

PLANT GENETIC RESOURCES FOR FOOD AND AGRICULTURE IN SITU AND EX SITU: WHERE ARE THE GENES OF IMPORTANCE FOR FOOD SECURITY LIKELY TO COME FROM?

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1. ABSTRACT

This paper approaches the questions of the scientific basis for the sole reliance on existing genebank accessions, and the continuing need for the conservation and collection of *in situ* genetic resources. It relates to the negotiation in progress in the inter-governmental forum of the FAO Commission for Genetic Resources for Food and Agriculture for the revision of the 1983 International Undertaking on Plant Genetic Resources for Food and Agriculture. The surveys presented here suggest that the first phase of genebanking has been marvelously successful in collecting and preserving a broad range of diversity of cultivars and wild relatives of the major food crops, but collection needs remain. Dynamic (as on-farm) and static (as serial increases in greenhouses) genebank strategies have both been proposed for the maintenance of diversity, but the relative costs and benefits of both approaches have yet to be assessed. There is a concern about loss of genetic diversity, especially in static genebanks, through genetic drift over serial increase cycles, genetic bottlenecks due to small sample sizes, and accumulation of deleterious mutations. Consequently, over the long-term, continuing germplasm collections from centers of diversity would be a wise strategy to regenerate the natural diversity in *ex situ* collections, assuming that these collections persist. Ideally, the world would preserve its genetic diversity through a coordinated multi-national effort involving a combination of core collection strategies, short- medium- and long-term static and dynamic genebanks, periodic recollections to maintain genetically variable germplasm, and habitat preservation.

The science and policy of these questions are strongly linked, and policy must be addressed as well to come to agreement on revision of the International Undertaking. A movement towards farmers' rights, costs for unimproved plant genetic resources for food and agriculture, and potential huge costs for funding a global Plan of Action without an appreciation of significant existing contributions of the "north" to Plant Genetic Resources for Food and Agriculture are hindering this agreement with the US. The scientific data suggest that for the major crops, the north could for many generations operate with its existing *in situ* collections. However this is an extreme scenario unlikely to occur as it would provide the north and the south alike with many scientific and economic disruptions. Most are working to avoid such a breakdown and wish to work cooperatively, stimulated by multilateral flow of benefits. Those questioning when the benefit stream will ever begin overlook the substantial benefits of the pre-CBD system and fail to see that many of the benefits are already here for poor and rich countries alike.

2. INTRODUCTION

As outlined by Hawtin and Reeves (1998), and Fowler (1998) the dominant paradigm regarding Plant Genetic Resources for Food and Agriculture (PGRFA) in the 1960's and 1970's was one of "common heritage for humankind". Germplasm then generally was available without restrictions internationally, at a time when the impacts of the Green Revolution were being felt in high-yielding varieties of wheat and rice. This period saw the initiation of the Consultative Group on International Agricultural Research (CGIAR) in 1971, the subsequent development of the International Agricultural Research Centers (IARCs, now numbering 16), including the International Board of Plant Genetic Resources (IBPGR) in 1974, now the International Plant Genetic Resources Institute (IPGRI; Ford-Lloyd and Jackson, 1986; Plucknett et al., 1987). The world then focused on building germplasm collections and genebanks, and the development of new high-yielding varieties. Much of this work was stimulated by an increasing awareness of the narrow genetic base of advanced agriculture and consequent potential susceptibility to crop failures (National Research Council, 1972). This system made tremendous strides in germplasm collection and understanding of distribution and systematics of crops and their wild relatives (Hawkes, 1985). In the US, the passage of the Plant Patent Act in 1930 enabled patents on vegetatively propagated plants, but had little effect on food crops. The passage of the Convention for the International Union for the Protection of New Varieties of Plants (UPOV) in 1961 legalized Plant Variety Protection (PVP) and introduced the concept of "breeders' rights." Subsequently, a Multilateral Trade Agreement made in 1995 under the Uruguay Round of negotiations included the Agreement on Trade-Related Aspects of Intellectual Property Rights (TRIPS), administered by the World Trade Organization (WTO, including 132 member countries; Lourie, 1998).

Few countries, and no IARCs, initially allowed the application of IPR protections for new varieties. Gradually, the growth of these protections, and growth of private sector breeding, stimulated developing countries to begin considering national sovereignty over their native germplasm and a move from the concept of common heritage to "national sovereignty" and a recognition of "farmers' rights". Also, concerns were raised about the socioeconomic (Cleaver, 1972), and environmental (Harlan, 1972; Mooney, 1979) effects of the widespread adoption of high yielding crop varieties (see also Harlan and Martini [1936], for perhaps the earliest reference to environmental concerns regarding the introduction of advanced varieties). Paradoxically, the adoption of advanced cultivars has the potential to stimulate genetic erosion of landraces often used in their pedigrees (Frankel, 1970); but see Brush (1995) who questions the conventional assumption of loss of diversity in centers of origins of crops. Ethical questions also were raised over benefit sharing from the utilization of PGRFA (Kloppenber and Kleinman, 1987; Kloppenber, 1988). These economic, ethical, and biological concerns surfaced at the 1981 Food and Agriculture Organization of the United Nations (FAO) Conference in Rome, and a debate about the value of the open access to PGRFA was well underway (Fowler, 1998). Eventually the Convention on Biological Diversity (CBD) reaffirmed an earlier statement of national sovereignty over all genetic resources, with a concept of mutually agreed terms and prior informed consent. After this reaffirmation, the FAO attempted to harmonize the Undertaking to the terms of the Convention. The ratification of the CBD in the United States however became stalled because of concerns of various political and industry groups and

ratification by the US has not moved forward (Lynch, 1996). Currently, many are considering how best to move the debate forward.

Farmers' rights was a new concept introduced into in the debate and open to considerable interpretation. The term variously was interpreted as a general political slogan vs. a legal concept (Fowler, 1998). At one end of the extreme it can be interpreted as direct monetary compensation to farmers (especially farmers from developing, "gene-rich", "southern" countries) for millennia of efforts in selection, maintenance, and ownership of landraces currently in genebanks and to be acquired in the future. Compensation would come from the developed "gene-poor" "north", who some viewed as unfairly exploiting the genetic resources of the poor for private gain. For example, as outlined in Paragraph 56 of the Revision of the IU, Rome, 1994, CPGR-Ex1/94/5, farmers' rights are interpreted to compensate farmers, and their communities and countries, for their past contributions and the continuation of their contributions through an international fund. Alternatively, it has been suggested that farmers' rights be interpreted as support for farmers' efforts to conserve and sustainably use PGRFA, perhaps through funding for genebanks and breeding efforts in developing countries or for education for their personnel. The term is still widely used in these different contexts, and is causing considerable confusion in the debate on PGRFA. The CGIAR Centers have the conflicting demands of trusteeship of holdings on one hand, and use of the collections on the other. Farmers' rights are recognized by the CGIAR (Hawtin and Reeves, 1998), but in necessarily vague terms that do not advocate a right for compensation. Alternative new interpretations that can possibly break the impasse over this issue are provided in a new FAO document, CGFRA-Ex5/98/REPORT, pages C9-C12.

This Workshop focuses on the negotiation in progress in the inter-governmental forum of the FAO Commission for Genetic Resources for Food and Agriculture (CGRFA) for the revision of the 1983 IU on Plant Genetic Resources for Food and Agriculture. Developed countries will consider their reliance on their existing *ex situ* genetic resources of some major staple food crops in these negotiations. Alternatively, developing countries will consider the value of their yet unexplored *in situ* genetic resources in the form of landraces and wild relatives.

This raises the question if these apparently polarized views will ever be able to be compromised to come to agreement in the IU. This paper address this question by exploring:

1. The scientific basis for the sole reliance on existing genebank accessions, and
2. The continuing need for the conservation and collection of *in situ* genetic resources.
3. The multilateral benefits of a system of open access to PGRFA.

3. METHODS

In this paper, PGRFA refer very broadly to a range of genetic resources from wild species to landrace populations. The World Wide Web provided much information for this subject. Because of extensive links among sites, I found the following sites most useful to begin searches:

- SINGER, The System-wide Information Network for Genetic Resources is the genetic resources information exchange network of the IARCs. It provides information on the collections of the CGIAR Centres - <http://noc1.cgiar.org/>
- FAO, Plant Genetic Resources Information home page with links to FAO documents and other selected sites relevant to plant genetic resources - <http://web.icppgr.fao.org/>

- FAO, World Information and Early Warning System on Plant Genetic Resources (WIEWS), provides a database on genebank holdings worldwide-
<http://web.icppgr.fao.org/WIEWS/wiews.html>
- USDA, ARS, The US National Plant Germplasm System (USNPGS) -
<http://www.ars-grin.gov/npgs/>
- Convention on Biological Diversity -
<http://www.biodiv.org/convtext/cbd0000.htm>

The US Crop Germplasm Committees (CGCs; link through site 4, above) are composed of experts on crops of interest to the USNPGS. I contacted members of this committee regarding references on taxonomy, gene pools, and international holdings of their crops. Data for major international collections (Table 2) were provided by FAO (1996). Data from FAO documents relating to the IU and the CBD were obtained on a CD ROM entitled "The State of the World's Genetic Resources for Food and Agriculture"

This includes:

- the Global Plan of Action
- the State of the World's Plant Genetic Resources
- 15 Sub-Regional Synthesis Reports
- 158 country reports
- The Global System (a guide to the FAO Commission on Genetic Resources for Food and Agriculture and other elements of the FAO Global System for the Conservation and Sustainable Use of PGRFA)
- reports on The International Technical Conference and its preparatory process.

Information on holdings in the USNPGS was obtained from the Germplasm Resources Information Network (GRIN; link through site 4), and with assistance from a GRIN database technician, Mark Bohning. Information on international holdings was obtained through the SINGER database (site 1), from the WIEWS database (site 3), and from web sites linked from there.

4. RESULTS PERCEPTION OF UNITED STATES CROP GERMPLASM COMMITTEES ON THE ADEQUACY OF THE US COLLECTIONS

The USNPGS receives advice on its operations from 40 Crop Germplasm Committees (CGCs), dealing with 85 major crops. These committees are composed of specialists within a crop or group of related crops of present or future economic importance. These committees represent their crop user community, and are composed of representatives from federal, state, and private sectors; various scientific disciplines; and with representatives of diverse geographical areas. They advise the USNPGS on acquisition of new germplasm, placing priorities on traits for evaluation and developing proposals to implement the evaluations, identifying discontinued breeding programs and other germplasm collections in danger of being lost, maintaining current reports on the status of their crops for various US government agencies, evaluating the potential benefits and problems associated with the development and use of core collections, and other issues.

These committees were surveyed recently (United States General Accounting Office, 1997) regarding issues facing their crops and the overall condition of the USNPGS. A major finding of this survey was that the CGCs reported that the genetic diversity for over half of the 85 major crops in the USNPGS collections is sufficient to reduce crop vulnerability. Moreover, when all widely accessible crops of the USNPGS and other [putatively] available collections were considered, almost three-fourths of the CGCs reported sufficient collections. Despite this perception, acquisition of new germplasm

was considered the top of 14 priorities. CGCs reporting insufficient collections were for grapes, cool-season food legumes, cucurbits (squash and melons), tropical fruits and nuts, walnuts, herbaceous ornamentals, *Prunus* (e.g., peach and cherry trees), and woody landscape plants. The CGCs however reported difficulties for crop curators to acquire new germplasm from some countries, most likely a result of changing policies caused by the placement of sovereignty over germplasm. A USNPGS policy of unrestricted international distribution of germplasm may not allow collections in countries imposing these restrictions. The survey also highlighted the increasing backlogs on needed increase cycles for existing USNPGS collections caused by insufficient funding of the USNPGS system.

4.1. MAINTENANCE OF GENETIC DIVERSITY IN EX SITU AND IN SITU COLLECTIONS

A critical issue affecting decisions of reliance on *ex situ* collections regards their long-term viability, maintenance of genetic diversity, and accumulation of deleterious mutations in long-term storage. The State of the World Report (FAO, 1996) documents 6.1 million *ex situ* germplasm accessions held world-wide in 1,300 separate collections. Since the early 1970s, the accessions have grown more than 12-fold. FAO (1996) identified regeneration as one of the major needs for *ex situ* collections in developing nations. This holds true for developed nations as well. For example, the USNPGS is a diverse system encompassing The National Germplasm Resources Lab (responsible in part for funding national and international collecting missions), the Germplasm Resources Information Network (GRIN), the National Seed Storage Laboratory, four Regional Plant Introduction Stations, ten National Clonal Repositories, the National Small Grains Center, the Inter Regional Potato Introduction Station, and support of several other crop-specific collections (Clark et al., 1997). Its funding is about \$20 million per year, only half of its projected needs (Strauss, 1998; American Genetic Resources Alliance website, <http://www.amgra.org/>). This serious fiscal shortfall in the US System is causing backlogs in needed regeneration cycles. The low funding of genebanks in developing nations however is much worse, and irreplaceable collections may be lost (FAO, 1996).

Even assuming all of the world's genebanks were adequately funded for regular regeneration cycles, some loss of diversity will occur over many serial increases, especially for heterogeneous out-crossing species. The extent and significance of this loss is not quantified empirically and studies mostly have relied on modeling. Brown et al. (1997) document how each subsequent increase of a heterogeneous population requires a two- to three-fold increase in parents to maintain more than 95% the alleles of the prior increase. The demands of increasingly growing collections make these population sizes impractical, with the trade off that alleles invariably will be lost. Typically 25 to 100 seeds are used for regeneration in genebanks (Breese, 1989). Furthermore, optimum regeneration requires detailed knowledge of the biology of the crop or crop relative regarding environmental requirements, pollination system, breeding system, and seed fecundity and longevity (Cross and Wallace, 1994; Frankel et al., 1995; Brown et al., 1997; Hamrick and Godt, 1997). These are known for only for some of the major crops. Serious backlogs in increases will certainly stimulate the need for reduction of collections by identification of duplicates.

Additional regeneration concerns relate to the pollination and seed sampling strategies (Crossa and Vencovsky, 1997). An additional concern is expressed by Hamilton (1994) who cautions that many current measures of maintenance of diversity improperly assesses simple neutral alleles and ignore genetic correlations of quantitative genetic variation and gene/environment interactions. He suggests that seeds not be bulked in initial collections but rather maintained as maternal families to allow for tracking of

quantitative variation, preventing inbreeding and selection, and preserving population differentiation. Alternatively, del Rio et al. (1997) found that there was little to no reduction in genetic diversity for most but not all accessions in one generation of a serial increase for two wild potato species, one an outcrossing diploid, the other an inbreeding tetraploid but such empirical studies are rare. In addition to problems arising from loss of diversity through serial increases, there are problems associated with the accumulation of deleterious mutations over long-term seed storage and serial increases (Schoen et al., 1998). This can be especially acute with small sample sizes, and such mutations can reduce fitness of collections.

Many problems associated with conservation of diversity and accumulation of deleterious alleles would be alleviated by conservation of genetic diversity *in situ* (Bretting and Duvick, 1997). *In situ* and *ex situ* strategies were shown by Bretting and Duvick (1997) to intergrade in many cases, as in the maintenance of fruit trees in genebanks vs. orchards. They proposed the alternative terms “static” vs. “dynamic.” Their primary point was that genebanks conserved the products of evolution but ceased evolutionary processes, while dynamic conservation sought to recreate the products of the evolutionary process. A dynamic genebank strategy attempts to maintain interactions with the plant’s natural environment, including pathogens, maintains gene flow (for outcrossing species), and maintains natural evolutionary forces, while a “static” strategy (as increases in greenhouses) does not.

For wild relatives *in situ*, dynamic conservation can be accomplished for some species by large nature preserves. This strategy serves many purposes, including conservation of a wide range of biodiversity, maintenance of ecosystems, and fosters societal goals such as recreation, environmental education, and ecotourism. Optimum design of preserves would be determined in part by allowing sufficient population sizes to maintain gene flow and mitigate drift (Ellstrand and Elam, 1993). However, preserves will not conserve all wild species diversity. For example, many species of wild potatoes are highly endemic (Hawkes, 1990; Ochoa, 1990; Castillo and Spooner, 1997), and are often found in areas already under development. Because preserves for wild crop relatives must take all crops into consideration, even the best system of preserves will not preserve all wild crop relatives in their native habitat. This practical consideration does not mitigate the need for designating preserves and conserving biodiversity, it only argues that it is only a partial solution.

One model for dynamic conservation would be the maintenance of traditional farming practices (Altieri and Merrick, 1987; Oldfield and Alcorn, 1987), retaining some advantages of a dynamic conservation model for wild crop relatives in preserves. This solution assumes that traditional practices and landraces still exist for many crops, and that farmers would maintain these practices to their economic benefit. Brush (1989, 1991) argues that such conditions still exist for some landraces, some that are still maintained for interesting culinary traits desired by consumers. Similarly, dynamic genebank preserves could be designed that attempt to recreate traditional settings (Bretting and Duvick, 1997).

In summary, dynamic and static genebank strategies have both been proposed for the maintenance of diversity, but the relative costs and benefits of both approaches have yet to be assessed. Static genebank strategies provide collections more readily available to germplasm users (farmers, scientists, and educators) than germplasm conserved in reserves. There is a concern about loss of genetic diversity, especially in static genebanks. Consequently, over the long-term, continuing germplasm collections from centers of diversity would be a wise strategy to regenerate the natural diversity in *ex situ* collections, assuming that these collections persist.

4.2. PGRFA OF FIVE SELECTED MAJOR CROPS

Relatively few crops supply the major foods and fibers for the world (Harlan, 1992). The top four food crops typically mentioned are wheat, maize, rice, and potatoes. In terms of estimated edible dry matter (the harvested tonnage reported in FAO Production Yearbooks, minus wastage, as peels, shells, or other non-edible plant parts, minus moisture content), the top four crops are wheat, maize, rice, and barley (potatoes ranked eighth, additionally after soybean, cane sugar, and sorghum). The conveners of this conference requested *in situ* and *ex situ* surveys of oilseed *Brassica* (rape; number 15 in EEDM production), peanuts (17), potatoes (8), soybeans (5), and tomatoes (27) (Harlan, 1992). These were chosen for this paper because of their major importance internationally, because of their relationship to other crops discussed in this conference, because of their modification by modern biotechnological methods, and because of the collections of these crops in a variety of genebanks internationally.

No country is independent in PGRFA, as all countries, rich and poor alike, rely on crops from outside their own country. The six highest producing countries for the five major crops treated here are presented in Table 1. Accessions of these crops are distributed in genebanks around the world (Table 2). Major *ex situ* germplasm collections are often in countries far removed from the origin of the crop. The raw numbers of genebank holdings from this survey suggest good representation of genetic diversity in current *ex situ* collections. Greater detail of these collections is provided below under the individual crop reports. The major genebanks listed below are only a fraction of the total genebanks holding collections (e.g., Juvik et al., 1985). Because collectors often provide duplicates to more than one genebank, and because genebanks often exchange materials, the number of unique accessions is likely to be inflated. Surveys analyzing unique and common accessions among genebanks are rare but greatly needed; to my knowledge the only one completed is for potato (see below).

TABLE 1. THE SIX HIGHEST PRODUCING COUNTRIES FOR FIVE SELECTED MAJOR CROPS (COMPILED FROM FAO, 1995).

Crop	World production, (100 MT), 1995	Country	Production by country (100 MT), 1995	% world production)
oilseed <i>Brassica</i> (rape)	34,685	China	9,777	28.2
		Canada	6,436	18.6
		India	5,888	17.0
		Germany	3,002	8.7
		France	2,782	8.0
		United Kingdom	1,330	3.8
peanuts	27,900	China	10,316	37.0
		India	7,100	25.4
		USA	1,578	5.7
		Nigeria	1,502	5.4
		Senegal	791	2.8
		Sudan	630	2.3
		potatoes	280,679	China
		Russian Feder.	37,300	13.3
		Poland	24,891	8.9
		USA	20,177	7.2
		India	19,000	6.8

soybeans	125,930	Ukraine	14,729	5.2
		USA	58,569	46.5
		Brazil	25,581	20.3
		China	13,581	10.8
		Argentina	12,088	9.6
		India	4,606	3.7
tomatoes	78,282	Paraguay	2,300	1.8
		USA	11,000	14.1
		China	8,928	11.4
		Turkey	7,150	9.1
		Egypt	5,050	6.5
		Italy	4,860	6.2
		India	4,800	6.1

TABLE 2. THE SIX LARGEST COUNTRIES, CGIAR CENTERS, OR REGIONAL GENEbanks HOLDING *EX SITU* GERMPLASM COLLECTIONS OF FIVE SELECTED MAJOR CROPS (FAO, 1996).

Crop	Total world accessions	Major holders (percent of world's holdings)
Oilseed <i>Brassica</i> (rape)	109,000	India (16), United Kingdom (10), Germany (9), US (8), China (6), Rep. Of Korea (3)
Peanut	81,000	US (27), India (20), ICRISAT (18), China (8), Argentina (6), Zambia (2)
Potato	31,000	CIP (20), Colombia (13), Germany (13), US (8), Argentina (4), Czech. Rep. (4)
Soybean	174,000	China (15), US (14), AVRDC (10), Brazil (5), United Kingdom (4), Russian Federation (3)
Tomato	78,000	US (30), AVRDC (19), Philippines (16), Russian Federation (8), Germany (45), Colombia (3)

a) Oilseed Brassica (rape)

Taxonomy and Distribution

The genus *Brassica* consists of a dozen or so highly polymorphic, broadly-defined species (Warwick, 1993). Prakash and Hinata (1980) provide the latest comprehensive treatment of the crop Brassicas. All are native to the Mediterranean Region. Some of them became agricultural weeds in antiquity and expanded their ranges northward into Europe or eastward into Asia (Sauer, 1993). The widespread nature of most of these species makes the discovery of centers of origin difficult or impossible and fits Harlan's (1971) concept of this crop as "non-centric". Selection produced a wide array of cultivars, including mustards, cabbages, turnips, rutabagas, and oilseed Brassicas (rapes). The major rape cultivar is *B. napus* L., but *B. rapa* L. (*B. campestris* L.), *B. carinata* A. Br., and *B. juncea* (L.) Czern. also are used as oilseeds. These species also

have vegetable and forage forms (Sauer, 1993; Downey and Rimmer, 1993; McNaughton, 1995).

Genepools

The interrelationships of Brassicas were elegantly elucidated by Morinaga (1934) and confirmed experimentally by U (1935), who showed three basic diploid species differing in basic chromosome numbers: *B. nigra* L. Koch ($2n = 16$, genome BB); *B. oleracea* L. ($2n = 18$, genome CC), and *B. rapa* ($2n = 20$, genome AA). Interspecific hybrids between species pairs followed by chromosome doubling formed the species *B. carinata* ($2n = 34$; genome BBCC), *B. juncea* ($2n = 36$, genome AABB), and *B. napus* ($2n = 38$, genome AACC).

Over 14-15% of the world's edible vegetable oil supply now comes from oilseed Brassicas making it the third most important oil after soybean and palm. The crop can be grown in cooler agricultural regions and at higher elevations than most other oilseed crops, and as a winter crop in temperate regions. The seeds yield on extraction over 40% oil on a dry weight basis and a meal containing 38 to 44% high quality protein (Downey and Rimmer, 1993; Downey and Ribbelen, 1989). Vegetable Brassicas were in common use in the Neolithic age, and Indian Sanskrit writings show the use of oilseed raps and mustard from 1500 to 2000 BC. Despite this early use, the crop gained wide market share in the western nations only after World War II after improved processing techniques and breeding for superior quality of oil and meal (Downey and Rimmer, 1995).

Crop improvement for rapes have involve increases in seed yield, winter hardiness and frost resistance, disease resistance (primarily blackleg, white rust, *Sclerotinia* stem rot, and *Alternaria* black spot), reduction in lodging, shattering resistance, and improved oil quality. The latter mainly involves reduction in erucic acid in the oil and glucosinolates in the residual meal. "Canola" was a term coined in 1986 to define seed, oil, and meal with low levels of both erucic acid and aliphatic glucosinolates, or "double low" (McNaughton, 1995). At present, only *B. napus* and *B. rapa* have been bred to canola quality crops, but it is likely that in the future *B. juncea* and *B. carinata* will be bred to this quality, making for a wider choice of oilseed *Brassica* crops for the future (Downey and Rimmer, 1993). These breeding objectives have involved many breeding techniques involving hybridization with related species (Downey and Ribbelen, 1989; Downey and Rimmer, 1993), making the germplasm collections very important.

Germplasm Collections

Because the four oilseed Brassicas listed above can also have vegetable or fodder use, it is difficult to know exactly the end use of all of the collections listed in the genebanks. Boukema and van Hintum (in press) provide a rough estimate of end use of the world's *Brassica* collections as 40% for feed or fodder, 30% for oilseed, and 30% unknown. Although duplication of collections likely inflate these numbers of unique accessions and not all are oilseed types, Boukema and van Hintum (in press) estimate that relative to the four oilseed *Brassica* species, the total worldwide accessions are: *B. rapa* (18,224 accessions, 25% of world total), *B. juncea*, 13,549, 18%), *B. napus* (13,543, 18%), and *B. carinata* (1,483, 2%). The six largest genebanks for these collections follow:

TABLE 3. THE SIX LARGEST GENE BANKS HOLDING THE THREE MAJOR SPECIES OF OILSEED BRASSICA (NOT ALL ACCESSIONS ARE OILSEED TYPES). DATA FROM BOUKEMA AND VAN HINTUM (IN PRESS).

Genebank	Genebank accessions		
	<i>B. rapa</i>	<i>B. juncea</i>	<i>B. napus</i>
Institute of Crop Germplasm Resources, Beijing, China	>5000	3000	1500
All India Coordinated Project on Rape and Mustard, Haryana Agricultural University, Hisar, India		5400	1700
North Central Regional Plant Introduction Station, Ames, Iowa, USA	1200	1030	560
National Bureau of Plant Genetic Resources, New Delhi, India	1040	1170	
Germplasm Management Office, Crop Experiment Station, Yongdang, North Korea			2200
Division of Genetics, Indian Agricultural Research Institute		1200	

Adequacy of Collections

According to Boukema and van Hintum (in press) from the available information sources it is difficult to determine which parts of the *Brassica* collections are still alive and available for exchange, and to determine the duplication of collections. Accordingly, it is difficult to trace possible omissions in the world's *Brassica* germplasm holdings and to place priorities on future collections. They argue for more world-wide coordination among genebanks to reduce duplication of efforts and to set priorities. This could be said for many germplasm collections and is a strong argument for the cost savings and efficiencies that could be gained from a more open system of availability of information and germplasm exchange.

b) Peanut

Taxonomy and Distribution

The latest taxonomy of the genus *Arachis* is Krapovickas and Gregory (1994). They recognize 69 species, four subspecies, and eight varieties (77 taxa in total). They are distributed in central and western South America in Argentina, Bolivia, Brazil, Paraguay, and Uruguay. New collections performed by CENARGEN/EMBRAPA and collaborators show the need to recognize eleven new species (J. Valls, pers. comm.). Krapovickas and Gregory (1994) divided the genus *Arachis* into nine sections based on morphology and artificial intercrossability. The largest section *Arachis* includes about 40% of the species, including the cultivated species *A. hypogaea* L. Most species are diploid ($2n = 20$) and are perennial. The cultivated species *A. hypogaea* is an annual tetraploid with $2n = 40$. This is divided into two subspecies and six varieties, and the varieties represent cultivar types "Virginia", "Peruvian", "Valencia" and "Spanish".

Genepools

Wynne and Halward (1989) recognized seven sections in *Arachis*. Section *Arachis*, containing *A. hypogaea* (genome AB), contains diploids and tetraploids designated genomes A, B, and D. His other sections were designated as genomes Am, C, E, E, Ex, and R. Crosses generally can be made within genome types. The tetraploid species *A. monticola* Krapov. and Rigoni is a putative progenitor of *A. hypogaea*, and occurs with this species in southern Bolivia and northern Argentina. Peanut breeding has involved crosses with *A. monticola* (Genome AB), and *A. cardenasii* Krapov and W. C. Gregory (genome A). (Wynne and Halward, 1989). Breeding has concentrated on yield, disease resistances (early leafspot, late leafspot, and rust), improvement in symbiotic nitrogen fixation, and fatty acid composition, but many other diseases, insect resistances, and quality traits are present in the wild species that could improve the cultivars (Stalker and Moss, 1987; Wynne and Halward, 1989).

Germplasm Collections

The major peanut germplasm resources are listed in Table 4. Data were obtained from Stalker and Simpson (1995), the SINGER database (for China), updated by unpublished data from Stalker, and data on the US collections from Mark Bohning (US GRIN System), and Merrelyn Spinks (US genebank at S9 in Griffin, Georgia).

TABLE 4. MAJOR PEANUT GERMPLASM COLLECTIONS.

Genebank	Genebank Accessions <i>Arachis hypogaea</i>	Other wild species
ICRISAT	13,740	413 accessions of 40 species
Southern Regional Plant Introduction Station (S9), Griffin, Georgia, US	8,725	894 accessions of 65 species
NRCG, ICAR	6,299	10 accessions of an unknown number of species
Texas A & M. University, Stephenville, Texas, US	3,563	798 accessions of 65 species
INTA	2,774	119 accessions of 35 species
Institute of Oil Crops Research, Wuhan, Hubei Province, China	2,377	23 accessions of an unknown number of species
Institute of Crop Germplasm Resources, Beijing, China	2,178	none
EMBRAPA/CENARGEN	1,600	953 accessions of 74 species

Adequacy of Collections

Landrace collections of cultivated peanut (*A. hypogaea*) make up the bulk of the world's genebank collections. More than 30 collecting expeditions have been made in South America, and many collections are made of landraces throughout the world. Despite these many collections, serious gaps still exist for landrace collections from Colombia, Venezuela, northern Brazil, Guyana, French Guyana, Surinam, most Central

American countries, and Mexico. The wild species have germplasm collections of nearly every species, but many with only a single accession. Wild species should still be sought in western Brazil, eastern and northeastern Bolivia, and northern Paraguay (David Williams and Karen Williams, unpublished report to peanut CGC, 1998). Thomas Stalker additionally mentions collecting needs of cultivated species collections from Peru, China, and East Asia (pers. comm.).

c) Potato

Taxonomy and Distribution

Solanum sect. *Petota* Dumort., the potato and its wild relatives, is distributed from the southwestern United States to southern Chile. About 30 species grow in the United States, Mexico, and Central America, and the rest grow in South America. Most species grow from about 2,500-3,500 m, with a concentration of diversity in the Andes. The latest comprehensive taxonomic treatment of the group (Hawkes, 1990) recognizes 232 species, partitioned into 21 series. Two of these series (containing nine of the 232 species) form a separate clades and are best treated as a separate section *Etuberosum* (Buk. and Kameraz) A. Child, section *Juglandifolium* (Rydb.) A. Child, and section *Lycopersicum* (Mill.) Wettst. (Child 1990; Spooner et al. 1993). Subsequent to Hawkes (1990), Ochoa (1990) published a potato flora of Bolivia. A comparison of these and other treatments shows several disagreements regarding the number of species and their assignment in series throughout sect. *Petota* (Spooner and van den Berg, 1992).

There is considerable controversy regarding the number of species in sect. *Petota*. The estimate of 232 species by Hawkes (1990) is largely concordant on a regional basis with the treatments of Ochoa (1962, 1990, and his many individual species descriptions). Alternatively, recent studies using morphological and molecular markers suggest that 232 species is a large overestimate of the species diversity in sect. *Petota*. For example, Castillo and Spooner (1997) examined 27 of the 40 species of *Solanum* ser. *Conicibaccata* Bitter with morphology and chloroplast DNA restriction site data. The results suggested that only 8 or 16 of these 27 taxa could be recognized, depending on a conservative or very liberal interpretation of the data. More dramatically, the 30 species of the *Solanum brevicaulis* Bitter complex was examined with morphology (van den Berg et al., 1998) and single- to low-copy nuclear restriction site data and Random Amplified Polymorphic DNA data (Miller and Spooner, 1998). All three data sets were remarkably concordant in suggesting that these 30 taxa should be reduced to only two or three. The number of series also has been suggested to be too many based on morphology (Spooner and van den Berg, 1992), and chloroplast DNA restriction site data (Spooner and Castillo, 1997).

One reason for the taxonomic difficulty in the group may be interspecific hybridization. Twenty-seven diploid or polyploid taxa wild and cultivated potatoes are of putative hybrid origin (Spooner and van den Berg, 1992). Molecular studies have failed to support two of these hybrid hypotheses (Spooner et al., 1991; Miller and Spooner, 1996), but have supported one of them (Clausen and Spooner, 1998). The taxonomy in sect. *Petota* is in need of revision, and future treatments likely will recognize fewer series and species than those outlined in Hawkes (1990).

Genepools

Most investigations of genomes in potatoes involved analysis of intra- and interspecific hybrids and their colchicine doubled products, and/or concomitant measures of fertility,

such as pollen stainability, and seed or fruit set. A comparison of different studies is complicated by different genomic formulae presented by different workers, but a major investigator on potato genomes (Matsubayashi, 1991) summarized his life's work on potato genomes and compared it to the work of others. Seventy three percent of the species with known chromosome numbers are diploid ($2n = 2x = 24$; Hawkes, 1990), with the others tetraploid and hexaploid, and a few triploid and pentaploid populations of other species. Matsubayashi (1991) designated all diploid species as A genome, with superscripts to designate eight minor variations. He designated all polyploid species as disomic polyploids, either as combinations with other variations of A genome, or with different genomes designated as B, C, or D. He designated the outgroup of potatoes and tomatoes, sect. *Etuberosum*, as an E genome.

In addition to genome differences, potato has other crossing barriers. One mechanism involves ratios of maternal/paternal effective ploidy in the endosperm, as evidenced by endosperm breakdown of interspecific hybrids (Endosperm Balance Number, EBN; Johnston et al., 1980; Hanneman, 1994). EBN data have been published by Hanneman and Bamberg (1986), Hawkes and Jackson (1992), Ochoa (1990), and Hanneman (1994). Yet another mechanism involves inhibition of pollen tube growth by stylar barriers (Abdalla and Hermsen, 1972; Fritz and Hanneman, 1989).

Despite these different genomes and ENB numbers in sect. *Petota*, breeders and geneticists have demonstrated that wide sexual crosses can be made among widely divergent species differing by genomes and EBN numbers by ploidy manipulation, rescue pollinations, and embryo rescue (Ortiz and Ehlenfeldt, 1992; Watanabe et al., 1995). In addition, genomes can be introduced by somatic fusion hybrids (Helgeson et al., 1998). These techniques are incorporating many valuable agronomic traits, environmental tolerances, and pest and disease resistances into advanced cultivars (Hawkes and Hjerting, 1969, 1989; Ross, 1986; Plaisted and Hoopes, 1989; Hawkes, 1990; Ochoa, 1990).

Germplasm Collections

Lawrence et al. (1986) provided a list of 58 institutions holding potato germplasm, including cultivated and wild species. According to Huamán et al. (1996, and submitted) the major world potato genebanks holding wild potato species germplasm are: CPRO-DLO/GCN (The Netherlands); CIP (Peru); NRSP-6 (USA); the Commonwealth Potato Collection (CPC) in Scotland, U.K.; the N.I. Vavilov Institute (VIR) at St. Petersburg, Russia; the Institut für Pflanzenzucht Gross-Lusewitz (GLKS) at Gross Lusewitz, Germany; the Instituto Nacional de Investigacion Agrícola (INTA) at Balcarce, Argentina; the Centro de Investigacion de Cultivos Andinos (CICA) at Cusco, Peru; and the Instituto Nacional de Investigacion Agropecuaria (INIAP) at Quito, Ecuador.

An intergenebank database of the world's collections of potato wild species collections was constructed by Huamán et al. (1996, and submitted), and duplicates were sorted by collector number. The latest version of this Intergenebank Potato Database for wild potato species is now available in electronic form and will soon be available on the internet through CIP's homepage (<http://www.cgiar.org/cip/>). It contains 7,311 unique accessions, which were reduced from a total of 11,871 total records (Table 5).

TABLE 5. MAJOR WILD POTATO GERmplasm COLLECTIONS.

Genebank	<u>Genebank Accessions (wild species)</u>
NRSP-6	3,661
CIP	1,908

CPRO-DLO/CGN	1,833
VIR	1,444
INTA	1,334
IPK	1,126
CPC	565

The countries where these 7,311 accessions were collected were: Argentina (2,126 accessions), Peru (1,539), Bolivia (1,296), Mexico (1,199), Colombia (186), USA (158), Ecuador (119), Chile (114), Uruguay (61), Venezuela (25), Paraguay (24), Guatemala (18), Brazil (9), and Costa Rica (2), and unknown source (435).

The largest holder of cultivated species, CIP, maintains 3,527 accessions of all seven of the cultivated species (Table 6; Huamán et al., 1997), but extensive collections of these also are held in other genebanks. The cultivated species collections at CIP are so extensive that the main research now is based on developing a core collection and identification and conversion of the duplicates to true seed.

TABLE 6. CULTIVATED POTATO SPECIES ACCESSIONS HELD AT CIP, THE MAJOR GENE BANK HOLDING CULTIVATED SPECIES (HUAMÁN ET AL., 1997).

Cultivated Species, (ploidy level; $2x = 24$)	Genebank Accessions
<i>Solanum</i> x <i>ajanhuiri</i> Juz. and Bukasov ($2x$)	10
<i>S.</i> x <i>chaucha</i> Juz. and Bukasov ($3x$)	97
<i>S.</i> x <i>curtilobum</i> Juz. and Bukasov ($5x$)	11
<i>S. goniocalyx</i> Juz. and Bukasov ($2x$)	48
<i>S.</i> x <i>juzepczukii</i> Bukasov ($3x$)	31
<i>S. phureja</i> Juz. and Bukasov ($2x$)	170
<i>S. tuberosum</i> L. subsp. <i>andigena</i> (Juz. and Bukasov) Hawkes ($4x$)	2,644
<i>S. tuberosum</i> subsp. <i>tuberosum</i> ($4x$)	144
<i>Solanum</i> $2x$ "hybrids"	56

Adequacy of Collections

Some of the above genebanks are continuing collections, with the greatest remaining collection needs of wild species from Peru. An expedition to Peru was completed in 1998, and four additional expeditions are planned from Peru from 1999-2002. When the Peruvian collections are completed in the next four years, all of the cultivated species and most of the wild species will be preserved in genebanks, making the potato one of the better conserved crops in the world. Remaining germplasm collecting expeditions then can be justified mainly in regions with low species diversity but with few collections. This is southern South America (Brazil, Paraguay, Uruguay) for *Solanum calvescens* Bitter, *S. chacoense* Bitter, and *S. commersonii* Dunal and in Central America (Honduras and Panama) for *S. agrimonifolium* Rydb., *S. morelliforme* Bitter and Muench, and *S. woodsonii* Correll.

d) Soybean

Taxonomy and Distribution

Glycine is divided into two well-defined subgenera, subgenus *Soja* (Moench) F. J. Herm., containing the cultivated soybean *G. max* (L.) Merr., and its wild relative, *G. soja* Sieb. and Zucc., and subgenus *Glycine*, containing sixteen other species. Both

species of subgenus *Soja* are annual and diploid with $2n = 40$ and hybridize readily. The sixteen species of subgenus *Glycine* are perennial and diploid (most $2n = 40$, one $2n = 38$) or polyploid (most $2n = 80$, one $2n = 78$). Ongoing field work in Australia is showing the need to recognize new species (Hymowitz, pers. comm.). The soybean grows only under cultivation, while *G. soja* grows wild in China, Japan, Korea, Russia, and Taiwan (Hymowitz et al., 1998). All 16 species of subgenus *Glycine* grow in Australia, and two of them additionally grow in the Pacific Islands or Papua New Guinea, Indonesia, Philippines, and Taiwan (Hymowitz et al., 1998). This subgeneric classification is strongly supported by many data sets including morphology, cytogenetics, seed proteins (summarized in Hymowitz et al., 1998); and restriction fragment analysis of mitochondrial DNA, nuclear DNA (Menancio et al. 1990), ribosomal DNA (Doyle and Beachy, 1985; Doyle et al., 1990b), chloroplast DNA (Shoemaker et al., 1986; Doyle et al., 1990a,b,c), and DNA sequences of nuclear ribosomal DNA (Kollipara et al., 1997); and AFLPs (Maughan et al. 1996).

Genepools

Hymowitz et al. (1998) summarize data from cytogenetics, biochemistry, the ability of species to hybridize, and molecular data, to designate genepools in the 18 species of *Glycine*. The cultivated soybean shares a genome (G) with its progenitor species *G. soja*, and all practical breeding has used *G. max* and *G. soja*. The perennial species have genomes designated as A, B, C, D, E, F, H, I. They are rich sources of many disease resistances (Dasshiell and Fatokun, 1997; Hymowitz et al., 1998). To date, all intersubgeneric hybrids have been obtained through embryo rescue techniques. These hybrids were vegetatively vigorous and with a growth habit resembling the perennial parent. All were sterile, but fertility was restored through colchicine-induced synthetic amphiploids (Hymowitz et al., 1998). To date, only the perennial relative *G. tomentella* Hayata has been successfully backcrossed with soybean but this has not yet been incorporated into a commercial cultivar (Singh et al., 1990, 1993).

Germplasm Collections

TABLE 7. MAJOR SOYBEAN GERmplasm COLLECTIONS (UPDATED FROM JUVIK ET AL., 1985; DASHIELL AND FATOKUN, 1997).

Genebank	Genebank Accessions	
	<i>Glycine max</i>	Other wild species
US National Soybean Collection, Urbana, Illinois	17,179	1925 of 14 species (1,081 of these <i>G. soja</i>)
AVRDC	14,138, mostly of <i>G. max</i> . Juvik et al. (1985) list 344 accessions of <i>G. soja</i> and 53 accessions other species.	
MAFF, NIAR	6,715	none
VIR	5,121	341 of 9 species (310 of <i>G. soja</i>)
EMBRAPA/CENARGEN	4,693	0
Jilin Research Institute, Jilin Academy of Agricultural Sciences, Jgongzhuling, China	4,200	600 (all <i>G. soja</i>)
IITA	2,500 accessions (Dashiel and Fatokun, 1977), no data on how divided between <i>G. max</i> and <i>G. soja</i>	

Nanjing Agricultural College, Nanjing, Jiangu Province, China	2,168	0
Heilongjiang Academy of Agricultural Sciences, Harbin, Heilongjiang Province, China	1,555	400
Economic Crops Research Institute, Jiangsu Academy of Agricultural Sciences, Nanjing, Jiangsu Province, China	1,199	0
CSIRO	None?	2042 of 16 species

Adequacy of Collections

Glycine max and *Glycine soja* are relatively well collected, but collections are needed for some areas in southern China, Burma, Viet Nam, and North Korea. Wild species should be sought in Australia, especially the northern rain forest areas of the country (Hymowitz, pers. comm.).

e) Tomato

Taxonomy and Distribution

Solanum sect. *Lycopersicum* (Mill.) Wettst., the tomato and its wild relatives, is distributed in the South American Andes from central Ecuador, through Peru, to northern Chile, and in the Galapagos Islands (that contains the single endemic species *S. cheesmaniae* [Riley] Fosb.). Additionally, some populations of *S. lycopersicum* L. var. *cerasiforme* (Dunal) Spooner grow in Mexico and Central America, and in Peru as well as scattered throughout much of the Peruvian Andes (Taylor, 1986; Rick, 1995). Tomatoes grow from near sea level to over 3,600 m in elevation. Muller (1940 and Luckwill (1943) provided the latest comprehensive taxonomic treatments of tomatoes. Rick et al. (1990) recognized nine species and two varieties (of the cultigen *Solanum lycopersicum* = *Lycopersicon esculentum* Mill.). Tomatoes have a bewildering array of morphological variability that has led to different taxonomic treatments, regarding both numbers of species, subspecies, and varieties, and in hypotheses of interspecific relationships. By far, the most variable tomato species is the highly polymorphic *S. peruvianum* L. (Rick, 1963).

The relationships of tomatoes, potatoes, and related genera in the Solanaceae were investigated by chloroplast DNA restriction site data and morphological data by Spooner et al. (1993). This work supported the previously suggested, but controversial hypotheses of sister-group relationships of potatoes and tomatoes (see taxonomy of potatoes above). More global molecular analysis of relationships the Solanaceae (Olmstead and Palmer, 1992; Olmstead et al., in press) are concordant in this sister group relationship. The results also are concordant with the extreme genome similarity of tomatoes and potatoes (with 12 linkage groups, with homosequential genomes, the order of genes the same, differing only by five paracentric inversions (Bonierbiale et al., 1988; Tanksley et al., 1992). Based on the above data, Spooner et al. (1993) recognized tomatoes under the genus *Solanum*, the treatment used here. The treatment of tomatoes under the genus *Solanum* is unfamiliar to many, but is not unprecedented. It was the first genus used for tomatoes at the beginning of formal taxonomic nomenclature (Linnaeus, 1753), and has been used by other taxonomists (MacBride, 1962; Seithe, 1962; Fosberg, 1987; Child, 1990).

Rick (1963, 1986) documented much morphological, ecological, and reproductive variability in *S. peruvianum*. The species grows from northern Peru to northern Chile, and from sea level to 3,600 m, throughout much of the range of tomatoes. He divided this variability into informally designated races, and noted that there are few widespread coastal races and many very locally distributed mountain races. Relative to potato taxonomy, the many races he illustrated for *S. peruvianum* (Rick, 1963, pgs. 218, 219) would be recognized as many separate species in potatoes. These variable races of *S. peruvianum*, like many diploid potato species, are self-incompatible obligate outcrossers.

Miller and Tanksley (1990) studied relationships in tomatoes using single- to low-copy nuclear RFLP's. They found ten times more genetic variability in the self-incompatible species relative to the self-compatible ones. Their phenetic analysis of RFLP data showed the self-compatible species to cluster apart from the self-incompatible ones, with a second cluster formed by the red-fruited species. The northern population and southern populations of *S. peruvianum* clustered separately.

Genepools

Based on crossing data, Rick (1979) divided tomato species into two major intra-crossable, inter-crossable groups. One (the "peruvianum group") consists of *S. peruvianum* and *S. chilense* (Dunal in DC.) Reiche, while the other (the "esculentum group") contains the remaining seven species. The barrier to gene flow between these groups can be broken down by the application of embryo culture, which succeeds only when a member of the esculentum group is employed as the female parent. The reciprocal cross can be made if highly selected inbred variants of *S. peruvianum* are used (Hagenboom, 1972a,b). Within the *S. peruvianum* complex, there are interspecific crossing barriers that can be broken down only with several bridging accessions. Within the esculentum group, taxa are more intercrossable. Fortunately, *S. lycopersicum* can be hybridized with all other eight tomato species. This has resulted in many superior cultivars (Stevens and Rick, 1986; Rick, 1987, 1991). In addition, tomato can be hybridized with great difficulty with close outgroup species (e.g., *S. lycopersicoides* Dunal, *S. sitiens* I. M. Johnston = *S. rickii* Correll; Taylor, 1986).

TABLE 8. MAJOR TOMATO GERMPLASM COLLECTIONS.

Genebank	Genebank Accessions	
Genebank	<i>S. lycopersicum</i> , including var. <i>cerasiforme</i> , breeding lines, and mutants	Other wild species
AVRDC	6,601	654 accessions of all wild species
USDA, Geneva, New York, USA	5,130	916 of all wild species except <i>S. pennellii</i>
National Plant Genetic Resources Laboratory, Laguna, Philippines	4,514	214 accessions of <i>S. cheesmanii</i> , <i>S. peruvianum</i> , and <i>S. pimpinellifolium</i>
IPK	2,913	Some <i>S. peruvianum</i> , some <i>S. pimpinellifolium</i>
VIR	2,540 (combination of <i>S. lycopersicum</i> and wild species, but not clear how many wild vs. cultivated).	

C.M. Rick Tomato Genetics Resources Center, Davis, California, USA	2,484	867 of all wild species
CPRO-DLO/CGN	1,033	90 of all species except <i>S. chemewiskii</i> , <i>S. neorickii</i> , <i>L. parviflorum</i>

Adequacy of Collections

The raw numbers of collections and numbers of wild species collections of tomato is considered as good or better than most other crop plants. Certain remote areas in the watershed of the Rio Marañon in Peru are targeted by the US Tomato Crop Germplasm Committee as of possible interest.

4.3. BENEFITS TO A SYSTEM OF OPEN ACCESS TO PGRFA

The foregoing discussion examined the scientific data regarding genetic diversity of crop germplasm, existing *ex situ* genebank holdings, and factors involved with the loss of this diversity in *ex situ* collections. These data were requested from the conveners of this Workshop in an effort to provide negotiators at the IU with facts to consider in its renegotiation. The science and policy of this issue are inextricably linked, and the exploration of negotiation points would be incomplete without a discussion of policy. This is certainly true in the US where many are uncertain how to best move the discussions at the IU forward. I believe this is partly a lack of appreciation of contributions from the north to scientific and food needs of south. Such discussions are being increasingly heard. These have included leaders in US Government agencies (US Agency for International Development [USAID], Chambers and Bertram, 1998); US Department of State (Kimble, 1998); the USNPGS (Shands, 1998); and the USDA, Research Education, and Economics (Woteki, 1998). A summary of many of these arguments and my arguments follow. The focus on contributions from the north are meant to provide a balance to this debate, but I understand the valid concerns of those from the south regarding IPRs. By “open access” I mean ready availability of unimproved wild species or landrace germplasm without compensation on a transactional basis.

➤ IARCs and National Crop Improvement Programs have been tremendously successful in producing and introducing new varieties and combating world hunger in developing nations. Open access stimulated and maintained this system without an expensive diversion of time and funds to tracking unimproved parents in advanced varieties or follow-up litigation for disputes.

➤ As a corollary to the above, open access to collections has provided the world scientific community unimproved materials needed for significant advance in basic research that supports crop improvement for *all* countries. An exemplary case can be made in the use of the extensive tomato collections that has advanced tomato breeding and genetics, as well as supporting disciplines of entomology, systematics, physiology, pathology, field management, etc. (e.g., Atherton and Rudich, 1986). If costs were associated with the use of these unimproved materials the research would have been greatly slowed.

➤ Advanced varieties produced by commercial breeders are widely grown in developing nations to their great economic benefit. Linking utilization of PGRFA directly to benefit sharing could potentially slow the continued production of new

varieties by taking away incentive to do so, e.g., sufficient profit margin. Under this view, user countries are not being exploited, but helped. The argument of the unfairness of payment by the south of an advanced variety incorporating southern germplasm is perhaps one of the most often mentioned examples of exploitation, but from my view is based more on nationalistic concerns than the realities of market forces. As long as unimproved germplasm is not protected, no country, even the poor ones, is hindered from its continued use.

➤ No individual country, even the “southern, gene-rich” ones is independent of genetic resources from elsewhere. Bread (from the Middle East) is as major a staple in Latin America as potatoes (from the central South American Andes) are in Eastern Europe, and the interdependence of food is worldwide (Table 1). In addition, many “southern” countries (e.g., Botswana, Chile, Honduras, Nicaragua) also are relatively gene poor and would be equally harmed by restrictions in open access. There is therefore as much potential for “south-south” restrictions in transfer and use of PGRFA as “north-south” restrictions. This has the potential to harm developed and developing countries by leaving them out of the benefit stream of continued crop improvement. *Everyone* will lose.

➤ As a corollary to the above, the projected doubling of the world’s population likely will place world hunger as a dominant need internationally and eclipse food sustainability over access concerns. Agriculture forms 16% of the US Gross Domestic Product and the US produces much more than it needs. The US is a strong supplier of grains internationally both through foreign trade and aid. The US is the third leading producer of wheat, exporting 50% of its production, and the leading producer of maize, exporting 20%. The exports of wheat alone currently meet the needs of the top four importing countries and maize exports enough to meet the needs of the top eight importing countries. It is the leading producer of soybeans (Table 1), exporting nearly 40%. In short, the world is interdependent on food production and the PGRFA that sustain it.

➤ Increased food productivity, stimulated by open access to PGRFA, is needed to more intensively farm existing lands, rather than opening new marginal lands and spoiling them for biodiversity conservation.

➤ A highly regulated approach to the transfer of genetic resources will have the unintended consequence of diverting funds from variety development and conservation to tracking germplasm in hybrids, followed by arbitration and litigation. This quickly could make access and use of PRGFA cost-prohibitive. Similarly, an overly bureaucratic and time consuming approach to obtaining collecting permits will hinder the ideal goals of stimulating collaboration.

➤ The debate on the value of PGRFA has been clouded by expectations of large funds possible by biodiversity prospecting for pharmaceuticals. In general, agriculture never operates on the profit margin of the pharmaceutical industry, and expectations of additional benefits to accrue from new varieties are inflated, factoring in research and development costs (Chambers and Bertram, 1998). Open access may be hindered by unrealistic expectations of benefits.

➤ Restriction of open access likely will make breeders bypass protected collections altogether and seek other sources of germplasm that are unencumbered by potential future high costs and legal liability. If the germplasm is not used, national and international collections have the potential to become expensive museums visited by only a very few.

➤ Similar to the above, the rapidly expanding field of transgenic technologies (Birch, 1997) often bypasses the need for working within traditional gene pools,

reducing the value of *in situ* collections. Reduced or closed access will stimulate the search for traits outside of restricted collections.

➤ The US makes many substantial contributions to PGRFA activities that have not been widely appreciated in the debate on the IU.

➤ US academic institutions are major contributors to training foreign scientists, particularly institutions in agriculture at the US land grant colleges and universities, training about 10,000 foreign scientists per year. Many of these students and other academics visit the US thanks to funds from the USAID and other US agencies.

➤ US agencies provide funds for international cooperation in PGRFA activities. One of these is the USDA Foreign Agricultural Service, International Cooperation and Development Program. I tried to summarize other programs focused in international cooperation in the US, but according to Henry Shands (USDA, ARS), and Marsha Stanton (USDA, Cooperative States Research Education and Extension Service [CSREES]), the many such contributions are very difficult to quantify. This is because international programs of different US agencies are not clearly outlined as separate budget items.

➤ The USNPGS provides a major service internationally through the maintenance of about 350,000 accessions in short, medium, and long-term storage. These genetic resources are openly available internationally. The US has distributed 560,899 accessions from the US germplasm system in the last five years (1993-1997); fully 30% of these (168,431), were sent internationally (data provided by Mark Bohning, USDA ARS Germplasm Resources Information Network Analyst).

➤ The US National Seed Storage Laboratory (NSSL) in Fort Collins Colorado provides long-term backup storage for some international collections at no charge to the IARCs. For example, NSSL keeps a backup collections of the rice germplasm from the International Rice Research Institute (IRRI), one of the 16 IARCs (Kaplan, 1998).

➤ The USNPGS works closely with other countries in extension work. For example, in collaboration with IPGRI, they have developed, made freely available, and trained others in a personal computer version of its GRIN System. Also, the USNPGS works closely with other National Programs in germplasm regeneration and characterization, and *in situ* conservation projects.

➤ The US provides substantial support to the CGIAR centers, with 1997 contributions totaling \$26 million. The US maintains that unrestricted free release policy within the CGIAR, like in the USNPGS, itself is a strong component of benefit sharing.

➤ The USNPGS contributes significantly to collaborative germplasm exchanges and collecting missions with full participation and funding for national cooperators. This often is followed by joint publication of results in the scientific literature, and the initiation of further scientific collaborations. A restricted system of collection and exchange will have the unintended result of hindering collection and preservation and ultimate loss of plants going extinct.

➤ While many of these benefits of open access focus on US contributions, examples from other nations would multiply them many-fold. Raymond and Fowler (1998) outline many significant “non-monetary benefits” of agricultural biodiversity that evolved under a policy of open access and can be maintained by it. They define non-monetary benefits as a diverse range of economic, societal, environmental, and scientific benefits in the open use and broad benefit sharing of PGRFA. They cite many non-monetary benefits that mirror those mentioned above. They additionally add that tracking parents in hybrids can be complex because of difficulty of determining “country of origin” (defined by the CBD as the country which possess those genetic resources in *in situ* conditions). It also can be complex because of complex pedigrees.

Raymond and Fowler (1998) mention a complex wheat hybrid, VEERY, with 51 parents from 26 countries. Complex pedigrees are also present in many other crops. Difficulty in determining parents also can be caused by difficulty in determining species-specific markers in a complex range of genotypes, as in the *Solanum brevicaulle* complex in potatoes (Miller and Spooner, 1998) where the close phylogenetic relationships of the cultivated species and their wild relatives may blur species boundaries. In addition species-specific markers may quickly become modified in interspecific hybrids making them difficult to use as markers (Song and Osborn, 1995). In short, a litigious approach to tracking germplasm is difficult, often impossible, and likely to be cost-prohibitive for all but the highest value commercial varieties.

5. DISCUSSION

This paper approaches the questions of the scientific basis for the sole reliance on existing genebank accessions, and the continuing need for the conservation and collection of *in situ* genetic resources. Research data include FAO statistics of genebanks in general, and data of five major and diverse food crops. These data are used to extrapolate general answers for all genetic resources. The questions have scientific relevance because 1) the world's genebanks (now numbering 1,300) are becoming so rapidly stocked (currently 6.1 million accessions) that collections are outstripping capacity of regeneration, 2) germplasm of wild relatives is becoming lost through disappearing habitats, and landraces may becoming lost through the adoption of advanced cultivars. The question also has political relevance because a rapid sea change in the politics and policies of germplasm ownership, exchange, and use.

The surveys presented here suggest that the first phase of genebanking has been marvelously successful in collecting and preserving a broad range of diversity of the major food crops. CGCs in the US reported collections to be the top priority, but priorities to collect many major crops are mainly for gaps in collections providing good but yet still incomplete coverage. For most major crops, genebanks are so relatively well stocked, at least in landraces, that they must be better organized to a manageable size by the development of smaller core collections (Frankel, 1984). For example, these have been established for annual alfalfa (Diwan et al., 1994), barley (Knupffer and van Hintum, 1995), common bean (Thome et al., 1995; Skroch et al. 1998), coffee (Hamon et al., 1995), peanut (Holbrook et al., 1993), and sorghum (Rao and Rao, 1995).

Many of the world's 6.1 million collections may become lost through lack of funds for regeneration. In addition, some genetic diversity will become lost in static *in situ* collections through genetic drift over serial increase cycles, genetic bottlenecks due to small sample sizes, and accumulation of deleterious mutations. Dynamic conservation strategies have the potential to alleviate some of these problems and maintain the evolutionary forces for the species. Most of these questions have been approached by theory and modeling, however, and we largely lack empirical data to suggest the severity of these problems. Ideally, the world would preserve its genetic diversity through a coordinated multi-national effort involving a combination of core collection strategies, short- medium- and long-term static and dynamic genebanks, periodic recollections to maintain genetically variable germplasm, and habitat preservation. A movement towards farmers' rights, costs for unimproved PGRFA, and potential huge costs for funding the GPA without an appreciation of existing PGRFA contributions are hindering this agreement with the US.

The *complicating* force behind these questions however is not the science, but the politics of germplasm, and a purely scientific answer to these questions will never bring

the world to agreement. In my view, this is part of a larger question of inequitable worldwide distribution of wealth, and germplasm is a suitable vehicle for these questions because it resides in the poorer countries. Stated bluntly, (many) in the south feel exploited regarding their native PGRFA by a vastly richer and technologically advanced north. The south is reacting by quickly regulating PGRFA access in sometimes very restricted ways. (Many) plant breeders and other users of PGRFA in the north are discouraged by potential increased costs, reduced productivity, and a change in a perception of their work from an ideal of feeding humankind to working under a cloud of distrust, litigation, and accusation of germplasm thievery.

World food security, continued production of new varieties, and international cooperation on PGRFA hinge on continued access to unimproved genetic resources for both rich and poor nations alike; in my view these would be optimized for everyone by open access. The scientific data suggest that for the major crops, the north could for many generations operate with its own *in situ* collections. However this is an extreme scenario unlikely to occur as it would provide the north and the south alike with many scientific and economic disruptions, especially for the under collected “new crops” (Roh and Lawson, 1991; Janick and Simon, 1990, 1993; Maynard, 1992; Janick, 1996; Schneider, 1996). In the (undetermined) long-term, genebank accessions may lose their utility through reduction in variability and viability. Most hope such a breakdown in agreements can be avoided, and wish to work cooperatively under a system of open access for unimproved germplasm, stimulated by multilateral flow of benefits such as described above (e.g., Raymond and Fowler, 1998) and funding of the GPA that factors in or redirects existing PGRFA contributions. However the direction of the debates at the IU are viewed by many as having failed to consider seriously the existing financial contributions and the concerns of the diverse parties of the north. This will be needed to build the political consensus to lead to agreement.

A major stumbling block for agreements concerns compensatory funding as the primary mechanism for benefit sharing. Recognition of collective rights (farmers’ rights) is not recognized by the US. Discussion for another fund concerns the expectations for funding the Global Plan of Action (GPA). During a meeting of FAO in December, 1996, the secretariat of the FAO introduced a document entitled “Revision of the Cost Estimates of the Global Plan of Action”. In this document, the costs expected to be borne by the international community were included, and provided three options: Option A, a basic or rudimentary approach; Option B, a moderate approach consistent with known and documented needs; and Option C “a more and ideal and comprehensive approach”. These three options would require an annual cost of \$150 Million, \$247 Million, and \$451 Million, respectively. The US Government and others hold that in the financing of the GPA, we should make use of existing funds already related to PGRFA rather than to establish another funding mechanism, and to see how these can be more efficiently used for this purpose. Clearly, cost savings by considerable consolidation of the world’s 1,300 genebanks is needed. International (CGIAR) programs appear to be a logical component in this consolidation. Ideally they would coordinate and integrate and share their work with the national programs.

The US economic view (and that of many other countries) is based on a belief that for the most part, market forces will provide a balance for the allocation of scarce resources (Lourie, 1998). I believe that restrictive policies on PGRFA access will disrupt the flow of personnel, ideas, and political will needed to stimulate the market of PGRFA benefits to even develop for the south. Development of consensus requires dialogue, and negotiations will require an appreciation of viewpoints from *both* sides of the debate, including trust that developed countries are eager to cooperate, not “steal [developing countries] golden germplasm egg” (Kimble, 1998). Those questioning

when the benefit stream ever begin ignore the substantial benefits of the pre-CBD system and fail to see that many of the benefits are already here for poor and rich countries alike. This view is unlikely to appeal to many who are politicized to a paradigm of exploitation, but it is shared as an honest, ethical, and practical view by many who are invaluable participants in our long-range goal of developing consensus (and funding for the GPA) in these debates. With an improved appreciation of contributions from both sides, I am convinced that we will be in a better political position to fund the GPA and work cooperatively to everyone's mutual benefit.

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8. EXPLANATION OF ABBREVIATIONS

AVRDC	Asian Vegetable Research and Development Center, Taiwan
CBD	Convention on Biological Diversity
CGC	US Crop Germplasm Committees
CGIAR	Consultative Group on International Agricultural Research
CGRFA	FAO Commission for Genetic Resources for Food and Agriculture for the revision of the 1983 International Undertaking on Plant Genetic Resources for Food and Agriculture
CICA	<i>Center for Investigation of Andean Cultivars, Cusco, Peru</i>
CIP	<i>International Potato Center, Lima, Peru (one of the 16 CGIAR Centers)</i>
CPC	<i>Commonwealth Potato Collection, Mylnfield, Invergowrie, Dundee, Scotland, U.K</i>
CPRO-DLO/CGN	Centre for Plant Breeding and Reproduction Research, Centre for Genetic Resources, Wageningen, The Netherlands
CSIRO	Commonwealth Scientific Industrial Research Organization, Australia
CSREES	US Cooperative States Research Education and Extension Service
EBN	Endosperm Balance Number
EMBRAPA/CENARGEN	The Brazilian Agricultural Research Corporation of the National Centre for Research for Genetic Resources and Biotechnology
FAO	Food and Agriculture Organization of the United Nations
GPA	Global Plan of Action for the Conservation and Sustainable Utilization of Plant Genetic Resources for Food and Agriculture, developed at the Leipzig Declaration, adopted by the International Technical Conference on Plant Genetic Resources in Leipzig, Germany on June 17 th 23, 1996.
GRIN	US Germplasm Resources Information Network
IARC	International Agricultural Research Center
ICRISAT	<i>International Crop Research Institute for the Semi-Arid Tropics, Patancheru, India (one of the 16 CGIAR Centers)</i>
IITA	<i>International Institute of Tropical Agriculture, Ibadan, Nigeria (one of the 16 CGIAR</i>

	<i>Centers)</i>
INIAP	<i>National Institute of Agrarian Research, Quito, Ecuador</i>
INTA	<i>National Institute of Agrarian Technology [potato genebank in Balcarce, Buenos Aires; peanut genebank in Manfredi, Córdoba], Argentina</i>
IPGRI	<i>International Plant Genetic Resources Institute, formerly International Board of Plant Genetic Resources, IBPGR (one of the 16 CGIAR Centers)</i>
IPK	<i>Institute of Plant Genetics and Crop Plant Research, Gatersleben, Germany</i>
IPR	<i>Intellectual Property Rights</i>
IRRI	<i>International Rice Research Institute, Manila, Philippines</i>
IU	<i>International Undertaking of the FAO</i>
MAFF, NIAR	<i>Ministry of Agriculture, Forestry and Fisheries, National Institute of Agrobiological Resources, Japan</i>
NRCG, ICAR	<i>National Research Center for Groundnut, Indian Council for Agricultural Research, Janagadh, India</i>
NRSP-6	<i>NRSP-6, National Research Support Program-6, formerly known as IR-1, the Inter-Regional Potato Introduction Station, Sturgeon Bay, US</i>
NSSL	<i>US National Seed Storage Laboratory, Ft. Collins, Colorado</i>
PGRFA	<i>Plant Genetic Resources for Food and Agriculture</i>
PVP	<i>Plant Variety Protection</i>
SINGER	<i>System-Wide Information Network on Genetic Resources of the CGIAR</i>
TRIPS	<i>Agreement on Trade-Related Aspects of Intellectual Property Rights</i>
UPOV	<i>International Union for the Protection of New Varieties of Plants</i>
USAID	<i>US Agency for International Development</i>
USNPGS	<i>US National Plant Germplasm System</i>
VIR	<i>N. I. Vavilov All Russian Institute of Plant Industry, St. Petersburg, Russia</i>
WIEWS	<i>World Information and Early Warning System on Plant Genetic Resources, FAO</i>
WTO	<i>World Trade Organization</i>