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A Sourcebook: Economics of conserving plant genetic resources in genebanks[1]

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[1] This sourcebook is intended as background for Genebank Impact Fellows and others interested in the economics of conserving plant genetic resources in genebanks. The summary draws from and updates earlier reviews of the literature (Smale and Koo 2003; Smale and Drucker 2005; Smale and Hanson 2010). Citing selected references, the sourcebook is accompanied by a larger bibliography of related literature in excel format that has been developed by Nelissa Jamora of the Crop Trust and Melinda Smale. The larger bibliography includes earlier work undertaken with Patricia Zambrano and Indira Yerramareddy at the International Food Policy Research Institute. It is our intention to update the sourcebook as new literature is identified.

Contents

I. Purpose of this sourcebook

Evidence on the economic returns to use of plant genetic resources in commercial agriculture is vast. The value of investing in crop improvement to society as a whole has been documented continuously for many decades. By contrast, applied research about the costs and benefits of conserving the diversity of plant genetic resources outside their place of origin (*ex situ*, in genebanks) is scant. Why is more research needed? For genebanks, "funding is inconsistent because genebanks have long-term objectives and are remote from eventual development outcomes" (Crop Trust 2015). Studies are needed in order to change these perceptions.

The purpose of this sourcebook is to compile, in an accessible form, a synopsis of previous research on this topic in order to motivate and frame new hypotheses in context. We intend to advance some of the empirical findings reported here with the work conducted by Genebank Impact Fellows under the guidance of CGIAR genebank staff and the Crop Trust during 2018-19. By implementing the work as a collaborative team, our hope is that the synergies and contrasts among individual studies will constitute a body of pertinent applied research that can be used for communicating in various ways with multiple audiences. The sourcebook is the first working paper of the 2019 series. Working papers led by Genebank Impact Fellows follow in the series.

Before proceeding, agreement on definitions is helpful. In economics, the definition of value is human-centric. While many have argued that genetic resources are invaluable (see examples in Wilson 1988), agriculture is fundamentally a human activity. By the diversity of plant genetic resources, we refer to both phenotypic and genotypic variation within and among all agricultural crop species, including varieties recognized as agro-morphologically distinct by farmers and those recognized as genetically distinct by plant breeders.[1] We include crop wild relatives and any other plant material that is a fundamental unit of heredity (or 'genetic material'). The genetic resources that are our focus are conserved as seed samples or "accessions."

There is an historical reason why we distinguish concepts of variety. During the Green Revolution, Jack Harlan (1972) and others expressed fears that valuable genes would be lost as farmers replaced their

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[1] A note on terminology: Typically, farmers' varieties do not satisfy breeders' or legal definitions of variety because they are heterogeneous, exhibit less uniformity, and segregate genetically. Often, farmers' varieties are called "landraces," while those bred by professional plant breeders are termed "modern varieties." Though definitions and concepts of landraces are numerous in the crop science literature, Harlan (1992) defined them broadly as variants, varieties, or populations of crops, with plants that are often highly variable in appearance. The genetic structure of landraces is shaped by farmers' seed selection practices and management, as well as by natural selection processes, over generations of cultivation. A plant phenotype is the observable manifestation of a genotype. A genotype is determined by its alleles, or types of genes. Morphology refers to physical characteristics or form.

landraces with more genetically uniform, modern varieties. The diffusion of modern varieties occurred on a massive scale, and entire farming systems were reshaped with greater use of fertilizers and irrigation. The corn leaf blight during the 1970s in the United States also underscored the potential crop devastation caused when large areas are planted to uniformly, genetically susceptible plants (NRC 1972). Then as now, genetic resource experts often hypothesized that rare, locally adapted genotypes might be found among the varieties maintained by farmers in isolated, extreme or heterogeneous environments. They led extensive and intensive efforts to collect diverse seed samples of landraces and crop wild relatives, protecting them for future use as “accessions” in cold storage units.

National and international organizations contributed to these efforts by investing in genebank construction. Criticisms then mounted that materials stored in genebanks were rarely used because little was known about them (Plucknett et al. 1987; Wright 1997) or they were poorly maintained (Kingwell et al. 2001), serving as little more than “seed morgues” (Raeburn 1995). Excess capacity, redundancy, or availability of close substitutes (Simpson, Sedjo, and Reid 1996) drives the marginal value of an accession toward zero. The expansion of collections is not justified if marginal value is negligible.

Since this work was published, the technical and operational management of genebanks has progressed enormously, and a much more insightful set of tools provides geneticists with new means of searching for useful traits and new ways of using materials (for example, see McCouch et al. 2012). At the same time, the geopolitical and environmental context in which genebanks conduct their work has evolved in new directions. We might argue that public concern for the physical security of seed samples, for the rate of loss of remaining landraces and wild relatives due to threatened habitat, and for finding ways to address human needs caused by weather extremes and variability are even greater today than they were during the 1990s. Yet, those who fund genebanks still want to know whether the long-term value of genebanks justifies their current operating costs, which are substantial. Other questions remain unanswered. For example, is there any justification for expanding the existing collections? Does the use of new information technology enable us substitute genetics “libraries” for accessions?

Next, in Section II, we lay out a few foundation concepts about valuation and measuring diversity, as understood by economists. Section III summarizes some of the economics research that sought to respond to early criticisms of genebanks and document genebank values.

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II. Foundations

A. What is meant by economic value?

To understand the impacts of a genebank, we need first to understand the sources of value in plant genetic resources. We are asked to value plant genetic resources because they are limited. When resources are limited, any choice is a value judgment. To economists, economic value is utilitarian and anthropocentric.

One way of conceptualizing sources of value is the total economic value framework developed by resource economists (Figure 1 is one version of the framework). Total economic value includes both use and non-use components. Use value can be direct, deriving from the food, fiber and medicinal products to which plant genetic resources contribute; use value can also be indirect, relating to the habitat or ecosystem. Both direct and indirect values have current and future expected values. A third component of use value is option value. Option value derives from uncertainty and implies the flexibility to respond to unexpected future challenges. Depending on the articulation of the framework, cultural services may be included in use or option values.

Non-use values are typically composed of existence and bequest values. Existence value refers to the satisfaction felt simply from knowing that something exists, whether or not it is used. Bequest value is defined as the satisfaction gained by individuals from knowing that in the future, others will have the opportunity to enjoy an asset. Endowing a genebank as a trust for future generations (e.g. The Crop Trust) might be viewed as an explicit recognition of bequest value. It has been argued, however, that the existence value of plant genetic resources is appreciated by relatively few individuals. Unlike "charismatic species" such as polar bears (e.g. in Svalbard), plant genetic resources are conserved precisely because they are thought to embody genes and gene combinations of future use to human society through crop improvement.

Years ago, an eminent resource economist admitted that he was "awed by how little economics could contribute to valuation of genetic resources" (Brown 1990). He explained that since most value components do not trade in markets, they have no market prices. Even when only the value components related to use are considered, few are measurable with quantities and observable prices. A genebank collection, as compared to a breeder's working collection, is maintained largely in order to respond to future demand. Thus, the expected future use and option value components of use value are sizeable in a genebank collection. Option value is more difficult to assess empirically than expected future use, which can be calculated from historical records. We do know that option value cannot be negative in sign.

Other aspects of plant genetic resources also contribute to the underestimation of total use value in such calculations. First, plant genetic resources have mixed good properties (Figure 2). Goods can be situated along two axes defined by rivalry over use and ease of exclusion in consumption. Plant genetic resources are public goods that are non-rival, and the costs of controlling their use are high. However, the seed in which they are embodied is a private good that is highly rival with low costs of exclusion. Farmers consume seed as a production input, and no two farmers can plant the same seed—though many can plant the same variety. The type of plant genetic resource, technological and institutional contexts influence the costs of exclusion. Halewood (2013) examines the natural and cultural commons attributes of plant genetic resources that have resulted from the International Treaty on Plant Genetic Resources for Food and Agriculture and changes in information technology. He shows that in the global institutional context, various types of plant genetic resources can be alternatively described as public, private, club and common pool resources.

Second, the commercial value of plant genetic resources may represent a relatively small component of their total use value when markets function poorly. In many developing agricultural economies, farmers obtain seed outside of formal markets, and although there is considerable value in the plant genetic resources they use, they may not sell their harvest. Third, each market-based analysis is generally fixed in time, and projections are based on assumptions that might not be borne out. Tastes and preferences are dynamic. Production shocks occur from which plant genetic resources that are rarely used in crop improvement derive substantial economic value, such as a genetic material that confers resistance to a new pathogen. Finally, since the potential usefulness of any single genetic resource is often highly uncertain, and time horizons for developing products from genetic resources are long, economists generally contend that private investors under-invest in conserving them at the levels needed by society. As a consequence, the public sector has played a pivotal role in conserving these resources and will continue to do so in the foreseeable future.

How do the mixed attributes of plant genetic resources relate to conservation approaches? First, suppose that genetic diversity serves as a proxy for current, future and option values from which society as a whole may benefit—public values. Then, the highest benefit-cost ratio for conserving a plant genetic resource in a genebank pertains where the contribution to genetic diversity is greatest but farmers no longer derive great private value from growing it (Figure 3, segment IV). Where the contribution to genetic diversity is low, no unique traits have been identified in the material (there are substitutes), and farmers currently value the resource little, there may be no great social loss from not investing in either on-farm or genebank conservation (segment III). In cases where farmers derive great value from growing a particular plant genetic resource, there is no immediate need to invest in conservation whether it contributes to diversity or not (segments I and II).

In closing, it is important to recognize that genebanks have multiple functions which are not strictly limited to conservation of plant genetic resources, including the documentation and the provision of scientific information for further research. Further, we are increasingly concerned about the loss of crop wild relatives in particular as we are beset by climate extremes. This would affect our depiction and interpretation of the vertical axis in Figure 3. We might incorporate the prospect of in-situ conservation in reserves by considering changes in land use and opportunity costs associated with exploitation of natural forest, grassland or desert-fringe areas by private actors. Halewood (2013) adds additional layers of value concepts in interpreting the emerging global commons of plant genetic resources for food and agriculture as our capacity to t synthesize massive amounts of data and genetic materials rapidly evolves with new technologies.

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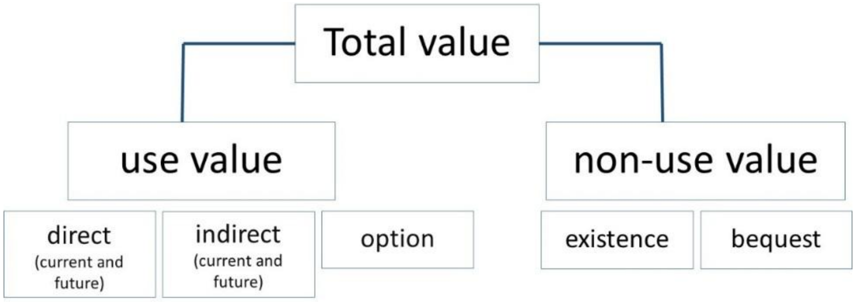

Figure 1. Total economic value

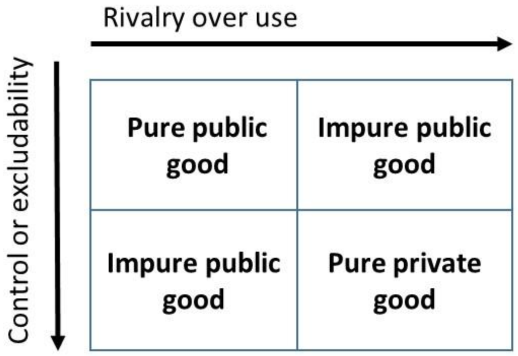

Figure 2. Public, private and impure public goods. Source: Romer 1999.

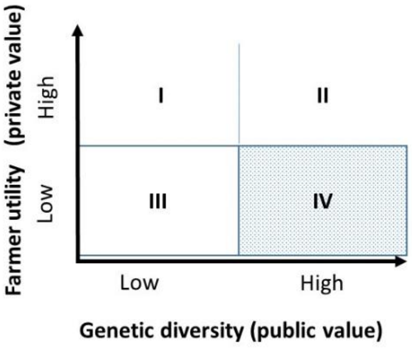

Figure 3. Benefit-cost ratios for conservation. Source: adapted from Smale and Bellon 1999.

B. Measuring crop genetic diversity for social scientists

Vavilov's theory (1926) about the origins of crops initiated decades of research on diversity within crops. Since then, the "science of diversity" has developed into a vast literature that is "balkanized into different disciplines, technical languages and popular understandings" (Brush 2004: 53). As explained by Brush (2004), diversity measurement depends on the disciplinary and analytical perspective. For example, from the crop species standpoint, plant diversity in any farming system is distributed between species, within species, within a population of species, and between populations of the species. Shifting to the farmer's viewpoint, diversity includes well-known plant types that can be obtained from a neighbor but also the novel types (such as modern varieties) found in the nearest market or offered by the extension agent. On a social scale, diversity is distributed among plots within the farming household, between households, among communities, regions and nations. Geneticists examine the variation and allele frequency in samples of the plant as cultivated by farmers, stored in collections, or found among wild relatives in natural reserves—including qualitative and quantitative traits, genetic markers and gene sequences. Ecologists are primarily concerned with spatial distributions of plant populations across a landscape. Anthropologists record the names and descriptors, or "folk" taxonomies, that farmers use to differentiate plant populations; agronomists study variability in functional traits such as flowering dates, plant height, and yield.

Here, we mention the full range of perspectives because there are important linkages and complementarities between plants managed *ex situ* and *in situ*, in reserves or on farms. Diversity indices or indicators based on any of these perspectives can be used as proxies for ranking the potential value of candidate plant populations for conservation when little is known about the monetary, cardinal value of benefits (Krutilla 1967; Figure 3, Section II.a). Greater public value might be associated with genes that are locally common but globally rare, assuming that these carry both the greatest potential for adaptation and scarcity value (Figure 2, Section II.a). In Nepal, Gauchan et al. (2006) proposed to conserve rice landraces that farmers, conservationists and plant breeders all ranked as important for future crop improvement. Conservation criteria included rare genes or gene variants, genetic diversity or heterogeneity, and adaptive traits.

Applied economists have given some attention to the *concept* of diversity represented by indices (Table 1). Meng et al. (1998) classified concepts according to "apparent" (agro-morphological characteristics) vs. "latent" (either molecular, or pedigree characteristics) diversity, and "spatial" as compared to "temporal" diversity. Spatial diversity indices drawn from the ecological literature have been among the most widely used, including measures of richness (e.g. Margalef), evenness (e.g. Pielou) and proportional abundance (e.g. Shannon or Simpson). Temporal diversity, or diversity in time (Duvick 1984) refers to the turnover of plant populations in breeding programs or in farmers' fields. Brennan and Byerlee (1991) proposed variety age (years from release) to measure this concept. When we use farm survey data as the basis of our analysis, the index of variety age and simple ecological indices of richness and relative abundance have strong overlaps with social science (e.g. the Herfindahl index) and are more easily interpreted in terms of farmer behavior compared to indices based on latent diversity. Indices of latent diversity, particularly when based on molecular or biochemical data, are likely to provide more information and explanatory power when analyzing genebank collections. However, finding evidence of polymorphism in molecular data is not the final answer because it does not necessarily relate to adaptive or evolutionary potential. Nor does the absence of it imply a lack of potential. The degree of polymorphism also depends on the species (Grimanelli, in Meng et al. 1998). Coefficients of parentage and pedigree analyses have often been applied, although these make assumptions about selection as compared to crossing, mutation, and genetic drift. In any case, in an economic analysis, it is crucial to be able to link genotypic to phenotypic variability for a trait of economic importance.

Taxonomic or phylogenetic trees have been employed to measure diversity both among and within species by biological scientists, but also be economists. Weitzman (1992; 1993) proposed a distance index based on maximizing diversity among the surviving members of a set, applying it to the study of cranes. He related his index to the Shannon index. The conservation goal associated with his index was to avoid redundant characteristics. Solow, Polasky and Broadus (1993) discussed an index that minimizes the distance between the surviving and extinct species, with the conservation goal of preserving a representative sample. The approach proposed by van Treuren et al. (2009) to optimize a genebank collection based on assigning weight to branches of a diversity tree is important to highlight in the context of the work described above, given its direct relevance for genebanks.

Solow, Polasky and Broadus identify three properties that should be associated with an index of diversity: 1) diversity should not be decreased by adding another species (monotonicity); 2) diversity should not be increased by the addition of an identical species (twinning); and 3) diversity should not decrease with a clear increase in the distances between species. The valuation approach of Nehring and Puppe (2002) depends on the phylogenetic tree, which has these features. As a counterexample, coefficients of parentage based on pedigrees of wheat varieties, which include backcrossing and selections of the same progenitor, do not have these properties.

Finally, Baümgartner (2007) emphasized that the measurement of diversity relies on prior value judgements about the role of diversity in an ecological-economic system: "the question of how to measure species diversity is intimately linked to the question of what is species diversity good for" (2007: 12). Similarly, Brown and Goldstein (1984) argued that if we have no way of knowing which species [or sub-species] will be important in the future, then relative importance in the short run is a fundamental parameter to consider in the decision to save or permit extinction. Further, they emphasized that how we choose to use, improve or alter plants determines which substitutes are more valuable today. Thus, science and technology choices affect our crop diversity choices.

Table 1. Examples of criteria to consider when choosing an index to measure diversity within crops.

Crop reproduction	Farming/breeding system	Diversity concept	Level or scale	Conservation goal	Data used to construct index
Self	Modern	Latent	Plot	Rarity	Biochemical
Cross	Traditional	Apparent	Household	Heterogeneity	Molecular
Vegetative	Mixed	Spatial	Village	Adaptation	Agro-morphological
	Microecosystem	Temporal	Eco-region		Pedigree
	Ex situ-in situ		Global		Ecological

Adapted from Smale 2006. Note: Table should be read by column, but not by row.

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III. Economics of conserving the plant genetic resources in genebanks

Considering the breadth of sources of value that can be ascribed conceptually to plant genetic resources, the documentation of these values is remarkably narrow. We synopsize some of that literature in this section, citing some key references.

A. What is the value of genebanks in crop improvement?

Findings. There is ample evidence that the continuous release of improved varieties by plant breeding programs has brought economic returns that far outweigh the costs of investment. Most of these net benefits have been generated by publicly-funded institutions. Society as a whole and consumers especially have benefited in the form of lower food prices, particularly in less advanced economies where consumers spend a larger share of their budget on food. Economists have repeatedly demonstrated that rates of return to investment are high (often within the 40-60% range; for example, see reviews of this literature by Alston et al. 2000; Evenson 2001; Evenson and Gollin 2003; Raitzer and Kelley 2008; Renkow and Byerlee 2010). Research on farm-level adoption and impacts of improved varieties is also voluminous. A smaller set of studies explores the effects of the certain categories of plant genetic resources (e.g. landraces), variety diversity or genetic diversity on yield or yield risk (e.g. Widawsky and Rozelle 1998; Smale et al. 1998, Smale et al. 2008; Di Falco and Chavas 2009).

Among the studies assessing the economic impact of using plant genetic resources in crop improvement, we know of only a handful that sought to relate productivity changes in farmers' fields explicitly to genebank accessions. Evenson and Gollin (1997) consulted the genealogies of rice varieties released by national programs and the International Rice Research Institute (IRRI) from 1965 to 1990, correlating productivity changes with changes in IRRI programs in an econometric model. They estimated that adding 1,000 cataloged accessions was associated with the release of 5.8 additional varieties. Assuming a 10-year lag for variety development, and a 10% discount rate, they calculated that these new accessions generated a present value (in 1990 dollars) of $325 million. A similar study by Gollin and Evenson (1998) focused on India.

Johnson, Pachico and Voysest (2003) identified the share of bean varieties released in Latin America that contain material from the collection of the International Center for Tropical Agricultural (CIAT), and used variety genealogies, combined with data on variety yields, to calculate the value contributed and received by each country via the genebank's distribution of materials. They estimated that 49% of bean area in Latin America was planted to varieties associated with CIAT and the genebank in 1998, with an incremental value of production to CIAT-related varieties of USD 177 million. Cumulated from 1970 to 1998, the authors estimated the value of increased production at USD 1154 million.

Robinson and Srinivasan (2013) estimated the benefits of a high-yielding cassava variety (Kasetsart 50) in Southeast Asia and a high-yield potato variety (Cooperation 88) in China, linking these explicitly to specific genebank accessions and the challenges addressed by the utilization of these accessions. They found aggregate economic benefits nearing USD 100 million from the diffusion of Kasetsart 50, as well as poverty reduction—arguing that these would not have been achieved without the use of the genebank. Benefits accruing to Cooperation 88 in China were predicted to reach nearly USD 500 million per year, with poor people earning the largest share. Diffusion also stimulated the processing industry because the potato was more suitable for table and chip consumption.

Methods. The compendium of methods used to assess the economic benefits of productivity gains in agriculture is Alston, Norton and Pardey (1998), although methodological challenges continue to be debated and refined. Partial equilibrium analysis, economic surplus methods and econometric approaches are commonly used. Econometric models of yield response and production functions may be estimated, incorporating diversity indices (see II.B.) as explanatory variables. Pedigree data and genealogies have been employed, in combination with data on variety transfers, or with farm survey data or secondary data measured at a district or regional scale. When pedigree data were used, simple Mendelian rules of inheritance were commonly assumed (each parent contributes 50% of genes). Forms of hedonic analysis were also applied to explore the value of genetic resource attributes.

Limitations. First, the literature on crop productivity documents the value of plant genetic resources used in plant breeding for commercial agriculture. For example, the value of crops not often used by breeding programs, about which relatively little scientific research has been conducted (sometimes referred to as “neglected and underutilized crops”), is not included. Semi-subsistence farmers, or farmers in remote areas who do not sell their crops are not represented. Nor are crop wild relatives, unless they were included as ancestors in the breeding program (e.g. Dresigacker et al. 2008). Second, analysts face challenges when estimating the share of the productivity gain that is attributable to genetic advance. The genetic component is only one of many factors that affects yields in farmers’ fields. Third, even when genetic gains can be estimated, apportioning these among the progenitors of the variety involves “rules of thumb.” For example, Mendelian rules of inheritance ignore the effects of selection. The Mendelian rule of inheritance assumes that each parent in the pedigree of a variety contributes equally in each generation, ignoring both the effects of random genetic drift and the effect of selection by breeders from crosses for traits of economic interest. Both the processes of attributing yield gains in farmers’ fields to their genetic component and apportioning the genetic component to individual ancestors are data-intensive. These require trial data, accurate genealogies, and extensive farm survey data with variety-specific information on areas and production (see summary in Smale 2004).

Future studies of the value of genebanks in crop improvement will need to clarify the direct linkage between a genebank accession and a productivity outcome, using genetics analyses, hedonics, or other recommended approaches. Gollin (pers.comm.) notes that the results obtained in his 1997 study should be considered with caution because the authors were not able to link the acquisition of landrace accession causally to variety release. The study by Robinson and Srinivasan (2013) is detailed with respect to the pedigree of the cultivars and direct linkage to the genebank, but not with respect to attribution and apportionment of value.

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B. What is the value of large collections?

Findings. Spurred by debates over whether the expansion of genebanks was justified (see Section I), Gollin, Smale, and Skovmand (2000) developed a model that portrays the relationship between genebank size and the search for new traits. They drew three major conclusions. First, there are occasional situations in which the chances of finding a trait are slim and the economic payoff to discovery is great. These are the situations from which large collections, like those of the International Center for Maize and Wheat Improvement (CIMMYT), derive their value. The threat of large economic problems in production of major food staples (such as wheat) therefore justifies large global collections.

For example, Russian wheat aphid spread from its center of origin in the Caucasus and Central Asia to a number of geographical areas, including the US, South Africa, parts of the Southern Cone of Latin American, and North and East Africa, but searches of advanced lines at USDA revealed the near absence of resistance in materials originating outside Central Asia (Robinson and Skovmand 1992). Applying their model to data assembled at CIMMYT about search costs and areas planted to potentially susceptible wheat, Gollin, Smale, and Skovmand (2000) simulated various scenarios to represent a range of adoption, cost and benefit outcomes. Across the scenarios, the range in discounted, expected net benefits was huge—from $1.2 to 165.8 million—depending most on the time lag from discovery of resistant material to adoption. When the time lag is as short as seven years, the value would justify a search that is larger than the number of landraces in the CIMMYT genebank.

In a second example, a trait of value is found in a tiny subset of the world's collection of genetic resources—among landraces from a particular geographic location. Searching a sample of Iranian landraces from the region of pest origin for resistance to Russian wheat aphid increases net benefits substantially in all cases, revealing the value of specialized knowledge and passport information. Further, although such sub-collections may be searched rarely, there are reasons for storing them “unused” for years.

Third, the observation that plant breeders search their own collections more frequently than they demand unimproved materials from gene banks in no way implies that the latter have no value. This was demonstrated by the case of Septoria leaf blotch. Despite the superior distribution of resistance among accessions of emmer wheat, the authors found that searching only within the collection of bred materials is optimal due to relative costs of search and trait transfer.

The examples presented by Gollin, Smale and Skovmand (2000) suggest that payoffs from genebanks may be modest in the short-term but great in the long-term—when both predictable and unpredictable challenges must be addressed—hinting at insurance and option values of genebank accessions.

Methods

The authors adapted the search theory framework used previously by Evenson and Kislev (1976) to model sugarcane breeding and by Simpson, Sedjo and Reid (1996) to model the search for pharmaceutical resources. Using numerical methods and Monte Carlo simulations, they applied the model to data from searches for new sources of pest and disease resistance by the CIMMYT wheat genebank and the Genetic Resource Information Network (GRIN) of the National Small Grains Collection at the US Department of Agriculture.

Economic principles dictate that a search should proceed until the costs of searching an additional accession outweigh the expected gains from search. The expected gains are defined as the product of: (1) the discounted stream of benefits from finding the trait; and (2) the change in the probability of success from searching one more accession. The probability of success is the chance of finding an accession with the desired trait in a search of a given size.

The probability of finding a targeted trait is sensitive to the frequency distribution of the desired trait. This distribution depends on the size of the collection and the distribution of the trait in the underlying plant population. The rarer the source of resistance, the larger is the size of search that is needed to find it. As in the analyses of the benefits of crop improvement described in II.A., the discounted stream of future benefits depends on many factors, including the time required for plant breeders to transfer effectively the new source of resistance into the variety, the time needed for the improved variety to pass any regulatory hurdles before release, and the time lag between release and actual use by farmers. Magnitudes depend on the size of the economic “problem” (how many hectares are affected by the pest or disease) and the popularity of the new variety among farmers (how many hectares are planted). The plant breeding process is known to be a race for the development and release of varieties with novel sources of genetic resistance to evolving strains of pests and disease. Thus, the time value of money is an important parameter in projecting benefits.

Fixed costs in this framework are affected by the type of genetic material and the technology of searching for and transferring the new source of resistance, but Gollin, Smale and Skovmand (2000) found that variable search costs did not change substantially with the size of the search. Thus, they assumed all costs to be variable with a constant average search cost equal to a constant marginal cost.

Limitations. A limitation of this study is that the authors were not able to examine the overall distributions of resistance across numerous traits, search costs, and benefits streams in order to draw more general conclusions about the optimal size of a genebank. If applied to larger databases on trait distributions, frequencies of search, benefits and costs distributions, the search model could be utilized to answer that question. Also, the model was applied to problems of pests and disease, but might be adapted to study problems of abiotic stress. Further, since that study was conducted, technological changes have affected the tools that might be used by genebank managers to find and confer sources of genetic resistance, with implications for costs. The model could be used to demonstrate the value of using more advanced genetic information, such as genotyping, in search processes. Gollin, Smale and Skovmand study (2000) did not estimate the expected value of an additional gene bank accession. This question, discussed next, is relevant for the decision to expand a collection, discard an accession, or restrict the use of an accession through imposition of property rights.

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C. What is the value of an individual genebank accession?

Findings. The important role of plant genetic resources in the historical development of world agriculture has been documented in general terms (e.g. Cox, Murphy and Goodman 1988), but the perception that individual plant genetic resources have great commercial value seems to be based on anecdotal cases in which substances identified in wild, indigenous plants generated large profits for pharmaceutical companies. Economists have cast doubt on the likelihood that the willingness to pay for these resources in commercial use would be sufficient to promote the conservation of their habitats (Simpson, Sedjo, and Reid 1996; Koo and Wright 2000a)—suggesting that the expected value of any single plant genetic resource is also likely to be too small to justify restrictions on its use.

There are many instances in which a single plant genetic resource has proved to have large commercial value by conferring a specific trait, but these cannot be generalized. Well-known examples include the *Rht* 1 and *Rht* 2 dwarfing genes, which were bred into modern wheats via Norin 10, and whose original source was named Daruma, a Japanese landrace. Sr2, the gene known as “Hope,” conferred resistance to devastating stem rust and was found in a genetic material named Yaroslav Emmer. Documented examples among crop wild relatives include the wild tomato and sunflower (Iltis 1988; Hunter and Heywood 2011; see subsection g, Tyack and Dempewolf 2015).

Generally, in the process of plant breeding, numerous genetic resources are continually shuffled and reshuffled in an uncertain search for traits that must be well expressed in a crop variety destined for highly differentiated conditions of production. Economically important traits are distributed statistically across plant genetic resources, with varying likelihood of useful levels. The traits demanded by societies, such as resistance to plant pests and diseases, and quality attributes preferred by consumers, also change frequently in response to environmental stress and economic changes. Breeding products (crop varieties) contain many “ingredients” that are also genetic resources and these products are in turn combined with others to produce the next variety. The marginal contribution of the last resource used may be slight.

The uniqueness of an individual accession is also a factor. The same trait may be apparent to one degree or another in multiple plant genetic resources. Even when rare in a given collection, accessions carrying useful traits may be duplicated among seed samples (accessions) in multiple collections. Seed samples of the same genetic resource may also be found in more than one genebank collection, in more than one political jurisdiction. Even when rare in a given collection, accessions carrying useful traits might be duplicated among seed samples (accessions) in multiple collections.

To say that the expected value of an individual accession may not be “enormous” does not imply that its expected benefits do not justify the costs of conserving it. Because many factors outside the control of genebank managers influence the magnitude of benefits from finding and transferring traits into crop varieties, predicting the benefits of conserving an individual accession, and deciding whether to keep or discard it based on economics principles (equating marginal expected benefits to marginal expected costs) is not as easy as would seem.

To our knowledge, the work by Zohrabian et al. (2003) was the first and remains the only published example of an attempt to estimate the marginal value of an accession. The authors found that the expected marginal benefit from exploring an additional unimproved gene bank accession in breeding resistant varieties of soybean, while small, more than covered the costs of acquiring and conserving it. They found an expected benefit-cost ratio in the range of 36 to 61 for investing in an additional accession to prevent losses from a single pest. In the terminology of Koo, Pardey and Wright (2004), the lower-bound benefits from utilizing a marginal accession were higher than the upper-bound costs of acquiring and conserving it in the US. Findings justified the expansion of the US soybean collection.

Methods. The approach of Zohrabian et al. (2003) drew on the search theoretic framework described in III.B and used a maximum entropy approach to model the distribution of a quantitative trait when data are sparse. The model was applied to the search for resistance to race 3 soybean cyst nematode in the US soybean collection. The expected benefit from testing an additional accession was calculated as the expected yield losses prevented multiplied by the area affected, with an adoption lag of ten years. Marginal costs included acquisition of the accession, its conservation and evaluation. The authors used the decision rule of Koo, Pardey and Wright (2004): if the lower-bound benefit from utilizing a marginal accession is higher than the upper-bound cost, the expansion of the collection is justified.

Limitations. The analysis involved only a single trait, although individual accessions may be useful in the search for more than one trait. Benefits included only estimated yield savings from genetic resistance, but positive externalities would also be likely. Application today of the maximum entropy approach also merits review. The authors note that they assumed no passport information was available about accessions, though conditional probabilities could be calculated in order to estimate the value of tagging genebank material with information. Is the question of the value of an individual accession still important?

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D. What is the value of accession information?

Findings. When some of the work by economists on the genebank management began, the lack of useful data about accessions was cited as an obstacle to greater utilization of accessions in plant breeding and scientific research (Wright 1997). In particular, evaluation data are of great value to plant breeders seeking to improve traits related to biotic or abiotic stress. Koo and Wright (2000) asked when genebank managers should decide to evaluate genetic materials and whether new technological tools might change this decision. Most genebank managers could not search ex ante (before problem onset) for traits, choosing to search ex post (after problem onset) due to funding constraints. Employing the example of disease infestation, they show that the benefit of ex ante evaluation is largest when the likelihood of disease infestation is at an intermediate rather than minimum or maximum level. When a disease is rare, the cost of searching today is great relatively to the expected present value of future benefits. When it is expected to occur soon, it will be evaluated in any case and the importance of timing is reduced. Examples of this situation include breeding for nonspecific resistance to the rusts of wheat. The marginal benefit of technology breakthroughs that reduce the time spent evaluating for resistance traits is larger when the development process begins earlier—favoring ex ante evaluation.

Based on a survey of requestors of genetic materials from the US National Plant Germplasm System (US NPGS), Day-Rubenstein, Smale and Widrlechner (2006), tested the effect of accompanying data on the share of seed samples reported to be "useful." They found that accompanying data improved the chances that a sample received was used within a five-year period in a breeding program, evaluated, or in other ways. A survey of users of the *Musa* International Transit Center revealed that receipt of ITC materials allowed them to based their research design on previous results, saving time and resources (Garming et al. 2010). Even so, a major weakness of the ITC was still perceived in the area of information about the germplasm.

Methods. The theoretical model proposed by Koo and Wright (2000b) is mathematical. The analyses of the US NPGS was based on two data sources: 1) a summary of all NPGS distributions from 1990 to 1999 for 10 major crops; and 2) a survey of US and international requestors of NPGS germplasm samples from

1995 to 1999. Access to both of these enabled aggregation from sample estimates to totals and regression analysis. The analysis of the *Musa* ITC involved numerous activities, including the compilation of data on: 1) the diversity and health status of germplasm held in the collection; 2) shipments of germplasm; 3) ITC users and intended use; 4) a user survey; 5) a survey of literature referring to ITC accession codes, and 6) an analysis of costs of conservation and distribution.

Limitations. The model by Koo and Wright (2000b) considers only a small aspect of genebank decision-making—the evaluation of resistance based on single genes. Although their model is not empirical, a testable hypothesis might be motivated by their analysis. New technologies have been developed for evaluating traits, with implications for the expected benefits and costs of genebank functions. The US NPGS survey was repeated in 2017, using SurveyMonkey rather than a mail survey. Response rates for both surveys were 35-40%. However, the question on accompanying information could not be included in 2017 because of length restrictions imposed by the US government. The question in the original survey did not specify the type of information provided. CGIAR databases, combined with focused user surveys, might be used to explore the relationship of various types of information to requests for seed samples and subsequent utilization. The survey of the Musa International Transit Center has also been repeated. Garming et al. (2010) suggest applying a transactions cost approach to value the extent to which the ITC facilitated research, virus indexing, or obtention of desirable germplasm.

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E. What is the value of germplasm flows from collections?

Findings. Studies by Evenson and Gollin (1997) and Johnson, Pachico, and Voysest (2003), noted above, and Smale et al. (2002) documented the reliance of individual countries on genetic materials obtained from numerous countries via gene banks and nurseries of the CGIAR. For example, of the 18 countries studied by Johnson, Pachico and Voysest (2003) in Latin America, 11 received over 70% of the genetic material in their released varieties from other countries. Only 8.5% of 1709 rice varieties studied by Evenson and Gollin (1997) had been developed entirely from own-country progenitors.

Fowler, Smale and Gaiji (2001) showed that developing countries were net recipients of germplasm samples from six of the CGIAR genebanks (CIAT, CIMMYT, ICARDA, ICRISAT, ILRI, and IRRI). More than 80 percent of the materials that had been distributed by that time, which totaled about one million samples, went to organizations in developing countries. The vast majority of these were universities and national agricultural research systems. While transfers from gene banks were substantial, the number of transfers of breeding lines through nurseries was much greater. Galluzzi et al. (2016) analyzed 25 years of distribution data from the CGIAR. They found that developing and transition economies dominated the flows, utilizing transferred germplasm within their public agricultural research systems and development programs. They argued for enabling the continuation of non-monetary benefits from international access to germplasm.

User surveys generally contradict the notion that genebanks are rarely used. The US NPGS survey indicated higher rates of direct utilization in plant breeding than had been suggested in earlier studies, secondary use through sharing within and outside respondents' institutions, and proportionately higher use rates among respondents in low- and middle-income countries (Smale and Day-Rubenstein 2002). Within the brief five-year period covered by respondents, 11 percent of germplasm samples received had already been incorporated into breeding programs. Another 43 percent were still being evaluated, and 19 percent were reported as useful in other ways, leaving 28 percent categorizes as "not useful." Breeders surveyed by Brennan et al. (2009) in Australia reported that they had made an average of five requests per year from the Winter Cereals Collection over the preceding five years. Breeders in general judged the material they obtained as "useful," "very useful," or "essential" in enabling them to expand the range of genetic materials they needed. It is noteworthy that the use rates calculated within such short time frames understate overall use rates.

Garming et al. (2010) found a continuous increase in the number of accessions available for distribution and in the number of samples distributed from the *Musa* ITC. The ITC had distributed germplasm to over 100 different countries since its foundation. For a number of countries, the ITC is the only source of superior Musa germplasm. In some cases, such as in countries with strict quarantine, survey respondents reported that they could not have conducted their research at all without the ITC since it was the only legal source of germplasm.

A recent analysis by Khoury et al. (2016) underscores the importance of international collaboration in genetic resource conservation by demonstrating that on average, 69% of national food supplies are derived from crops originating outside the nation. Dependence on "foreign crops" has increased significantly over the past half century—even in countries with high indigenous crop diversity. A brief by Vernooy and

Clancy (2017), which synthesizes the findings of eight country studies, also demonstrates the interdependence of countries on externally-provided plant genetic resources for their food staples.

Methods. The early studies relied on detailed documentation of germplasm distributions over time from CGIAR centers, combined with genealogical information. The analysis by Fowler, Smale, and Gaiji also consulted 15 detailed case studies on germplasm exchanges from 1972 to 1990/91 and data from FAO's State of the World's Plant Genetic Resources for Food and Agriculture (1998), which was based on 154 country reports. Other aspects of the user surveys are noted in III.d. Khoury et al. (2016) combine FAO databases with published data on crop centers of origin.

When implementing user surveys, researchers have often considered the application of stated preference methods such as contingent valuation or choice experiments but to our knowledge, these have been applied only in the case of Tyack and Ščasný (2018). Tyack and Ščasný estimated the willingness-to-pay for conserving additional crop varieties in the genebank for ten years by the Czech population as a whole and the population in the agricultural region of South Moravia. A major finding of their research is that Czechs who are provided with information about the meaning and importance of crop diversity would be willing to pay a total of $68 million USD crop conservation during the coming decade. This amount represents about 4.5 times more than current conservation costs.

Limitations. Of these studies, only Johnson, Pachico and Voysest (2003) and Evenson and Gollin (1997) reported economic values and these were simply estimated. A number of case studies demonstrating co-dependence were prepared using the SINGER database (now part of Genesys) of the Systemwide Genetic Resources Program, now the Genebank Platform), but none of these studies placed an economic value on the flows. User surveys have documented use of resources conserved in genebanks, which has implications for use value, but have not estimated economic value per se with the exception of the study on willingness-to-pay by Tyack and Ščasný (2018). Experimental analysis or auctions may also be feasible with users.

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F. What are the costs of genebank conservation?

Findings. The costs of conserving accessions in gene banks are relatively easy to tabulate compared to their expected benefits. The landmark studies compiled by CGIAR genebank managers and Koo, Pardey and Wright (2004) confirmed the relatively low costs of maintaining large collections of some major crops. They provided realistic resource projections for an endowment under the Crop Trust to support globally important collections in perpetuity.

The analysis showed that the present value of conserving and distributing an accession into perpetuity varied significantly by crop, reflecting in part its reproductive biology. For example, the costs of conserving an existing accession of maize was estimated at $141 in 1996 dollars with 6% initial regeneration, compared to only 10 for an accession of wheat. New accessions of maize and wheat cost more. Comparable figures for wild groundnut at ICRISAT were $19 for an existing accession and $121 for a new accession, $28 for cultivated rice and $49 for wild rice. At ICARDA, the costs of conserving a cereals accession into perpetuity, in 1998 prices, was estimated to be $27, as compared to about $30 for chickpea, $31 for lentil, and $34 for faba bean. At CIAT, conserving an accession of beans into perpetuity was estimated to cost $13 in 2000 prices with a 6% regeneration, compared to $23 for an accession of forages. Wages, plant maintenance and operational costs also differ with the location of the physical plant.

Other cost studies of national genebanks have been implemented (see volume edited by Virchow 2003). These included a study on the conservation of crop genetic resources in Kenya (Andama and Wandera), India (Saxena et al.) and Colombia (Moreno et al.). Like Koo et al. (2004), these studies reveal variation in conservation cost by method of conservation, crop, and genebank location. Garming, van Den Houwe and Roux (2010) also noted the important share of collection costs in the national conservation effort of nations located in centers of origin and diversity.

In 2010, Horna and a task force of the Systemwide Genetic Resources Program built on work of Koo, Pardey and Wright (2004) by developing a decision-support tool aimed at enhancing the cost-effectiveness of collection management (Horna et al. 2010). The authors found again that the reproductive biology of the crop is a major determinant of the relative costs of operations, and in particular the cost of regeneration. Characterizations and regeneration were often the most resource-intensive operations for materials that are seed-propagated. The average costs of some operations are similar across materials (such as distribution and seed health testing, which follows a formula) but distribution costs were higher than expected and particularly so if shipping was done by courier. Import clearance was a large component of costs. They concluded that molecular characterization to prevent duplication or for pre-breeding purposes added value to the collection.

Schreinemachers, Ebert and Wu (2014) applied the decision-support tool to an analysis of the World Vegetable Center (AVRDC) collection. They found that seed regeneration, seed processing, characterization and seed dissemination where the four most expensive operations of the genebank. Storage itself represented only 17% of the cost.

Methods. The theoretical approach of Koo, Pardey and Wright (2004) is cost minimization. If, as they showed, the costs of conserving an accession are lower than any sensible lower-bound estimate of benefits, undertaking the expensive and challenging exercise of benefits estimation is not necessary to justify its conservation. The methodology of Horna et al. (2010) followed the approach of Koo et al. (2004). The decision support tool was an excel file used to store detailed data on input use and related costs per operation. The file could be used to calculate cost reports by categorizing total costs as capital, variable, or quasi-fixed. Three types of outputs were then generated: 1) costs per input category, genetic material and operation; 2) total and average costs per input accession; and 3) a graphic representation of the distribution of total costs per input type. Two reports could be produced: a report of the per accession cost of conservation and distribution, and report of the total annual and in-perpetuity cost of conserving and distributing all existing genebank accessions.

Limitations. For further work, Horna et al. (2010) recommended applications of the tool to identify potential cost savings, addition of an input sheet for entering performance indicators, examination of how costs can be structurally linked to performance indicators, and econometric analysis as a means of evaluating the system. Initially, their work was designed to relate performance indicators to cost in order to evaluate cost-effectiveness. Data needs, and lack of consensus on performance indicators at the time that the decision-support tool was developed meant that although simple in concept, the goal of evaluating cost-effectiveness was difficult to attain within the project life-cycle. One possible conceptualization of performance indicators was suggested in a monograph by Calles et al. (2007). Initial attempts at defining performance indicators are also included in an appendix to the Horna et al. (2010) report. As noted above, the way that molecular characterization "adds value" to a genebank might be investigated in specific cases. An expert analysis was also conducted by Hawtin, Shands and MacNeil (2011) for the Consortium Board of Trustees. The CGIAR Genebank Platform is currently reviewing work on costs of conservation (2017-2019).

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G. What is the economic value of crop wild relatives?

Findings. Crop wild relatives often contain genes that are no longer found in cultivated crops, widening the diversity of the gene pool and contributing potential for plant breeders to address particular challenges. The habitats where crop wild relatives often survive are vulnerable to changes in use of land and forests for commercial purposes, with varying opportunity costs. On the other hand, only wild bananas propagate with seed. That makes it easier to store reproductive material long-term. Commercial banana cultivars have three sets of genes (triploid) rather than two, produce no seed, and must be stored under challenging *in-vitro* conditions.

Tyack and Dempewolf (2015) summarized the findings of a number of studies that estimated the economic value of crop wild relatives in crop improvement. Annual benefits range from 8 mill to 165 bill USD (2012), for activities ranging from providing genes from wild tomato to contributing to "the world economy."

Methods. Methods utilized in early studies were not always clearly stated. Tyack and Dempewolf (2015) review these, but also propose a new conceptual framework for analysis. They argue that previous studies focused narrowly on production value resulting from the introgression of wild genetic material. First, they suggest researchers consider the cost reduction due to reduced use of pesticides and herbicides, or nutrients such as phosphorus or nitrogen. Second, they recommend efforts to measure positive externalities, such as reduced emissions of carbon dioxide from lower use of fertilizers, pesticides, herbicides, and irrigation. Carbon savings have a dollar value in carbon markets. Reduced threat of habitat loss, because of less need for water, is another benefit that might be valued. Health benefits from reducing toxic substances in runoff are another benefit though could be measured. The long-term cost of fertilizer subsidies, as compared to other means of increasing productivity, is mentioned with reference to programs in Sub-Saharan Africa.

Limitations and directions. The conceptual framework of Tyack and Dempewolf (2015) might be adapted and applied, although this would require extensive data to be tenable. The authors note that the estimates reported in the literature they reviewed was based in most cases on "back-of-the-envelope" calculations. In a number of cases, the entire value of the increase in the yield or quality of the finished variety was attributed to the wild crop relative with the known trait. The authors cite the study of Prescott-Allen and Prescott-Allen (1986) as seeking to apportion the value more carefully by source, also recommending a study by Hein and Gatzweiler (2006) on wild coffee that took costs into consideration.

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IV. Future directions

The synopsis provided here reveals that much of the literature on genebank value (benefits and costs) is dated. On costs, new applied research is underway by Horna and CGIAR genebank managers. With regard to benefits, the brochure by the Crop Trust hints at some new directions.

These include documenting the value of accessions distributed directly to farmers. Direct use is the usual option for forages and trees, which are not highly bred. Superior lines are selected and distributed to farmers. There are some outstanding examples of direct distribution of genebank materials to farmers (Major 2018; Hawkes, Maxted and Ford-Lloyd 2000; King 2003). Westengen et al. (2018) discuss different approaches to linking genebanks and farmer seed systems, including: 1) reintroduction; 2) emergency seed interventions; 3) community seed banks; 4) participatory plant breeding; 5) variety introduction; and 6) integrative seed system approaches. There are also numerous examples of restoration of materials to farming areas beset by natural or human-made disaster (Varma and Winslow 2005). Valuing direct use does not require apportioning value by ancestry. Analysis of observational data or stated preferences collected in surveys might be considered, depending on whether market prices are available.

Another direction is economic analysis of genetic resource policy impacts. Gotor and Caracciolo (2010) used an econometric framework applied to data provided by IRRI, supported by key informant interviews, to investigate the effects of the In-Trust Agreements on germplasm distributions. Their results were consistent with the hypothesis that there was a switch in distributions of materials before and after the time that the In-Trust agreements were enacted (pre- and post- 1994), but given the sample data at hand, they were unable to draw conclusions regarding the value of the material held In-Trust because of the policy change. Visser et al. (2000) estimated the costs of bilateral transactions, concluding that the transactions costs that would have been involved in negotiating all of the transfers that are facilitated by the multilateral system would have been prohibitive, and acceptable only for a very restricted number of industrial, medicinal, and ornamental crops. Noriega et al. (2013) discuss how the International Treaty has affected the CGIAR. A recent review by Halewood et al. (2018) discusses the impact of new genetic technologies, and how their equitable, international use will require new institutional forms and partnerships. There may be a way to formulate and test related hypotheses.

The changing structure of diets worldwide has led to concern about the “triple burden of malnutrition”, which refers to undernutrition, micronutrient inadequacy, and obesity. Research has indicated that climate change reduces the micronutrient availability in some food staples, such as rice (Washington Post May 23

2018). Biofortification is one means of enhancing micronutrient content in varieties grown by farmer-consumers living in remote areas. Linkages between the diversity of sources in genebank collections that can be tapped to breed for biofortification and diet outcomes have not been adequately explored.

Finally, other values have scarcely been touched by the literature. Indirect values, such as those related to ecosystem function and habitat preservation, have been claimed but not documented. Xepapadeas et al. (2014) is the only example we have found where insurance values have been estimated. The authors develop scenarios corresponding to "trigger events" that could negatively affect production of food staples and be addressed by utilization of the Greek genebank. They conclude that insurance values exceed current operating costs.

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