4 million per year. Part of the costs of the breeding process that gave rise to the variety Victoria are shared with other varieties that originated from the same population (Thiele et al. 2008). Hence, the rate of return on the investment in the CIP genebank is indeed high.

A possible refinement of our analysis for future studies would be to refine apportioning based on genetic contribution while considering the real genetic composition of the genotypes in the pedigree. This can be accomplished by taking advantage of DNA 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, such as in haplotype blocks. However, costs would be high—especially for polyploids, which contain several copies of a set of chromosomes, sometimes with more than one form of each gene or allele—and the process is still not yet fully understood. Time and information are necessary for experimental implementation, given the need for material acquisition, DNA extraction and sequencing, bioinformatic analysis, identification of relationships between genotype and phenotype under determined environmental conditions, among others, required to fully realize complex linkages between genotype and phenotypes. Access to the DNA of at least a minimum number of ancestors would be required to run the analysis. Obtaining this access could be challenging 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 on obtaining the correct samples for analysis, especially for varieties that were developed several decades ago.

## 5 Conclusion

We evaluated a three-step analysis that incorporates biological, agricultural, and market-related data to measure the share of the CIP genebank in economic benefits derived from the use of an improved potato variety.

We built the pedigrees of two varieties reported as CIP genebank-derived varieties and linked information about the provenance of the pedigree members and their relation to the CIP genebank. This allowed us to perform a Relative Contribution of Provenance (RCP) analysis to estimate the contribution of the CIP genebank to the varieties. We found a CIP genebank contribution of 35% for the variety Pallas Poncho (CIP 399085.23), based on the use of germplasm in the CIP genebank base collection. For the variety Victoria (CIP 381381.20), we found a 72% contribution based on the use of germplasm in the CIP genebank base collection (30%) and the collection of CIP-derived breeding materials supported by the CIP genebank (42%). These values correspond to the apportioned component of benefits estimation and represent the benefits share of the genebank.

Adoption of Victoria in Uganda led to farm-level productivity gains (Kaguongo et al. 2008). Yield gain is estimated at about 8% compared to other varieties being adopted in Uganda. The valuation of the productivity gain and other market-related information were used in an economic surplus analysis to estimate gross economic benefits.

Excluding the genebank, breeding and extension costs, the estimated benefit from adopting Victoria in Uganda over a 25-year period is about USD \$42 million per year. Considering

that Victoria's germplasm has also been widely adopted in other countries, under other names, the total benefits from Victoria and the related CIP genebank contribution may be significantly greater. The total cost of running the genebank is estimated at USD \$4 million per year, less than a tenth of the economic benefits derived from a single variety in one country.

Our study of Victoria illustrates how germplasm used in a variety development process can be traced and related to an estimated economic benefit. This highlights how the use of conserving genetic resources, like the germplasm safeguarded in the CIP genebank, can impact the agricultural development of lower-income, potato-producing countries, such as Uganda. There are numerous improved varieties like Victoria and C-88 that include important genetic contributions from the CIP collection and that have been used in various places around the world.

Complementary and more exhaustive studies should be conducted by making available more detailed information about new improved varieties 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 more precisely calculate ancestral contribution with more robust biological significance. Additional information about varietal 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 presented here correspond to a current, direct 'use value'. However, the economic value of plant genetic resources comprises different types of value, as described by Smale and Jamora (2020, in this issue). Direct use value, related to derived food, fibre and medicinal products, is only one component of the total value. Total value also 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. Additional studies with different analytical frameworks are needed to assess other types of economic values related to the genebank.

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**Authors' contributions** The first author contributed to the research conceptualization and design, data gathering, data analysis, writing, and editing. The second author contributed to research conceptualization and design, data analysis, writing, and editing. The third, fourth, and fifth authors contributed to research conceptualisation and design, data gathering, data provision, and editing. The sixth author contributed to research conceptualisation and design, data analysis, writing, and editing. The seventh author contributed to research conceptualization and design and editing. The eighth author contributed to the research conceptualization and design. The final author contributed to data provision.

## Compliance with ethical standards

**Conflict of interest** The third author was the Genebank Manager of CIP at the time this research was conducted. The fourth author is the current Genebank Manager of CIP. The fifth and last authors are scientists at CIP. The seventh author is an agricultural economist at the Crop Trust. The remaining authors declare no conflict of interest.

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