



Centro Internacional de Agricultura Tropical
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Conservation of *Phaseolus* beans genetic resources

A strategy

D.G. Debouck

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The above picture of terracotta bottle from the author's collection is of double significance about crop origin and crop movement. First, it is that of a Moche pottery, a human civilization that flourished on the coast of today northern Peru in 100-700 a.D.. It clearly depicts seeds of Lima bean, a crop that was domesticated in the area (Motta-Aldana et al. 2010) and key to food security for that pre-Columbian people. There is good evidence (Diamond 2005; Fagan 1999) that this civilization became extinct because of severe climatic alterations caused by 'El Niño' around 700 a.D.. Second, the seeds put in the front of the bottle are that of 'Jaspé de l'Ituri'; Ituri refers to a mountainous region of eastern Congo, where they were still grown in the 1950s a.D. The morphological similarity with those pictured on the pottery is striking. Surely, the Lima Painter (as identified by Donnan & McClelland 1999) was not aware that the seeds he or she depicted on the bottle would be grown

in eastern central Africa fourteen centuries later, and kept recently in CIAT genebank and Svalbard vault. Seeds are part of our own nutritional and historical fabric !

But the picture above also brings two reflections for this strategy: to whom belong the Moche Lima beans ? And who should care and pay for the conservation of these beans ? Obviously the Moche Lima beans belong to the Moche, but the Moche no longer exist. And one should note that the Moche themselves receive/ inherit these seeds from people living high up the Sechura Desert some 5-6,000 years before the Moche exist namely as an organized state and civilization (Piperno 2012; Piperno & Dillehay 2008)! One modern Andean state (a republic since 28 July 1824) will likely claim the heritage of the Moche, but this is likely to be without 'prior informed consent' (Convention on Biological Diversity, 1992, Art. 15.5) because the generators of these genetic resources are dead since millenia. So, our current legal, economic and social frameworks and standards might be ill prepared for the problem to be tackled; yet the same Lima beans are key for the food security of poor people in the highlands of Cochabamba in Bolivia (Cárdenas 1989), of Hararghe in Ethiopia (Westphal 1974), of Mahafaly in Madagascar (Baudoin 1989), and of Mandalay in Myanmar (Purseglove 1968).

So, the cover photograph showed a doubly (in space and in time) orphan bean crop that benefited different peoples millennia afterwards: the Moche benefited from a crop domesticated outside their coastal oasis, and the farmers of eastern Congo grew a crop introduced from a land thousands of miles apart!

Conservation of genetic resources of *Phaseolus* beans

OUTLINE

1. THE QUESTION AT THE START AND ITS IMPLICATIONS

2. WHICH ARE THE GENETIC RESOURCES OF PHASEOLUS BEANS?

- 2.1. How many species of beans are there, and which are they?
- 2.2. What are the genetic relationships between the different bean species?
- 2.3. Where are the different beans species distributed today?

3. HOW DID SUCH GENETIC RESOURCES DEVELOP?

- 3.1. what is wild? what is cultivated?
- 3.2. the bean domestication process as a reduction of genetic diversity
- 3.3. locations *versus* durations

4. WHAT HAS BEEN USED IN BEAN GENETIC RESOURCES?

- 4.1. importance of bean germplasm for food and feed across the world
- 4.2. which bean varieties have been used so far?
- 4.3. considerations about the unrealized economic potential

5. WHAT HAS BEEN LOST IN GENETIC RESOURCES?

- 5.1. what has been lost as landraces and traditional varieties?
- 5.2. what has been lost in wild species and wild populations?

6. CURRENT CONSERVATION EFFORTS

- 6.1. Status of the *ex situ* conservation of bean genetic resources
- 6.2. Status of the *in situ* conservation of bean genetic resources
- 6.3. What does not work properly nowadays in conservation of bean genetic resources?

7. STRATEGY FOR THE CONSERVATION OF BEAN GENETIC RESOURCES

- 7.1. The rationale for a strategy
- 7.2. The drives of the Strategy, major activities and time sequence
- 7.3. Implementation of the Strategy, and funding mechanisms
- 7.4. Conditions to and indicators of success

8. CONCLUDING REMARKS

ACKNOWLEDGMENTS

LITERATURE CITED

1. THE QUESTION AT THE START AND ITS IMPLICATIONS

The question at the start set by the Global Crop Diversity Trust – and purpose of this Strategy - was: “What are the activities and resources required to safely conserve bean genetic resources in perpetuity?”. As we see below, the last two words introduce another dimension - time, assuming that the first part of the question could be fully answered today. It quickly suggests other questions tightly interrelated, particularly in view of a practical implementation. These are – and set the plan of this document:

2. which are the genetic resources of *Phaseolus* beans?
 - 2.1. how many species of beans are there, and which are they?
 - 2.2. what are the genetic relationships between the different bean species?
 - 2.3. where are these species naturally distributed today?
3. how did such genetic resources develop?
 - 3.1. what is wild? what is cultivated?
 - 3.2. the bean domestication process as a reduction of genetic diversity
 - 3.3. locations *versus* durations

The questions in parts 2 and 3, logically expected at the beginning, set the scene in concrete terms from the object perspective, and will help to quantify many elements of the Strategy. From these the reader will understand our focus on the primary centers of diversity, that goes together with the current revolution in genomics.

4. what has been used in bean genetic resources?
 - 4.1. importance of bean germplasm for food and feed across the world
 - 4.2. which bean varieties have been used so far?
 - 4.3. considerations about the unrealized economic potential

Part 4 is related to use by human societies and uses in agronomy and bean breeding, with the hope to open minds to shifting priorities and evolving markets. Uses through time are briefly discussed, showing how a wide genetic diversity met and continues to meet breeders and human societies’ needs.

5. what has been lost in genetic resources?
 - 5.1. what has been lost as landraces and traditional varieties?
 - 5.2. what has been lost in wild species and wild populations?

Part 5 brings a time perspective to past and ongoing losses, that we need urgently, because as a paradox, current production patterns and ways of living contribute to eliminate the bean diversity that made possible such breeding efforts and urban life.

6. the current conservation efforts
 - 6.1. Status of the *ex situ* conservation of bean genetic resources
 - 6.2. Status of the *in situ* conservation of bean genetic resources
 - 6.3. What does not work properly nowadays in conservation of bean genetic resources?

Part 6 presents the current situation in *ex situ* and *in situ* conservation, ending up with a brief analysis of shortcomings. Then, we will examine some reasons behind the strategy, the major activities encompassed by the strategy, and a logical time sequence. We will then address the questions: How to implement the strategy? How to fund the strategy?, ending that part 7 with indicators of success. The document ends up with a couple of concluding remarks (part 8), and some references.

7. Strategy for the conservation of genetic resources of *Phaseolus* beans

7.1. the rationale for a Strategy

7.2. the drives of the Strategy, major activities and time sequence

7.3. Implementation of the Strategy, and funding mechanisms

7.4. Conditions to and indicators of success

8. Concluding remarks

The boxes in the main text sum up points of importance for the development and implementation of the Strategy.

2. WHICH ARE THE GENETIC RESOURCES OF *PHASEOLUS* BEANS ?

2.1. How many species of beans are there, and which are they?

The first international legume conference held in Kew, United Kingdom, in 1978 set a landmark because a clear definition of the genus *Phaseolus* as compared to other genera of tropical legumes (e.g. *Vigna*, *Macroptilium*, *Ramirezella*, ...) finally came up (Maréchal et al. 1978, 1981). Lackey (1983) confirmed these generic limits further, and indicated that *Phaseolus* might have fifty species. In a review of the genus using that same definition, Delgado-Salinas (1985) reported the presence of thirty-six species in four sections. In the last review of *Phaseolus*, Freytag & Debouck (2002) indicated that seventy-four species distributed in fifteen sections may exist. One should note from these reviews that *Phaseolus* is strictly of Neotropical origin, and therefore *P. massaiensis* and *P. nakashimae* in WCMC's (1991) Conservation Status Listing are doubtful taxa. Table 1 gives an indication about the current number and names of possibly valid taxa (let us consider them all as wild for the time being), date of description, and their geographic distribution on the basis of herbarium voucher specimens and seed accessions kept in genebanks. Most of the original data can be seen in 'Cahiers de Phaséologie', compilations organized by sections of the genus as currently defined, at <http://www.ciat.cgiar.org/urg>. The list of Table 1 comes from a study of voucher specimens in 81 Herbaria visited in the period 1978-2013 (Table 1 will also be used as reference for the authors of *Phaseolus* taxa who will not be mentioned in the main text). Some synonyms (e.g. *P. teulensis* and *P. pyramidalis*, merged into *P. grayanus*) as proposed by Delgado-Salinas et al. (2006) are here endorsed, while others (e.g. *P. purpusii*) are kept on hold till more material becomes available for study. Table 2 gives an indication about contents of the different sections. The number of species climbs now up to seventy-seven without entering into subspecies; if these are proven valid, the number of taxa might be even higher. From the dates of the descriptions of the species, it is clear that the periodical reviews of the genus (e.g. Piper 1926; Delgado-Salinas 1985, 2000; Freytag & Debouck 2002) being forcefully more exhaustive come up with new species. But even after the last review of 2002, recent field work continues to disclose new species (e.g. Delgado-Salinas & Carr 2007; Salcedo-Castaño et al. 2006, 2009, 2011), and the final number might not be definitive at this time. It is true that in the case of *P. dasycarpus*, the section *Paniculati* lost one species to the benefit of section *Pedicellati* (Table 2) (Mercado-Ruaro et al. 2009), but with *P. novoleonensis* the former section might have a net gain in a wide crossing perspective for Lima bean (Salcedo-Castaño et al. 2006). A somewhat similar story is that of *P. persistentus*: described in 2002 by Freytag & Debouck and located in the *Falcati* by error because of the scarce herbarium material at hand, it was indicated as belonging to the phylum of *P. vulgaris* by Delgado-Salinas et al. (2006), but unfortunately not found again in the field (Debouck 1995). Interestingly, Shrire (2005) considered that the genus may have 60-65 species distributed in North and Central America, with only three species endemic to South America and the Galapagos Islands. Indeed, one can note that the number of species remains stable for the later geographic regions, while it continues to increase in Central and North America (including Mexico). For the region north of Isthmus of Panama, one cannot at this time discard a final number of 85 species, namely because of the endemic species, since most likely the species with wide distribution have already been found (at least once).

Box 1

Because it increases possibilities of success in future bean breeding, a set of activities of the Strategy must continue to define the number of bean species. The region north of Isthmus of Panama seems rewarding towards that goal. This could be achieved in two steps:

- Study of voucher specimens in Herbaria
- Filed explorations

Table 1 – Tentative list of possibly valid *Phaseolus* species and general indication about geographic distribution and qualification of their range R (E= endemic, I= intermediate, W= widespread).

Bean species (only as native wild plants)	Area of geographic distribution	R
1. <i>acutifolius</i> Asa Gray (1850)	SW USA, NW Mexico down to Neo-volcanic axis	W
2. <i>albescens</i> McVaugh ex Ramírez & Delgado (1999)	W of Neo-volcanic axis of Mexico	E
3. <i>albiflorus</i> Freytag & Debouck (2002)	N of Sierra Madre Oriental in Mexico	E
4. <i>albinervus</i> Freytag & Debouck (2002)	Chihuahua of Mexico	E
5. <i>albiviolaes</i> Freytag & Debouck (2002)	Sierra Madre Oriental in Mexico	E
6. <i>altimontanus</i> Freytag & Debouck (2002)	Sierra Madre Oriental in Mexico	E
7. <i>amabilis</i> Standley (1940)	Sierra Madre Occidental in Mexico	E
8. <i>amblyosepalus</i> (Piper) Morton (1944)	Durango and Sinaloa border in Mexico	E
9. <i>angustissimus</i> Asa Gray (1853)	SW USA and NW Mexico	W
10. <i>anisophyllus</i> (Piper) Freytag & Debouck (2002)	Durango of Mexico	E
11. <i>augusti</i> Harms (1921)	Andes, from S Ecuador to NW Argentina	W
12. <i>campanulatus</i> Freytag & Debouck (2002)	W end of Neo-volcanic axis of Mexico	E
13. <i>carteri</i> Freytag & Debouck (2002)	S end of Baja California of Mexico	E
14. <i>chiapasanus</i> Piper (1921)	Parts of Veracruz, Oaxaca and Chiapas in Mexico	I
15. <i>coccineus</i> L. (1753)	From Chihuahua, Mex., down to Jalapa, Guatemala	W
16. <i>costaricensis</i> Freytag & Debouck (1996)	Central and E Costa Rica to W Panama	I
17. <i>dasycaarpus</i> Freytag & Debouck (2002)	S end of Sierra Madre Oriental	E
18. <i>dumosus</i> Macfadyen (1837)	Volcanic mountains of SW Guatemala	E
19. <i>esperanzae</i> Seaton (1893)	Central and E of Neovolcanic axis of Mexico	I
20. <i>esquinensis</i> Freytag (2002)	Central Chiapas of Mexico	E
21. <i>filiformis</i> Bentham (1844)	Gulf of California to NW Mexico to Texas	W
22. <i>glabellus</i> Piper (1926)	Gulf of Mexico, Tamaulipas to Chiapas	W
23. <i>gladiolatus</i> Freytag & Debouck (2002)	San Luís Potosí and Hidalgo of Mexico	E
24. <i>grayanus</i> Wootton & Standley (1913)	NW to N Mexico to Arizona through Texas	W
25. <i>hintonii</i> Delgado (2000)	Central W Mexico	E
26. <i>hygrophilus</i> Debouck (2011)	Central S Costa Rica	E
27. <i>jaliscaanus</i> Piper (1926)	S Sierra Madre Occidental of Mexico	I
28. <i>juquilensis</i> Delgado-Salinas (2000)	Central S Oaxaca of Mexico	E
29. <i>laxiflorus</i> Piper (1926)	E of Neovolcanic axis of Mexico	E
30. <i>leptophyllus</i> G. Don (1832)	Central Guerrero of Mexico	E
31. <i>leptostachyus</i> Bentham (1837)	Arizona through Mexico to Central Costa Rica	W
32. <i>lignosus</i> Britton (1918)	Bermuda	E
33. <i>lunatus</i> L. (1753)	Central and South America, Caribbean	W
34. <i>macrolepis</i> Piper (1926)	Central and SW Guatemala	E
35. <i>maculatifolius</i> Freytag & Debouck (2002)	N of Sierra Madre Oriental in Mexico	E
36. <i>maculatus</i> Scheele (1848)	Arizona through Texas to Puebla of Mexico	W
37. <i>macvaughii</i> Delgado-Salinas (2000)	Coastal W Mexico from Sinaloa down to Guerrero	I
38. <i>magnilobatus</i> Freytag & Debouck (2002)	Central W Mexico	E
39. <i>marechalii</i> Delgado-Salinas (2000)	Central and E of Neovolcanic axis of Mexico	E
40. <i>micranthus</i> Hooker & Arnott (1838)	W of Neovolcanic axis to S Pacific, Mexico	I
41. <i>microcarpus</i> Mart. (1831)	Central Mexico, from Durango down to Costa Rica	W
42. <i>mollis</i> Hooker (1847)	Archipelago of Galapagos Islands	E
43. <i>neglectus</i> Hermann (1948)	N of Sierra Madre Oriental	I
44. <i>nelsonii</i> Maréchal, Mascherpa & Stainier (1978)	Central and southern Mexico to Chiapas	E
45. <i>nodosus</i> Freytag & Debouck (2002)	W of Neovolcanic axis of Mexico	I
46. <i>novoleonensis</i> Debouck (2006)	N of Sierra Madre Oriental	E
47. <i>oaxacanus</i> Rose (1903)	Central Oaxaca of Mexico	E
48. <i>oligospermus</i> Piper (1926)	Chiapas of Mexico to central Costa Rica	E
49. <i>pachyrrhizoides</i> Harms (1921)	Andes of northern and central Peru	I
50. <i>parvifolius</i> Freytag (2002)	Arizona down to E Guatemala through W Mexico	W
51. <i>parvulus</i> Greene (1881)	SW of USA and Sierra Madre Occidental of Mexico	I
52. <i>pauciflorus</i> Sessé & Mociño ex G. Don (1832)	Northern and central Mexico	I

53. <i>pedicellatus</i> Bentham (1837)	Neovolcanic axis, Sierra Madre Oriental of Mexico	I
54. <i>persistens</i> Freytag & Debouck (2002)	Central volcanoes of Guatemala	E
55. <i>plagiocylis</i> Harms (1921)	Eastern central Nuevo León of Mexico	E
56. <i>pluriflorus</i> Maréchal, Mascherpa & Stainier (1978)	Western central Mexico	I
57. <i>polymorphus</i> Sereno Watson (1882)	Northern and eastern central Mexico	I
58. <i>polystachyus</i> (L.) Britton, Stern & Poggenberg (1888)	Eastern USA from New York to Florida to E Texas	W
59. <i>purpusii</i> Brandege (1912)	Western San Luís Potosí of Mexico	E
60. <i>reticulatus</i> Freytag & Debouck (2002)	SW of Durango in Mexico	E
61. <i>ritensis</i> Jones (1908)	SW of USA and NW of Mexico	W
62. <i>rotundatus</i> Freytag & Debouck (2002)	Central Jalisco of Mexico	E
63. <i>salicifolius</i> Piper (1926)	Eastern Sinaloa of Mexico	E
64. <i>scrobiculatifolius</i> Freytag (2002)	Western central Veracruz of Mexico	E
65. <i>sinuatus</i> Nuttall (1838)	SE of USA from North Carolina to Florida	I
66. <i>smilacifolius</i> Pollard (1896)	Central Florida of USA	E
67. <i>sonorensis</i> Standley (1940)	SE Sonora and SW Chihuahua of Mexico	E
68. <i>talamancensis</i> Debouck & Torres (2001)	SE of Costa Rica	E
69. <i>tenellus</i> Piper (1926)	Central Neovolcanic axis of Mexico	E
70. <i>texensis</i> Delgado & Carr (2007)	Central Texas of USA	E
71. <i>tuerckheimii</i> Donnell-Smith (1913)	Chiapas of Mexico to western Panamá	I
72. <i>venosus</i> Piper (1926)	E Jalisco, Aguascalientes, SW Zacatecas of Mexico	E
73. <i>viridis</i> Piper (1926)	Veracruz of Mexico to Alta Verapaz of Guatemala	I
74. <i>vulgaris</i> L. (1753)	SW Chihuahua Mexico to NW San Luís Argentina	W
75. <i>xanthotrichus</i> Piper (1926)	Chiapas of Mexico to central Costa Rica	W
76. <i>xolocotzii</i> Delgado-Salinas (2000)	E Sierra Madre del Sur of Mexico	E
77. <i>zimapanensis</i> Delgado-Salinas (2000)	SW Sierra Madre Oriental of Mexico	I

N.B.: in the list above, the species *P. coccineus*, *P. lunatus* and *P. vulgaris*, while originally described on cultivated forms, are considered as wild.

2.2. What are the genetic relationships between the different bean species?

Authors (Delgado-Salinas 1985; Delgado-Salinas et al. 2006; Freytag & Debouck 2002) seem to agree that sections within the genus as currently understood mean groups of species that share morpho-, eco-, and physiological features; hencefore it is likely that they share a common phylogeny and thus genetic affinities among them. Defining sections (Table 2) is thus not the sole interest of taxonomists, but has significant consequences for breeding programmes (and thus can be justified). Table 3 expanding on previous work (Debouck 1999) summarises some opportunities of widecrossing for the different bean crops, which are five: *P. acutifolius*, *P. coccineus*, *P. dumosus*, *P. lunatus* and *P. vulgaris*. The Lima bean is quite distant from the common bean, and has to date the largest tertiary genepool (we adopt here the concept of genepool developed by Harlan & de Wet 1971, and adapted to *Phaseolus* beans by Debouck & Smartt 1995). Because of its likely Andean origin (Debouck 1996; Fofana et al. 1999; Serrano-Serrano et al. 2010), the Lima bean has three species in its secondary genepool (i.e. *P. augusti*, *P. mollis* and *P. pachyrrhizoides*). There is a good probability that *P. mollis* is closely related to the Andean wild form of Lima bean (synonym = *P. rosei* Piper: Freytag & Debouck 2002), because of an oceanic migration into the Galapagos Islands from the South American coast at that latitude thanks to the Humboldt Current (McMullen 1999), as it has happened for the wild tomato and wild cotton present in this archipelago (Marshall et al. 2001; Wendel & Percy 1990, respectively). The tertiary genepool of Lima bean includes species of the sections *Coriacei* and *Paniculati*, distributed in the USA, Mexico and the Caribbean, from the Revillagigedo Islands up to Bermuda (Delgado-Salinas et al. 2006; Freytag & Debouck 2002). The common bean, the year-bean and the scarlet runner make each other a secondary genepool, although the latter is a bit more distant. As noted by Maunder and co-authors (2004), there is intraspecific variation in interspecific

crossability: some accessions – particularly wild ones - of a species of section *Phaseoli* cross better with those of another species. In addition, *P. albescens* and *P. costaricensis* can be considered as belonging to the secondary genepool of common bean (Delgado-Salinas et al. 2006; Freytag & Debouck 2002). The case of *P. persistentus* still may need additional evidence. Finally, the tepary bean is an early separation of the *Phaseoli* branch with which it still has some affinities (Debouck 1999 for a review; Delgado-Salinas et al. 2006); its closest taxon – *P. parvifolius* Freytag would be the sole species in its secondary genepool so far (Muñoz et al. 2006). Early separation might be an appropriate terminology as practical possibilities for introgression seem to be limited (Muñoz et al. 2004).

One can note that all possibilities for widecrossing tested so far have been in clade B as defined by Delgado-Salinas and co-workers (2006) (Table 2), not in the other clade A which comprises the *pauciflorus* group (with section *Minkeliersia* according to Delgado-Salinas 1985 and Freytag & Debouck 2002), the *pedicellatus* group (with section *Pedicellati* according to Freytag & Debouck 2002, amended in Debouck 2013g), the *tuerckheimii* group (with sections *Brevilegumeni* according to Freytag & Debouck 2002 and Salcedo-Castaño et al. 2011, and *Chiapasana* and *Xanthotricha* according to Delgado-Salinas 1985), and a few miscellaneous species. This is because as we will see (part 3 below), no bean species has been domesticated in clade A. One should note that the species not assigned to any section, i.e. *P. glabellus* and *P. microcarpus*, have no relationships between themselves. The separation of clade A from clade B might have taken place five or six millions years ago, and thus the possibilities of widecrossing between them by use of current technologies might be nil. In clade B the genetic distance of the Lima bean in relation to the common bean might be due to different evolutionary histories in the Andes for the former (Serrano-Serrano et al. 2010), and in Central America for the latter (Chacón-Sánchez et al. 2007; Bitocchi et al. 2012). The separation of these two taxa together with their related species might trace back as far as four millions years ago (Delgado-Salinas et al. 2006; Serrano-Serrano et al. 2010), clearly explaining why widecrossing between common and Lima bean has not been successful (reviewed by Debouck 1999). The claim of a successful cross between *P. vulgaris* and *P. lunatus* (Honma & Heeckt 1959) was found unproven (Hucl & Scoles 1985), possibly because the taxonomic identity of the parents was incorrect; this example stresses the importance of the right taxonomy.

Box 2

Because of its importance to effective bean breeding, a set of activities of the Strategy must continue to define the relationships between bean species, namely to identify the ones belonging to the secondary genepools of the cultigens in clade B. This could be achieved in two steps:

- interspecific hybridization often with help of embryo rescue through *in vitro* culturing
- molecular markers (AFLPs, introns of cpDNA, sequences)

For both there is ‘prior art’.

Table 2 – *Phaseolus* species and sections as currently recognized (partly based on Delgado-Salinas et al. 2006; Freytag & Debouck 2002).

Sections	Species	total
Clade A (8)	38	
Not assigned	<i>glabellus, microcarpus</i>	2
<i>Bracteati</i> Freytag	<i>macrolepis, talamancensis</i>	2
<i>Brevilegumeni</i> Freytag	<i>campanulatus, hygrophilus, oligospermus, tuerckheimii</i>	4
<i>Chiapasana</i> Delgado	<i>chiapasanus</i>	1
<i>Digitati</i> Freytag	<i>albiflorus, albiviolaceus, altimontanus, neglectus</i>	4
<i>Minklersia</i> (Mart. & Gal.) Maréchal, Mascherpa, Stainier	<i>amabilis, amblyosepalus, anisophyllus, nelsonii, parvulus, pauciflorus, plagiocylix, pluriflorus, tenellus</i>	9
<i>Pedicellati</i> (Benth.) Freytag	<i>dasycarpus, esperanzae, grayanus, laxiflorus, oaxacanus, pedicellatus, polymorphus, purpusii, texensis</i>	9
<i>Revoluti</i> Freytag	<i>leptophyllus</i>	1
<i>Xanthotricha</i> Delgado	<i>esquincensis, gladiolatus, hintonii, magnilobatus, xanthotrichus, zimapanensis</i>	6
Clade B (6)	39	
<i>Acutifolii</i> Freytag	<i>acutifolius, parvifolius</i>	2
<i>Coriacei</i> Freytag	<i>maculatus, novoleonensis, reticulatus, ritensis, venosus</i>	5
<i>Falcati</i> Freytag	<i>leptostachyus, macvaughii, micranthus</i>	3
<i>Paniculati</i> Freytag	<i>albinervus, augusti, jaliscanus, juquilensis, lignosus, lunatus, maculatifolius, marechalii, mollis, nodosus, pachyrrhizoides, polystachyus, rotundatus, salicifolius, scrobiculatifolius, sinuatus, smilacifolius, sonorensis, viridis, xolocotzii</i>	20
<i>Phaseoli</i> DC	<i>albescens, coccineus, costaricensis, dumosus, persistentus, vulgaris</i>	6
<i>Rugosi</i> Freytag	<i>angustissimus, carteri, filiformis</i>	3
Total (no. sections): 14		
Total (no. species):		77

Table 3 – Sections and sources of variability that can be exploited for the different bean crops.

Bean crop	Secondary gene pool; species of	Tertiary gene pool; species of
Common bean <i>vulgaris</i>	section Phaseoli: <i>albescens</i> , <i>coccineus</i> , <i>costaricensis</i> , <i>dumosus</i> , <i>persistentus</i>	section Acutifolii: <i>acutifolius</i> , <i>parvifolius</i> ; section Rugosi: <i>angustissimus</i> , <i>carteri</i> , <i>filiformis</i>
Scarlet runner <i>coccineus</i>	section Phaseoli: <i>albescens</i> , <i>costaricensis</i> , <i>dumosus</i> , <i>persistentus</i> , <i>vulgaris</i>	section Acutifolii: <i>acutifolius</i> , <i>parvifolius</i>
Year-bean <i>dumosus</i>	section Phaseoli: <i>albescens</i> , <i>coccineus</i> , <i>costaricensis</i> , <i>persistentus</i> , <i>vulgaris</i>	
Tepary bean <i>acutifolius</i>	section Acutifolii: <i>parvifolius</i>	section Phaseoli: <i>albescens</i> , <i>coccineus</i> , <i>costaricensis</i> , <i>dumosus</i> , <i>persistentus</i> , <i>vulgaris</i>
Lima bean <i>lunatus</i>	section Paniculati: <i>augusti</i> , <i>mollis</i> , <i>pachyrrhizoides</i>	section Paniculati: <i>albinervus</i> , <i>jaliscanus</i> , <i>juquilensis</i> , <i>lignosus</i> , <i>maculatifolius</i> , <i>marechalii</i> , <i>nodosus</i> , <i>polystachyus</i> , <i>rotundatus</i> , <i>salicifolius</i> , <i>scrobiculatifolius</i> , <i>sinuatus</i> , <i>smilacifolius</i> , <i>sonorensis</i> , <i>viridis</i> , <i>xolocotzii</i> section Coriacei: <i>maculatus</i> , <i>novoleonensis</i> , <i>reticulatus</i> , <i>ritensis</i> , <i>venosus</i>

Table 4 – Numbers of *Phaseolus* species with respective distribution patterns (not human made).

Widespread	Intermediate	Endemic	Total
16	18	43	77

2.3. Where are the different beans species distributed today?

The geographic distribution of the different wild species (Table 1) is far from being completely surveyed, and it is of course a priority in view of further collecting or for *in situ* conservation, through a set of concrete figures: the number of populations and their precise location. The latter can also be a step towards germplasm evaluation, at least for some abiotic stresses such as drought, extreme temperatures (heat and frost) or salinity. It is however possible to propose three distribution ranges (Table 4): widespread with a large number of populations (100-500 or more) thriving in more than one vegetation type, intermediate with a substantial number of populations (25-100) inhabiting one vegetation type with its variants in amounts of annual rainfall, and an endemic range with a small number of populations (< 25) and restricted to a specific niche within a broad vegetation type. While additional data could turn some species with an intermediate range into the widespread category (e.g. the case of *P. pauciflorus*, being pending on more data about its presence in Guatemala; Debouck 2013d), there are possibly fourteen widespread species now (or in the very recent past because of changes in land use by humans after 1900 – this date marking arbitrarily the beginning of massive transportation based on fossil oil). Typically widespread are wild *P. lunatus*, wild *P. vulgaris*, *P. microcarpus*, *P. polystachyus* and *P. leptostachyus*. Four of the five ancestors of cultivated species have a widespread distribution, contrasting with that of wild *P. dumosus* which can be seen as endemic (Debouck 2013f; Freytag & Debouck 2002; Schmit & Debouck 1991), pending on more information about its presence in Chiapas. One cannot forget the hypothesis of the colonizing behaviour of many of our crop wild relatives (Anderson 1952; de Wet & Harlan 1975; Heiser 1969), that is, the capacity to reproduce and expand quickly in human made habitats, and it is likely to be the case for wild *P. coccineus*, *P. lunatus* and *P. vulgaris* (see also Sousa-Sánchez & Delgado-Salinas 1993). The higher number of molecular polymorphisms – and their inheritance and intrinsic nature - in the wild as compared to the cultivated forms are an indication that the former are not weedy escapees from the later.

It is important to mention that for widespread species genetic diversity is not uniformly distributed along the range; instead it seems that bean populations in the wild are genetically highly structured. Wild *P. vulgaris* has been the species most studied, with differences revealed among (Nanni et al. 2011; Tohme et al. 1996) and within its three to four major gene pools (Khairallah et al. 1992; Chacón-Sánchez et al. 2007). And a similar structuring is also found in wild *P. lunatus* (Maquet et al. 1997; Martínez-Castillo et al. 2014; Serrano-Serrano et al. 2012). A good example of the genetic variation among populations of wild *P. vulgaris* within the Mesoamerican gene pool is found in the variation of seed storage proteins called arcelins (Osborn et al. 1988; Romero-Andreas et al. 1986). Arcelins seem not to be present outside Mexico (Acosta-Gallegos et al. 1998; Zaugg et al. 2013), and the variants with insecticidal properties against bruchids seem mostly restricted to the Jalisco-western Guerrero area (Acosta-Gallegos et al. 1998; Osborn et al. 1986). Another example of the structuring of genetic diversity in the same taxon is given by the variation of photosynthesis parameters across the geographic range (González et al. 1995).

To be considered as with an intermediate range of distribution are species like: *P. esperanzae*, *P. micranthus*, *P. nelsonii*, *P. parvulus*, *P. pedicellatus*, *P. sinuatus*, and *P. xanthotrichus*. Again important for conservation and use is the matter of structure of genetic diversity; evidence accumulated so far in wild *P. acutifolius* shows that many populations not too distant from each other in their wild habitats are genetically different (Muñoz et al. 2006).

Typically endemic are species such as *P. amblyosepalus* (growing at the border between Sinaloa and Durango in Mexico: Debouck 2013d), *P. hygrophilus* (central southern Costa Rica: Salcedo-Castaño et al. 2011), *P. mollis* (part of the Galapagos archipelago: Debouck 2013e; Wiggins & Porter 1971), *P. novoleonensis* (SE of Nuevo León in Mexico: Debouck 2013b; Salcedo-Castaño et al. 2006), or *P. macrolepis* (part of the volcanic mountainous range of Guatemala: Debouck 2013a; Standley 1946). The case of *P. talamancensis* call for caution in concluding about endemic species: it was initially thought to be restricted to the Talamanca mountainous range in Costa Rica with two populations (Torres-González et al. 2001), and it currently has four known populations, one of them outside that mountainous range (Debouck 2013a). In other words, the total number of populations is not fully known yet, even for the endemic species. Our knowledge has however increased dramatically if one sees the change over the last twenty years (Delgado-Salinas 1985; Freytag & Debouck 2002; Debouck 2013a,b,c ...), with the prospect of conservation planning becoming more and more a reality (Ramírez-Villegas et al. 2010). The existence of a population can be testified by a herbarium voucher and/or a genebank seed accession, and from there a population can be converted into a conservation unit that can be georeferenced and mapped. A step into that direction can be seen in ‘Cahiers de Phaséologie’ (at <http://www.ciat.cgiar.org/urg>) – currently the largest verified database of that kind in the public domain -, where geographic coordinates have been estimated to the extent possible. One should note that the number of populations or conservation units is a finite one, and a good example of this reality has been provided by the case of wild *P. vulgaris* in Costa Rica: twenty-three populations (out of which two are endangered or extinct), all located, georeferenced and with partial molecular characterization (González-Torres et al. 2004). With each population being converted into a conservation unit, it is worth mentioning that populations for most species will fall within the range of two top biodiversity hotspots – the Tropical Andes and Mesoamerica – as identified by Myers and co-workers (2000).

Box 3

Because of its critical importance for collecting, *in situ* conservation and evaluation for some abiotic stresses, a set of activities of the Strategy must continue to define the number and location of all populations of the different bean species, and firstly the wild ancestral forms of the five cultivated species. This could be achieved in three steps:

- study of voucher specimens in Herbaria
- field explorations
- georeferencing

For these there is ample ‘prior art’.

3. HOW DID SUCH GENETIC RESOURCES DEVELOP?

3.1. What is wild? What is domesticated?

Authors (Debouck & Smart 1995; Pickersgill 2007) seem to agree, on the basis of multidisciplinary (including botany, phytogeography, anthropology, genetics, and molecular biology) evidence, that five wild species in the genus *Phaseolus* have been affected by domestication (Table 5). These are: *P. acutifolius*, *P. cocineus*, *P. dumosus*, *P. lunatus*, and *P. vulgaris*. All belong to clade B (Delgado-Salinas et al. 2006), and three of them belong to the *Phaseoli* section as here defined (also Debouck 2013f). This multiple domestication has happened possibly in response to different needs in contrasting environments, and is outstanding because of its rarity in the plant kingdom (with the

exceptions of *Capsicum*, *Cucurbita* and *Solanum* sect. *Petota*, which curiously enough are all found in the Neotropics). Two species viz. *P. lunatus* and *P. vulgaris* have been domesticated at least twice, in Mesoamerica and in the Andes (Debouck et al. 1987, Gutiérrez-Salgado et al. 1995, Motta-Aldana et al. 2010; and Chacón-Sánchez et al. 2005, Khairallah et al. 1992, Kwak et al. 2009, McClean et al. 2012, respectively), from wild forms that were already widely distributed in both regions before the domestication events took place. It is possible though not yet demonstrated that other species, e.g. *P. maculatus* (Nabhan et al. 1980), might have been affected by an incipient domestication process, but if so the process did not come to completion. *P. dumosus* from a domestication process in western Guatemala was introduced into the Andean region in late pre-Columbian or early historic times (Schmit & Debouck 1991), and continues to expand there often as weed (Debouck 1992, 2013f) (previously named *P. flavescens* in the northern Andes: Freytag & Debouck 2002). This is the fifth case of domestication in the genus, and we have no evidence so far that *P. dumosus* could have been domesticated twice, possibly because the range of its wild form is rather small. One should note that the five bean species were all domesticated at least once within Mesoamerica as traditionally understood (from the parallel of the watersheds of rivers Santiago-Panuco in Mexico down to the region of Guanacaste of Costa Rica; León 1992), or very close to it. While the range of each of the wild progenitors varies considerably in tropical America, the range of the derived cultigen is much wider, and expands far beyond the original domestication area. One should note that the two species viz. *P. lunatus* and *P. vulgaris* with the widest ranges in the wild are also the ones which spread most in late pre-Columbian and historic times after 1492 (Debouck & Smartt 1995; Kaplan & Kaplan 1992).

Table 5 – Cases of domestication in *Phaseolus* beans and possible areas; note the double domestication in the case of *P. lunatus* and *P. vulgaris*.

Bean species	Possible area (s) of original domestication	Source(s)
<i>P. acutifolius</i> A. Gray	NW of Neo-volcanic axis in Mexico	Garvin & Weeden 1994; Muñoz et al. 2006
<i>P. coccineus</i> L.	Southern Honduras	Spataro et al. 2011
<i>P. dumosus</i> Macfady.	Volcanic mountains of SW Guatemala	Schmit & Debouck 1991
<i>P. lunatus</i> L.	W of Tehuantepec in Mexico; SW of Ecuador and NW of Peru	Motta-Aldana et al. 2010; Serrano-Serrano et al. 2012; Andueza-Noh et al. 2013 Motta-Aldana et al. 2010; Debouck et al. 1987; Chacón et al. 2012
<i>P. vulgaris</i> L.	W of Neo-volcanic axis in Mexico; Central Peru: Apurimac and around it	Chacón et al. 2005; Kwak et al. 2009 Chacón et al. 2005

3.2. The bean domestication process as a reduction of genetic diversity

Domestication first means dependence on humans for reproduction, either directly thanks to harvest and planting or indirectly through the modification of natural habitats. Gepts and Debouck (1991) indicate the five traits (i.e. seed dispersal, seed size, seed dormancy, growth habit, and flowering under short or long days) and their genetic control, that separate the domesticated from the wild forms, out of which perhaps the first and definitive one to mark the transition is alteration of pod dehiscence. Because of the frequent presence of antinutritional factors in the wild relatives of bean (Johns 1990;

Mirkov et al. 1994; Lioi et al. 2010), one can assume the little incentive to go back to the wilds. The richness in molecular polymorphisms in the wild forms as compared to the respective cultigens of the five species – taking into account the rate of generation and inheritance of polymorphisms in the markers – points to what has been called the ‘founder effect’, that is, a very significant reduction of genetic diversity in the derived domesticated forms (Table 6). Significant, because the reduction has been estimated at 50% in common bean in both gene pools (Mamidi et al. 2011), and at 60% or more in the Andean gene pool of Lima bean (Motta-Aldana et al. 2010). Interestingly, at least in common bean, selection by early farmers seems to have affected larger fractions of the genome beyond the target genes (Papa et al. 2007). The founder effect in beans might be the way it is because of the presence of such antinutritional factors, the genetics of the ‘domestication syndrome’, and that of traits such as the seed testa. In this regard, beans are almost unique in the plant kingdom in displaying so numerous unique patterns and colors in the seed testa, ‘promoting’ selection (the “aesthetic selection”: Hawkes 1983, p. 11), distribution - and indirectly selfing - by humans.

Table 6 – Founder effects associated with the domestication of bean species.

Bean species	Source(s)
<i>P. acutifolius</i> A. Gray	Garvin & Weeden 1994; Muñoz et al. 2006; Schinkel & Gepts 1988; Blair et al. 2012
<i>P. dumosus</i> Macfady.	Schmit & Debouck 1991
<i>P. lunatus</i> L.	Gutiérrez-Salgado et al. 1995; Motta-Aldana et al. 2010; Chacón-Sánchez et al. 2012; Serrano-Serrano et al. 2012
<i>P. vulgaris</i> L.	Beebe et al. 2001; Mamidi et al. 2011; Papa et al. 2005; Sonnante et al. 1994

3.3. Locations *versus* durations

Since Alphonse de Candolle (1883) scholars have not escaped from the curiosity to put on the world map where the different bean species entered into the human domain. In trying to locate the place of origin of the bean crops, there are three calls for caution however. First, what the evidences in molecular genetics actually bring, because of the intrinsic properties of the markers, is information about the “parental” populations from which the cultigens are derived. One should note that the wild “parental” populations are actually derived ones, often after thousands of cycles of germination, fruit setting and seed dispersal. From this close association between two biological forms scholars often conclude about places or “centers” of domestication. One should further note however that locations of initial domestication events are hypothetical, under the assumption that the “parental” wild populations did not move over the last millenia. Over the last five thousands years, this assumption is possibly correct (see below, about timing), although with some oscillations in altitude (for example in the Andes: Cardich 1985). But over the late Tertiary-early Quaternary in tropical America (long before humans entered into the Americas, some 12-20,000 years ago: Cavalli-Sforza et al. 1994; Dillehay 2000), it seems that some wild bean species, namely *P. lunatus* and *P. vulgaris*, have travelled extensively (Chacón-Sánchez et al. 2007; Rossi et al. 2009; Serrano-Serrano et al. 2010), likely because of climate changes (Graham 2010, 2011), and that these travels have shaped significantly the structure of their genepools. For both species gene pools were formed through a genetic bottleneck followed by an expansion through migration and then geographic isolation (Mamidi et al. 2013; Martínez-Castillo et al. 2014; Schmutz et al. 2014).

A second call for caution in pinpointing to a place of domestication is about the process itself: domestication is a series of conscious and unconscious actions applied to the plant populations, resulting in a series of changes in the plant material which do not happen overnight. The changes, most of them initially affecting mechanisms of seed dispersal, seed color and size (Blumler & Byrne 1991; Gepts & Debouck 1991), would not have happened and been kept if not by farming communities over centuries. Since the former trait is controlled by a few genes, so at least that part of the domestication process could have been fast (Koinange et al. 1996), possibly longer for complex traits controlled by many genes (2,000 and 1,500 years in Mesoamerica and in the Andes, respectively: Mamidi et al. 2011). In other words, domestication rather than a single place is a process by which the wild ancestors of beans were able to reproduce in human made habitats and in response to human selections. As aforementioned, because of the frequent presence of antinutritional factors in the wild relatives of bean (Seigler et al. 1989; Mirkov et al. 1994), one can assume the little incentive to go back to the wilds and re-initiate the process, but rather through the exchange of seeds between farming communities to capitalize on the advancing domesticated materials. But if the mutation affects an antinutritional factor (detectable!), and with little incentive to try other populations in other locations, then the possibility to track origin to a single population – the founding population - growing at a single location would still be warranted.

The third call for caution stems from the gene flow between wild and cultivated forms: the wild forms that are used as landmarks have the genes under scrutiny borrowed from beans that were moved around by people! Studies have shown that such gene flow occurs in both Mesoamerica (Papa & Gepts 2003) and in the Andes (Beebe et al. 1997), predominantly from the cultivated into the wild in the former study. Without a careful selection of the marker, the wild forms might thus be useless in tracking down places of origin. Bearing these observations in mind, a few locations can be proposed (Table 5). One will note that these locations fall outside the most significant historic (e.g. the Mayan area for Lima bean) and current (e.g. the northern highlands of Mexico for common bean) bean production areas, suggesting that the whole genetic diversity might not be concentrated there.

The question of timing of these different domestication events is important first because longer durations would be correlated to higher accumulations of (positive or at least neutral) genetic diversity under cultivation. One would expect that longer durations because of drift, piling up of mutations or of variants from crosses would progressively compensate for the founder effect that has been shown associated with the domestication events in beans (Table 6) (Mamidi et al. 2011). But the timing of these different domestication events is still a largely unresolved issue, with possibly younger dates revealed recently (Kaplan & Lynch 1999; Smith 2001) as compared to early archaeological records (Kaplan 1965, 1967), although Mamidi et al. (2011) date the beginning of the bottleneck of domestication at 8,000 years before present for both gene pools. Under corrected dating domestication could have been an earlier event in the Peruvian Andes as compared to Mesoamerica, for both common and Lima beans (Kaplan & Lynch 1999; Piperno & Dillehay 2008; Piperno 2012). With the present data, and after recalibration, one could suggest a domestication time of about 2,000 years before present (b.p.; it is meant 1950, when that sort of dating came into use) in Mesoamerica, and about 4-5,000 years b.p. in the Central Andes (8-9th millennia b.p. in northern Peru on the lower western slopes of the Andes: Piperno 2012). If so, we have no indications available now that the respective wild ancestral forms have experienced a drastic change in their natural distribution since; pinpointing to populations of wild ancestral forms is therefore possible, and through them locations of initial domestication events (Table 5). In contrast with maize, a progressive transition from the wild into the cultivated derived material has not yet been found in beans (Kaplan & Kaplan 1988). And this may mean older domestication processes as compared to the current evidence, but we do not

have archaeological data. The tracking of the origin of the race ‘Nueva Granada’ to the Central Andes of Peru (Chacón-Sánchez et al. 2005) provides enough indication that the whole domestication process did not occur fully in a single place, but extended over space and time. If the landraces of Mesoamerican origin could be 2-3,000 years old, the species themselves *P. vulgaris* and *P. lunatus* - in the wild – in contrast could be 1,000,000 years old (Chacón-Sánchez et al. 2007, Delgado-Salinas et al. 2006; and Serrano-Serrano et al. 2010, respectively). The diversity is thus in the wild forms and species, and not only because of the founder effect but because of the duration of their respective evolutions. This incites us to reconsider the secondary centers of diversity.

Authors (Delgado-Salinas et al. 2006; Lavin et al. 2005; Serrano-Serrano et al. 2010) have presented evidence that the genus *Phaseolus* is relatively young (as compared to the age of the legume family: 60 million years: Lavin et al. 2005), about 7-10 millions year old. Two clades of possibly the same age separate about 5-6 million years ago, and clade B includes all cultivated species. Within the latter, the phylums of the common bean and the Lima bean might have separated about four million years ago and thus their genetic incompatibility today. As we have seen, part of the genesis of Lima bean has occurred in the Andean region, from an initial root in Mesoamerica (its tertiary gene pool). Another scenario of migration through the Isthmus of Panama may have happened for common bean, with a later entry into the Andes. One plausible explanation might be in geographic isolation and migrations in opposite directions at different times (Mayr 2000; Wilson 1992). These migrations happened long before the arrival of humans in the Americas, estimated in the range of 12-20,000 years ago (Dillehay 2000; Zimmer 2005). *Phaseolus* is by no means an exception in such transisthmic migrations that have affected the oaks (Graham 1999), the lupines (Hughes & Eastwood 2006), wild cassava (Chacón et al. 2008), or the blueberries (Graham 2010). As a result, there is the structure of genetic diversity as presented above and already a divergence between the Mesoamerican and Andean gene pools. The divergence already exists prior to domestication (Koinange & Gepts 1992; Rossi et al. 2009), but has not gone (yet) to a complete biological barrier (Mumba & Galwey 1998).

The same mechanisms of generation of genetic variability – drift, migration (this time through people), mutation and natural outcrossing – have affected beans in secondary centers outside the primary focuses in mountainous tropical America. McClean and co-workers (2004) have indeed shown the importance of the role of mutations in the generation of variation within landraces, and at a higher rate in the Mesoamerican genepool. There are thus possibilities of finding new mutations within and recombinants between genepools – a valuable step forward for breeding programs, sometimes already tested in adverse conditions. And these are good reasons for considering the acquisition of germplasm from secondary centers. Perhaps we should consider Brazil first, because of its land mass favoring important bean demography, and the antiquity of bean cultivation there as compared to the Old World (Freitas 2006). It can be considered as secondary center, because wild common bean has not yet been found in that country (Debouck 2013f). Authors (Blair et al. 2013; Lobo-Burle et al. 2010, 2011) showed that although the two gene pools exist in Brazil, the Mesoamerican small-seeded one is dominant with a reduction of diversity upon introduction into Brazil; they also found that a significant number of Brazilian landraces were of hybrid origin, resulting from crosses between Mesoamerican materials, although not much between gene pools. One should note that the introduction of Lima bean in Brazil might be older as compared to that of common bean, and as a result the former is more interesting in terms of genetic variation. Further, the presence of wild Lima bean in Brazil is plausible (Debouck 2013e), and one cannot discard the possibility of one domestication event there (Serrano-Serrano et al. 2012).

A sure region where the two gene pools might have been in contact for long and intercrossed is the Northern Andes, namely Colombia, because of multiple introductions from both Mesoamerica and the Central Andes at different times (Debouck 1996). This is particularly what studies with help of molecular markers have revealed (AFLP markers: Beebe et al. 2001; isozymes: Debouck et al. 1993; microsatellites: Blair et al. 2007; RAPD markers: Islam et al. 2004; seed proteins: Islam et al. 2002). What makes this region uniquely rich in genetic diversity is in addition the presence of wild forms with which the landraces have crossed too (Beebe et al. 1997).

Arrival of beans into the Old World might have been through southwestern Europe and could have included *P. vulgaris* and possibly *P. coccineus* (Spataro et al. 2011; Zeven 1997). Lack of land mass (being replaced by the Mediterranean Sea!) and winter period with killing frost did not prevent however the formation of some novel variants, apart from accessions of the two well-known gene pools (in Italy: Lioi 1989, Raggi et al. 2013; in Spain: Ocampo et al. 2005, Rodiño et al. 2006, Santalla et al. 2002; in Portugal: Rodiño et al. 2001). However, the frequency of hybrids between gene pools might be lower there as compared to other parts of central and southeastern Europe (Angioi et al. 2010). The landraces are predominantly of Andean origin. A contrasting situation seems to be present in China (Zhang et al. 2008), with prevalence of Mesoamerican types, but more diversity in the introduced Andean landraces; some introgression between the major gene pools seems to have happened in southern China too. Africa, namely the eastern part from Ethiopia down to South Africa (Wortmann et al. 1998), where beans could have been grown for 350-400 years (Sauer 1993), is another area where to look for rare variants and recombinants between gene pools. The two well-known gene pools are clearly present in Burundi and Kenya (Gepts & Bliss 1988), Malawi (Khairallah et al. 1990), and Tanzania (Briand et al. 1998). The prospect for finding rare variants seems however limited in eastern Africa (Pickersgill 1998), namely because of genetic incompatibilities between gene pools (Singh & Gutiérrez 1984), and when happening such variants are found outside commercial classes (Adams & Martin 1988). Again, the point is not that the variant falls outside commercial classes, but that it represents a bridge between gene pools, and as such is of value for breeding and genetic resources.

Finally, the United States could have been a place where to look for recombinants between the Mesoamerican types introduced into the southern states (Gepts et al. 1988), and the Andean types re-introduced into the American continent through the European immigration from the northeast (Kaplan & Kaplan 1992), if time would have been longer and monocropping (single varieties) absent. A similar situation could exist in Argentina where the commercial production is getting in contact with the wild (native) form in spots of Salta and Tucuman (Santalla et al. 2004), or between commercial varieties of different origins and seed types in vast areas of Santiago del Estero, but the duration for the intercrossing has so far been too short, because farmers change varieties in response to prices of such varieties on foreign markets, namely those of Brazil and Mexico (bean is produced almost only for export in that country: Voysest 2000).

Jack Rodney Harlan (1978, p. 351) once wrote: “Resistance is where you find it”, in order to warn us that any source of resistance should be welcome, and that “there may not always be a geographic correspondence of crop and pathogen” (*ibidem*, p. 350), although in the same paper the author acknowledged that the wild progenitor of a crop would have been subjected to all endemic diseases affecting the crop for a much longer duration than any cultivated races. Therefore, wild progenitors are often good sources of genetic defense against diseases and pests. And yes, eventually time is one of the most important factors, putting the focus back on the early American landraces and the wild relatives.

A final consideration coming from studies on bean domestication, crop movements and on the founder effect deals with genetic uniformity in the bean crops. This aspect has been studied most in *P. vulgaris*, and this is perhaps where it matters most given the current large scale monocropping, since with few exceptions (e.g. baby Lima in the southern USA) in the other bean crops acreages are small or scattered and a diversity of landraces continues to be planted, thus lowering risk of total damage (Simons & Browning 1983). And the available evidence (Adams 1977; Becerra-Velásquez & Gepts 1994; Sonnante et al. 1994; Wilkes 1983) indicates risks of genetic uniformity. In small red- and black-seeded varieties of Central America it seems that the combination of selection and breeding has led to a reduction of genetic diversity as compared to original landraces (Beebe et al. 1995), although there are cases in race ‘Mesoamerica’ where the breeding process has resulted in an increase of genetic diversity (Voyses et al. 1994). If the bean varieties in hands of farmers produce well this is not a problem in the short term but a potential hazard in case of a disease outbreak, for example of bean rust the pathogenicity of which changes frequently (Beebe & Pastor-Corrales 1991; Stavely 1984). In the case of snap bean, the technical conditions of production and the requirements of specialized markets make the production of the bred seed expensive and thus the genetic base narrow (Myers & Baggett 1999); snap bean breeders often commercialize sister lines.

Box 4

There is a consequence from the studies about the founder effect, for the Strategy: most of the diversity was left in the wild, untouched, not because of intrinsic negative traits, simply because the domestication events took place elsewhere in only a few sites, thus involving few original populations and *de facto* just a fraction of the diversity existing in the species. The material that should be the focus of the conservation effort in the primary gene pools involves the wild forms of the five bean cultigens.

The evolutionary forces at work in the primary centers of diversity (Mesoamerica, Central Andes) resumed once beans were brought into new lands (southern Europe, eastern Africa, south and southeastern Asia) with favorable ecological conditions. From a genetic resources viewpoint what matters is duration, originality (where human cultures will be critical) of such selective pressures, and the amount of original variation brought in. This is where sequencing could be key at the decision making of introducing novel germplasm from these secondary centers into *ex situ* collections.

4. WHAT HAS BEEN USED IN BEAN GENETIC RESOURCES?

4.1. Importance of bean germplasm for food and feed across the world

Table 5 sums up some domestication sites in Mesoamerica, where work is still needed for the small-seeded Lima bean, tepary and the scarlet runner. But for the common bean, after the initial domestication event(s) (Chacón et al. 2005; Kwak et al. 2009), it seems that at least three races were selected (Beebe et al. 2000; Blair et al. 2006; Díaz & Blair 2006; Singh et al. 1991). In pre-Columbian and early historic times, race ‘Mesoamerica’ seems to have been highly successful with diffusion up to southeastern Central America, the northern coast of South America and Brazil (Gepts et al. 1988; Lobo-Burle et al. 2010), while races ‘Jalisco’ and ‘Durango’ have had a more restricted distribution. On the Peruvian Coast a small white seeded navy bean ‘Panamito’ has been reported (Voyses 1983). A few landraces with a phaseolin type found in Central American materials have been reported in

Central Chile (Paredes & Gepts 1995). In recent times, race ‘Mesoamerica’ is important in eastern Africa and in Canada, for both local consumption and export (Gepts & Bliss 1988; Martin & Adams 1987; Navabi et al. 2012). Race ‘Durango’ with the pinto cultivars has experienced a significant development in the western USA over the last century because of the prospects for export (Singh et al. 2007). On the other hand, many varieties of snap bean are of Andean origin (Myers and Baggett 1999; Singh 1989); yet some belong to the Mesoamerican genepool, like ‘Princesse Double de Hollande’ or ‘Merveille du Marché’ (Gepts & Bliss 1988). Table 7 indicates some statistics about human consumption of common bean, and most likely of race ‘Mesoamerica’, and there is no doubt about its critical importance for food security in countries like Brazil (Lobo-Burle et al. 2010), Mexico (Lépiz & Ramírez 2010), Cuba, and Central America (Singh 1999b). There, Nicaragua might be a net exporter towards its neighbors, but the amounts do not suffice, and Central America is a net importer of seed types of race ‘Mesoamerica’. One should note that yields although twice as much as the productivity of several traditional landraces are however about one third of the yield (or even lesser) obtained in experimental stations, mainly because of diseases, problems of soil fertility, or weeds. In any case there is ample room for improvements, and thus use of bean genetic resources of race ‘Mesoamerica’ and beyond.

Table 7 – Population, common bean (race ‘Mesoamerica’) consumption per capita, import (-)/ export (+), average yield in 2007-2009, for selected countries (sources: FAO Stat 2010, US Census Bureau 2010).

Country	Population (million)	Intake (kg/ capita/ year)	Import (metric tons)	Yield (kg/ Ha)
Cuba	11.4	20	- 117,346	736
Nicaragua	5.9	19	+ 50,608	739
El Salvador	6.0	18	- 79,377	770
Honduras	7.8	15	- 37,147	679
Mexico	111.2	11	- 73,360	746
Brazil	198.7	16	-65,422	849
Costa Rica	4.4	11	- 38,682	610
Total (7)	345.4	15.7	- 360,726	732.7

Table 5 indicates that for the common bean an initial domestication event took place in an area today including Ayacucho, Apurimac and western Cuzco in Peru. From there and likely over centuries or millenia (9,000 years B.P.: Piperno 2012) three races were formed (Blair et al. 2007; Singh et al. 1991): ‘Chile’, ‘Nueva Granada’ and ‘Peru’. Some statistics indicating the importance of the Andean germplasm of common bean are provided in Table 8 (keeping in mind that such statistics do not differentiate at the race level). They likely reflect races ‘Nueva Granada’ and ‘Peru’ (Singh et al. 1991), as race ‘Chile’ quite possibly unique (Becerra-Velásquez et al. 2011; Johns et al. 1997; Paredes & Gepts 1995) seems to be limited to this country. Likely, the same Andean races went up to the Pamirs (Vavilov 1997) and the foothills of the eastern Himalayas (Salick et al. 2005). As aforementioned, most of the varieties of snap beans are of Andean origin and on the rise in most cities of the world (a five-times increase over the last fifty years to 17 million tons: FAO Stat 2010). Rwanda with one of the highest levels of consumption of dry beans in the world, in spite of a production of 327,497 tons in 2010, still imports over six thousand metric tons (FAO Stat 2010).

Table 8 – Population, common bean (likely of races ‘Nueva Granada’ and ‘Peru’) consumption per capita, import (-)/ export (+), average yield in 2007-2009, for selected countries (sources: FAO Stat 2010; US Census Bureau 2010).

Country	Population (million)	Intake (kg/ capita/ year)	Import (metric tons)	Yield (kg/ Ha)
Colombia	44,2	2.7	- 26,232	1,173
Ecuador	14,8	0.1	- 377	309
Peru	28,9	1.7	- 4,965	1,142
Rwanda	11,0	27.0	- 6,321	1,026
Total (4)	99,0	7.8	- 37,895	912.5

Race ‘Nueva Granada’ in the form of improved varieties ‘Cranberry’, ‘Light Red Kidney’, ‘Dark Red Kidney’, ‘Alubia’ or ‘Calima’ (Voysesst 2000) makes a significant contribution to bean exports of countries such as Argentina, Canada, the US, and several African countries (Beaver 1999) (note: outside the original range of ‘Nueva Granada’!). A reason behind its success lies in the large cylindrical or kidney shaped grain (100 seed weight: 45-65 g).

Accurate statistics about the other bean cultigens in other parts of the world are badly missing, partly because in the reports about production of pulses in the countries, beans are reported as a generic commodity, often with no distinction among species and races (*Phaseolus* beans might even be confused with Asiatic *Vigna* species!). The definition and use of commercial market classes (Voysesst & Dessert 1991; Voysesst 2000) could progressively correct this shortcoming. Under this caution note, small seeded Lima beans of sure Mexican origin (Motta-Aldana et al. 2010; Serrano-Serrano et al. 2012) have been reported in Nigeria (Rachie 1973), the eastern USA (Purseglove 1968; Sturtevant 1919), Java, Burma (Purseglove 1968) and the Philippines (Mackie 1943). The large seeded Lima beans of NW Andean origin (Debouck et al. 1987; Motta-Aldana et al. 2010) have been or are grown in Ethiopia (Westphal 1974), California (Hendry 1918), coastal South Africa and Madagascar (Baudoin 1988a; Purseglove 1968). Pearman (2005) reported that Lima beans are used as sprouts in Asia – non conventional, but likely after soybean - but without country indication. The scarlet runner is grown for food in Britain and Holland (Sturtevant 1919), in Ethiopia (Westphal 1974), South Africa (Pearman 2005), Spain (Cubero 1992), Greece (Albala 2007), the USA (Kaplan & Kaplan 1992), and as an ornamental in the USA (Kaplan & Kaplan 1992; Albala 2007). There are reports about the presence of tepary bean in different parts of Africa (Pearman 2005; Shisanya 2002). Curiously enough, there are very few reports about the presence about the year-bean outside the Americas, unless it continues there as well to be confused with the scarlet runner as it long used to be in tropical America (Schmit and Debouck 1991).

Although not frequently mentioned, apart from the use of its leaves (Westphal 1974), bean is also used as feed (Purseglove 1968; Smartt 1989). Once Amerindians filled their deficit in livestock by adopting domestic animals of the Old World (Crosby 2004), they had to feed them, and a couple of cattle and donkeys feeding on dried stalks of maize and bean vines have been a traditional harvest scenery since the 16th century.

Concluding, germplasm of the different bean cultigens of Mesoamerican origin have diffused much beyond their respective nuclear area of original domestication to become full part of the diet in different parts of the world; *Phaseolus* beans are the first edible grain legumes after soybean and peanut (Broughton et al. 2003) (note the oil value of the latter two legume crops).

Box 5

While beans continue to be important for the daily food of millions of people in their original homelands, they have become as critically important for the same daily protein intake in many parts of Africa, less so in Asia because of soybean and the indigenous *Vigna* species. As a vegetable, common bean has gained a place of choice in almost every city in the world (as lettuce, onion and tomato). The countries at the new frontier should realize that they share together with the homeland countries the same interest in having bean genetic resources well conserved; for both groups of countries it is the same food security issue.

4.2. Which bean varieties have been used so far?

Since the beginning of scientific (common) bean breeding in the 1930s (Voyses 1983), (common) bean genetic resources have been used extensively, although bean breeders have often been constrained to work for and within market classes. Such market classes (Voyses & Dessert 1991) are very much linked to the consumption as dry bean and its local preferences in color and seed types, but this set of constraints may change dramatically if food processing gains importance (Singh 1999a) as it did for wheat and maize.

Table 9 is an attempt to show which materials have been used and for which purposes. There is an ironic note here: while Gregor Mendel was a pioneer in crossing *P. vulgaris* and *P. coccineus* (Mendel 1865), widecrossing has had limited impact (Hucl & Scoles 1985) until recently (Navabi et al. 2012), when bean breeders are equipped with new tools and far deep knowledge about the bean crop (s) they are improving (see Acosta-Gallegos et al. 2007; Porch et al. 2013, for synthesis).

Table 9 – Some bean germplasm identified/ used to overcome limiting factors in commercial production.

Trait looked for	Material used	Source
Abiotic stresses		
aluminium toxicity	G35346 (<i>coccineus</i> , from Oaxaca)	Butare et al. 2011, 2012
drought	Common Red Mexican G11212; G21212 landrace from Colombia	Singh 2007; Miklas et al. 2006
low phosphorus	G19227A; Chaucha Chuga G19833	Ribet et al. 1997; Beebe et al. 2006
salinity (NaCl)	<i>filiformis</i> , <i>lunatus</i> , <i>macvaughii</i>	Bayuelo-Jiménez et al. 2002
low T° C seedling growth	<i>coccineus</i> G35171 from Rwanda	Rodiño et al. 2007
freezing during growth	<i>angustissimus</i> G40550 from New Mexico	Balasubramanian et al. 2004
Diseases		
angular leaf spot	G10613 from Guatemala	Pastor-Corrales et al. 1998
angular leaf spot	interspecific hybrids with <i>coccineus</i> ; G4691	Pastor-Corrales et al. 1998; Mahuku et al. 2003; Islam et al. 2002
anthracnose	Aliya G02333	Young & Kelly 1996
anthracnose	Kaboon G1588; Cornell 49-242 G5694	Melotto & Kelly
anthracnose	interspecific hybrids with <i>coccineus</i>	Mahuku et al. 2002
ascochyta blight	<i>dumosus</i> G35369 from Costa Rica	Schmit & Baudoin 1992
ascochyta blight	<i>dumosus</i> G35182 from Guatemala	Garzón G. et al. 2011
bean Golden BGYMV	<i>coccineus</i> G35172 from Rwanda	Beaver et al. 2005

bean Common BCMV	Porillo Sintético G04495, Royal Red G04450	Singh et al. 2000
beet curly top virus	California Pink G06222, Red Mexican G05507	Larsen & Miklas 2004
beet curly top virus	Porillo Sintético G04495, Burtner, Tio Canela 75	Singh & Schwartz 2010
common bacterial blight	interspecific hybrids with <i>acutifolius</i> VAX4, MBE7	Singh & Muñoz 1999; Michaels et al. 2006; Navabi et al. 2012; Zapata et al. 1985
common bacterial blight	Montana No. 5; PI 207262	Miklas et al. 2003, 2006
halo blight	Montcalm G06416, ICA Tundama G14016	Beaver 1999
halo blight	Palomo G12669	Schwartz 1989
halo blight	Pinto US 14 G18105	Singh & Schwartz 2010
halo blight	Wis HBR 72 G03954	Taylor et al. 1996
<i>Fusarium</i> root rot	Porillo Sintético G04495; wild <i>vulgaris</i> G12947	Beebe et al. 1981; Acosta et al. 2007
<i>Pythium</i> root rot	PI 311987 G02323	Beebe et al. 1981
<i>Rhizoctonia solani</i> rot	N203 G00881	Beebe et al. 1981
rust	Compuesto Negro Chimaltenango G05711	Stavelly 1984
rust	Ecuador 299 G05653	Stavelly & Pastor-Corrales 1989
rust	Redlands Pioneer G05747	Liebenberg et al. 2006
rust	PI 260418	Singh & Schwartz 2010
web blight	BAT 93; Flor de Mayo G14241	Beaver et al. 2002
white mold	<i>coccineus</i> PI 175829 from Turkey	Abawi et al. 1978
white mold	<i>dumosus</i> PI 417603 from Mexico	Hunter et al. 1982
white mold	interspecific hybrids with <i>coccineus</i> G35172	Singh et al. 2009
white mold	interspecific hybrids with <i>costaricensis</i> G40604	Singh et al. 2013
Pests		
<i>Acanthoscelides</i> weevil	wild <i>vulgaris</i> from western Mexico G12952; QUES	van Schoonhoven et al. 1983; Zaugg et al. 2013
<i>Apion godmani</i> pod weevil	Amarillo 154 G03982; G03578	Garza et al. 2001; Beebe et al. 1993
<i>Empoasca</i> leafhoppers	Turrialba 1 G03712	Galwey 1983
<i>Empoasca</i> leafhoppers	California Dark Red Kidney, from USA G17638	Schaafsma et al. 1998
<i>Ophiomyia</i> bean fly	<i>P. coccineus</i> G35023 and G35075, and interspecific hybrids	Kornegay & Cardona 1991
whiteflies Aleyrodidae	DOR 303	Blair & Beaver 1992
<i>Zabrotes</i> weevil	wild <i>vulgaris</i> from Chiapas, Mexico G24582	Acosta-Gallegos et al. 1998
Nitrogen fixation		
N2 fixation	Puebla 152 G03353	Bliss 1990
N2 fixation under low P	Bituyano from Cajamarca, Peru, G19348	Vadez et al. 1999
nodulation efficiency	wild <i>P. vulgaris</i> (origin not indicated)	Petrônio et al. 2010
Yield		
favourable QTLs	wild <i>vulgaris</i> from Colombia G24423	Acosta-Gallegos et al. 2007
favourable QTLs	wild <i>vulgaris</i> from Colombia G24404	Blair et al. 2006
photosynthesis traits	wild <i>vulgaris</i> from Mexico and Guatemala	González et al. 1995
Nutrition		
amount of seed protein	PI 229815	Sullivan 1988
amino acid content	wild <i>vulgaris</i> from several locations	Montoya et al. 2008
high zinc content	Peruvian landrace G23823	Blair et al. 2011
high iron content	Peruvian landrace G23823	Blair et al. 2011
percentage seed protein	wild <i>vulgaris</i> from Mexico	Baldi & Salamini 1973
polyphenols	wild <i>vulgaris</i> from Mexico G11025	Espinosa-Alonso et al. 2006

The above information has been concentrated on common bean, for which data are more numerous as compared to the other four cultigens; but it is an indication of what genetic resources can do if breeders realize they have four more beans to breed! There are a couple of take-home lessons from

this compilation. **First**, the diversity of sources of useful traits is striking (the passport data of CIAT G numbers can be seen at: <http://www.ciat.cgiar.org/urg>). Sure, certain bean lines have been the much used source of positive characteristics (e.g. Cornell 49-242, Ex Rico 23, Jamapa, Porrillo Sintético: Voyses et al. 1994, Voyses 2000), but with the widening of breeding objectives so have been the sources of variability. The finding of genetic incompatibility genes limiting recombinations (Shii et al. 1980; Singh & Gutiérrez 1984) between genepools has also provided additional help for focusing on the right parents (which may mean to be forced to find alternate sources!). In addition, this biological/ geographical diversity of sources highlights the dependence of countries on each other for the progress of their bean crops (Johnson et al. 2003). **Second**, the breeding objectives have been evolving (and with them the sources of variability): from securing the primary productivity of landraces with resistances to pests and diseases in the 1960-70s (Zaumeier 1973), yield *per se* in the 1990s has become a priority in order to compete against soybean in different (sub-) tropical agroecosystems. Breeding methods are evolving too: in addition to finding good traits, bean breeders are nowadays after good genes (Tanksley & McCouch 1997) that can be re-assembled into favorable genotypes with help of marker-assisted selection (Miklas et al. 2006). And this brings us to a **third** consideration: the useful traits or genes could come from completely unexpected parts of the genepool, stressing the importance of large scale evaluations (in turn based on the conservation of a wide genetic basis). Who could have predicted that Amazonas of Peru would be a ‘pocket’ of landraces with tolerance to low phosphorus in the soil (Lynch & Beebe 1995; Beebe et al. 2006)? Who could have predicted that wild forms with a poor architecture and tiny seeds would contribute QTLs for yield (Acosta-Gallegos et al. 2007)? F1 heterosis for yield is high enough (reviewed by Kelly 1999) to plan ahead of time for the conservation of the ‘building blocks’ from within the primary and secondary gene pools (Bannerot & Charbonnier 1988), as recommended by Krull & Borlaug (1970). Over the last decade nutritional quality has come at the forefront (Broughton et al. 2003), and nothing could tell us that few ordinary landraces from Colombia, Peru or the USA (Beebe et al. 2000; Blair et al. 2010, 2011) could combine high iron and high zinc contents, or that wild forms could bring twice as much calcium and phosphorus as compared to cultivated forms (Beebe et al. 2000). And now there is an increased concern for the bred materials to withstand heat and drought in relation to climate change (Porch et al. 2013). So, demands in human societies are changing – in rather unpredictable ways, and accordingly are changing breeding objectives. If human societies want quickly performant bean varieties in the field, the widest base of genetic variability and of documented traits seems to be the sole insurance.

4.3. Considerations about the unrealized economic potential

Beans as snap beans

In bean history, snap bean is an ‘invention’ of the period 1880-2000 that goes together with urbanization and the progress of other vegetables (e.g. Bell pepper, broccoli, lettuce, and tomato) in human diet. Most varieties of snap beans are of Andean origin (Myers & Baggett 1999; McClean et al. 2004), because they were initially selected in dry beans of Andean background introduced into Western Europe, in response to a short growing season at these high latitudes. Two elements may however indicate that such selection pressures might be ancient. First, snap beans are traditionally known as ‘ejote’ in Mexico, and ‘éxotl’ has been the term in nahuatl used by the Aztecs for snap bean in pre-Columbian times (Aguilera 1985). One variant of common bean with little pod dehiscence has been found in the caves of Tamaulipas, Mexico, and is dated of 500-900 years old (Kaplan & McNeish 1960). Second, young developing seeds of different bean species, namely *P. vulgaris* and *P.*

xanthotrichus, have been seen as eaten by birds (Debouck et al. 1993), suggesting that young pods could have been looked for as food in preceramic times (a hypothesis also considered by Piperno & Pearsall, 1998, for Lima bean). Green beans seem to be a product in expansion: in 1991, the world production was of 6,384,688 tonnes, 11,080,065 tonnes in 2001 and 20,394,746 tonnes in 2011 (FAOStat 2013). Snap beans are a good source of bioavailable calcium (Grusack & Abrams 2010).

Beans as toasted food

We have seen that archaeological evidence available so far points to an earlier domestication of common bean in the Andes as compared to Mesoamerica (Kaplan & Lynch 1999; Piperno & Pearsall 1998; Piperno 2012). That archaeological evidence also indicates a duration of at least 1-2,000 years without the ceramics to soak and cook the beans in water. However, there is a group of traditional landraces of common bean (named ‘nuñas’, ‘reventones’, ‘k’opuros’: Cárdenas 1989, León 1964), grown in the highlands of Peru and Bolivia (Gade 1999; Tohme et al. 1995), which are eaten toasted (Zimmerer 1992), after being cooked just in contact with a hot surface. It is possible that these varieties are the ones domesticated during the preceramic period (Kaplan & Lynch 1999), and thus for some with an age older than 4,000 years. One should note that the oldest landraces of corn in the Americas (in Mexico: Wellhausen et al. 1952; in Colombia: Roberts et al. 1957; or in Peru: Grobman et al. 1961) were popcorn, also consumed toasted. There is now a collection of about 300 landraces of popping beans conserved at CIAT, and it seems to be genetically diverse on the basis of phaseolin data (Tohme et al. 1995), possibly because of its long evolution. Although it has today a limited distribution in the Andes, this bean crop has potential for a much wider use, namely in the heavily deforested highlands of East Africa (National Research Council 1989). There are also efforts going on to adapt the nuñas to higher latitudes with photoperiod insensitivity and compact growth habit in the USA (Brick et al. 2013) and in Spain (Campa et al. 2011). Although once a truly neglected crop in its homeland nowadays it is making a comeback in Peru (Voyssest 2000). Strangely enough the oldest bean might be the one to bring the most novel products.

Beans bringing health benefits

Evidence is accumulating that dry beans consumed on a weekly basis improve glycemic control (Bennink 2010), and thus reduce risk of Type 2 diabetes (Thompson 2010). Beans also reduce risk of colon cancer (Bennink 2010) and mammary carcinogenesis (Thompson et al. 2008; Thompson 2010). On the other hand, dry beans are good sources of iron and zinc (Blair et al. 2009), particularly in the Andean and in the Mesoamerican gene pools, respectively.

Box 9

In contrast with the major cereals and soybean, the five bean species have not entered much in the food processing industry, although canning and deep-freezing products with beans are on the rise. If energy to cook and process food would be fully computed, popping beans may make a breakthrough. Equally if the costs of cardiovascular accidents to health systems because of excessive consumption of meat products would be computed, many bean products would be on the rise. Bean genetic resources and breeding should already take into account these future needs. These needs in turn call for a wide vision when defining the scope of the conservation efforts.

5. WHAT HAS BEEN LOST IN BEAN GENETIC RESOURCES?

5.1. What has been lost as landraces and traditional varieties?

Because a full inventory with georeferencing has never been done in the Americas for landraces of the five cultigens, we have to rely on examples and cases studies. The risk over the last 3-4 decades has been the demographic extinction of landraces and with it the total loss of alleles. For example, in northeastern Campeche, Mexico, landraces of Lima bean have experienced a complete replacement by new/ other varieties (Martínez-Castillo et al. 2012). In the western part of Mexico (highlands of Nayarit, Jalisco, Michoacán), the traditional association of climbing bean and maize grown there for two millennia is almost gone, and with it many landraces of race ‘Jalisco’ (Núñez-González 1997). In another part of central Mexico – Aguascalientes, traditional varieties have been discontinued because the market does not require them anymore (Andrade-Aguilar & Hernández-Xolocotzi 1988, 1991). In Chimaltenango, Guatemala, the traditional maize-bean (common, year-bean and scarlet runner varieties) association has been replaced by growing-outs of Old World vegetables (cabbages, onions) since the 1990s (Debouck 1995). It seems that the same economic drivers have brought to extinction two hundreds traditional landraces of common bean (out of three hundreds) in the period 1950-1980 in Spain (Cubero 1992). In Calabria of South Italy, Hammer and co-workers (1996) found a genetic erosion of almost 70% in landraces of common bean between 1950 and 1983/1986. Many varieties grown in France or in the USA (Chopin et & Trébuchet 1950; Jarvis 1908, respectively) less than a century ago are not anymore in the sale lists of seedsmen today. Hopi farmers of Arizona “do not bother to grow pinto beans because they are so easy and inexpensive to buy” (Soleri & Cleveland 1993, p. 224). From these few concrete examples it is clear that the current loss of landraces is massive (70% and above) and irreversible.

5.2. What has been lost in wild species and wild populations?

As aforementioned, vouchers in herbaria can be seen as samples representative of a population that can be georeferenced. Botanists might have sampled the same population at different times, but it is still the same population occupying the same site. The land uses affecting that site may mean the *in situ* conservation or the extinction of that population. By checking original sites, some estimate can be made about extinction of populations. Areas around cities that were sampled in the period 1800-1900 have been since significantly altered, with several wild populations not sampled timely for *ex situ* conservation (Table 10). All efforts carried out so far to find germplasm of *P. leptophyllus* and *P. persistentus* have failed; both species are known only by one population and a few herbarium (type) specimens.

Clearly all urban surroundings of capitals and towns from New York City down to Cochabamba with favourable ecological conditions have experienced another use of the land since 1900 resulting in the physical elimination of wild bean populations. This is a sure (and present) risk as compared to a coming 1-2° C increase in temperature because of greenhouse gases!

Place and year	Population (by collector and no.; where seen)	Species (as wild)
Durango, Mexico; 1896 Mazatlán, Mexico; 1934 Chihuahua, Mexico; 1886 Guadalajara, Mexico; 1903 Culiacán, Mexico; 1904 Nogales, Arizona; 1926	<i>E Palmer 645</i> ; NY <i>J González-Ortega 7437</i> ; MIN <i>CG Pringle 1128</i> ; F <i>JN Rose 7370</i> ; US <i>TS Brandegeee</i> ; US <i>ME Jones 22498</i> ; UC	<i>acutifolius</i> <i>acutifolius</i> <i>acutifolius</i> <i>acutifolius</i> <i>acutifolius</i> <i>acutifolius</i>
Calderas, Guatemala; 1874	<i>O Savin s.n.</i> ; K	<i>macrolepis</i>
Cartago, Costa Rica; 1857 Concepción Las Lomas, Guatemala; 1987 Guatemala, Guatemala; 1928 Sta María de Dota, Costa Rica; 1966 Concepción Las Lomas, Guatemala; 1987 Las Calderas, Guatemala; 1938	<i>Oersted 30</i> ; K <i>DG Debouck & JJ Soto 2472</i> ; AGUAT <i>J Morales 1128</i> ; F <i>Wm Burger 4028</i> ; F <i>DG Debouck & JJ Soto 2473</i> ; MICH <i>PC Standley 59991</i> ; F	<i>oligospermus</i> <i>oligospermus</i> <i>oligospermus</i> <i>tuerckheimii</i> <i>tuerckheimii</i> <i>tuerckheimii</i>
Cd. Mexico, Mexico; 1820 Santa Fé, Mexico; 1865 Tacubaya, Mexico; 1865 Chapultepec, Mexico; 1827 Durango, Mexico; 1896 Acapulco, Mexico; ? Cd. Oaxaca, Mexico; 1938 Hda. Noria de Puebla, Mexico; 1909	<i>Berlandier 620</i> ; P <i>E Bourgeau 334</i> ; G <i>E Bourgeau 580</i> ; FI <i>Karwinsky s.n.</i> ; M <i>E Palmer 624</i> ; K <i>E Palmer 573</i> ; ARIZ <i>RE Schultes 463</i> ; ECON <i>Nicolas 221</i> ; K	<i>coccineus</i> <i>coccineus</i> <i>coccineus</i> <i>coccineus</i> <i>coccineus</i> <i>coccineus</i> <i>coccineus</i> <i>coccineus</i>
Aguascalientes, Mexico; 1839 Tula, Hidalgo, Mexico; 1896 San Luis Potosí, Mexico; 1876 Silver City, NM, USA; 1880	<i>Hartweg 59</i> ; K <i>CG Pringle 6360</i> ; BM <i>JG Schaffner 252</i> ; PH <i>EL Greene sn</i> ; NY	<i>maculatus</i> <i>maculatus</i> <i>maculatus</i> <i>maculatus</i>
Cochabamba, Bolivia; 1932 Curahuasi, Peru; 1950 Barranquilla, Colombia; 1929 Cartagena, Colombia; 1920 San José, Costa Rica; 1893 Guatemala, Guatemala; 1987 Coatzacoalcos, Mexico; 1895 Managua, Nicaragua; 1922 Caracas, Venezuela; 1854 Washington, DC, USA; 1878 New York, NY, USA; 1898 Philadelphia, PA, USA; 1846 Jacksonville, FL, USA; 1894 Miami, FL, USA; 1918	<i>Julio 247</i> ; US <i>Marín 1856</i> ; LIL <i>Elias 263</i> ; SI <i>Heriberto 326</i> ; US <i>AO Tonduz 1565</i> ; US <i>DG Debouck & JJ Soto 2469</i> ; AGUAT <i>CL Smith 996</i> ; SI <i>JM Greenman 5709</i> ; GH <i>A Fendler 260</i> ; K <i>JW Chickering sn</i> ; MO <i>Menand 22</i> ; FI <i>G Watson 428</i> ; FI <i>HD Keeler sn</i> ; F <i>HB Meredith sn</i> ; PH	<i>augusti</i> <i>augusti</i> <i>lunatus</i> <i>lunatus</i> <i>lunatus</i> <i>lunatus</i> <i>lunatus</i> <i>lunatus</i> <i>lunatus</i> <i>polystachyus</i> <i>polystachyus</i> <i>polystachyus</i> <i>sinuatus</i> <i>sinuatus</i>
Ochomogo, Costa Rica; 1896 Sn Isidro Coronado, Costa Rica; 1937 Panajachel, Guatemala; 1972 Sn Miguel Dueñas, Guatemala; 1985 Merlo, Sn Luis, Argentina; 1943 Zarcero, Costa Rica; 1998 Cd. Guatemala, Guatemala; 1995 Cd. Durango, Mexico; 1896 Morelia, Mexico; 1909	<i>A Tonduz 10914</i> ; US <i>PH Allen 555</i> ; F <i>A Gentry 6516</i> ; MO <i>DG Debouck & JJ Soto 1621</i> ; K <i>R Batallanez sn</i> ; SI <i>DG Debouck 3121</i> ; CR <i>DG Debouck 3057</i> ; CIAT <i>E Palmer 866</i> ; UC <i>G Arsène 3161</i> ; MO	<i>costaricensis</i> <i>costaricensis</i> <i>dumosus</i> <i>persistentus</i> <i>vulgaris</i> <i>vulgaris</i> <i>vulgaris</i> <i>vulgaris</i> <i>vulgaris</i>
Flagstaff, AZ, USA; 1884 Todos Santos, Mexico; 1928 La Paz, Mexico; 1928	<i>ME Jones 4052</i> ; ARIZ <i>ME Jones 24141</i> ; GH <i>ME Jones 24280</i> ; NA	<i>angustissimus</i> <i>filiformis</i> <i>filiformis</i>

Table 10 – Some populations of wild species likely that have gone extinct (additional information in Debouck 2013a,b,c, ...) (organized by sections).

6. CURRENT CONSERVATION EFFORTS

6.1. Status of the *ex situ* conservation of bean genetic resources

Three considerations are pertinent here: i) what do we have in the genebanks?, ii) how much has been evaluated and for which traits?, and iii) what has been done in terms of documentation?

Most of the genetic collections of *Phaseolus* beans that exist *ex situ* across the Americas (and likely elsewhere too) were established in response to needs for variability expressed by breeders for their programs. It is thus not a surprise that commercial lines – and materials related to commercial classes (Voysset & Dessert 1991; Voysset 2000) – followed by landraces form the bulk of these genetic collections. Table 11 shows some of the important collections. No single institution has at least one population of all taxa of the genus, and overall the number of samples of wild forms/ wild species is still largely under-represented in *ex situ* collections (being on average 5% of total holdings or less). The situation is quite unequal among taxa, in terms of number of accessions, but also in terms of geographic coverage. For example, wild *P. vulgaris* from Mesoamerica is not badly represented in *ex situ* collections, although there are gaps for Venezuela, and possibly Panama (Jones et al. 1997; Ramírez-Villegas et al. 2010). Overall, landraces and commercial lines under the status of ‘cultivated’ are well represented in the collections. Some may rightly argue that *P. vulgaris* as a species and as commercial lines/ breeding materials are excessively represented in the collections. In relation to this comment, the first call for caution would be to avoid internal genetic copies, viz. accessions repeated 2-3 times in the same collection. While storing beans is not hugely expensive (Koo et al. 2004), the problem and costs are on the side of field multiplications and evaluations where internal genetic copies do not add anything new.

Table 11 – Some genebanks keeping genetic resources of *Phaseolus* beans.

Institution, location	Number of accessions	Number of taxa
CIAT, Cali, Colombia	36,221	44
USDA-ARS, Pullman, WA, USA	14,674	50
INIFAP, Texcoco, Mexico	12,752	3
University UACH, Chapingo, Mexico	1,422	5
CENARGEN, Brasilia, Brazil	14,069	40
Botanic Garden, Meise, Belgium	699	46

source: FAO-WIEWS, December 2010.

Because the first priority was to stabilize the yield of common bean varieties in the major commercial classes, in the work at CIAT in 1970-1980 emphasis was put on screening germplasm and then breeding for diseases and pests resistances. As a result, sources of resistance have been identified in many germplasm accessions with quite a variation of promising materials (Hidalgo & Beebe 1997). In viruses, materials have been evaluated against BCMV (Gálvez & Morales 1989a; Hidalgo & Beebe 1997), BGMV (Gálvez & Morales 1989b; Hidalgo & Beebe 1997, BYMV (Gálvez & Morales 1989a) and BSMV (Morales & Gámez 1989). Important screening has been done against common bacterial blight (Hidalgo & Beebe 1997; Singh & Schwartz 2010), halo blight (Schwartz 1989), angular leaf spot (Hidalgo & Beebe 1997; Pastor-Corrales et al. 1998), anthracnose (Hidalgo & Beebe 1997), and rust (Stavelly & Pastor-Corrales 1989). In insects, screening has been done against leafhopper (Hidalgo & Beebe 1997), *Apion* (Beebe et al. 1993; Garza et al. 1996) and bruchids (Dobie et al. 1990; Hidalgo & Beebe 1997). In the years 2000, drought and nutritional aspects were added as

priorities for breeding, capitalizing on previous and limited evaluations, so results of large scale evaluations will not appear.

Documentation in passport data might be seen as satisfactory at CIAT, USDA, and the European genebanks, and a lot of valuable data are already available on the internet. Documentation seems less satisfactory about agronomical traits (at accession level) and in many other genebanks along the criterion of data availability on the internet; it is possible that they have a state-of-the-art documentation but not available! Lack of availability may lead to question the purpose of keeping a collection, especially if supported by public funds.

About distribution, taking the genebank at CIAT as an example, one can see in the following figure (Fig. 1) that bean genetic resources have been used substantially over the period of work (1973-2012). With a total close to 37,200 accessions at time of this compilation, one could say that almost the entire collection has been requested and distributed once. Sure the breeding and other programs of CIAT have benefited a lot from the presence of the genebank (Gaiji & Debouck 2008), but external users outside the CGIAR have received a substantial share of bean accessions too. The current status of bean breeding – a crop preferentially autogamous, where the private sector would have difficulties in protecting innovations – is also reflected in these figures. Private companies mainly focused on snap bean breeding do request from time to time specific accessions with known traits but not much, as compared to the national agricultural research systems (NARS) and university departments. On the other hand, with germplasm originating in 95 countries, one can note that a larger number of countries have benefited from this collection, evidencing the advantage of a multilateral system such as the one of the International Treaty (FAO 2002).

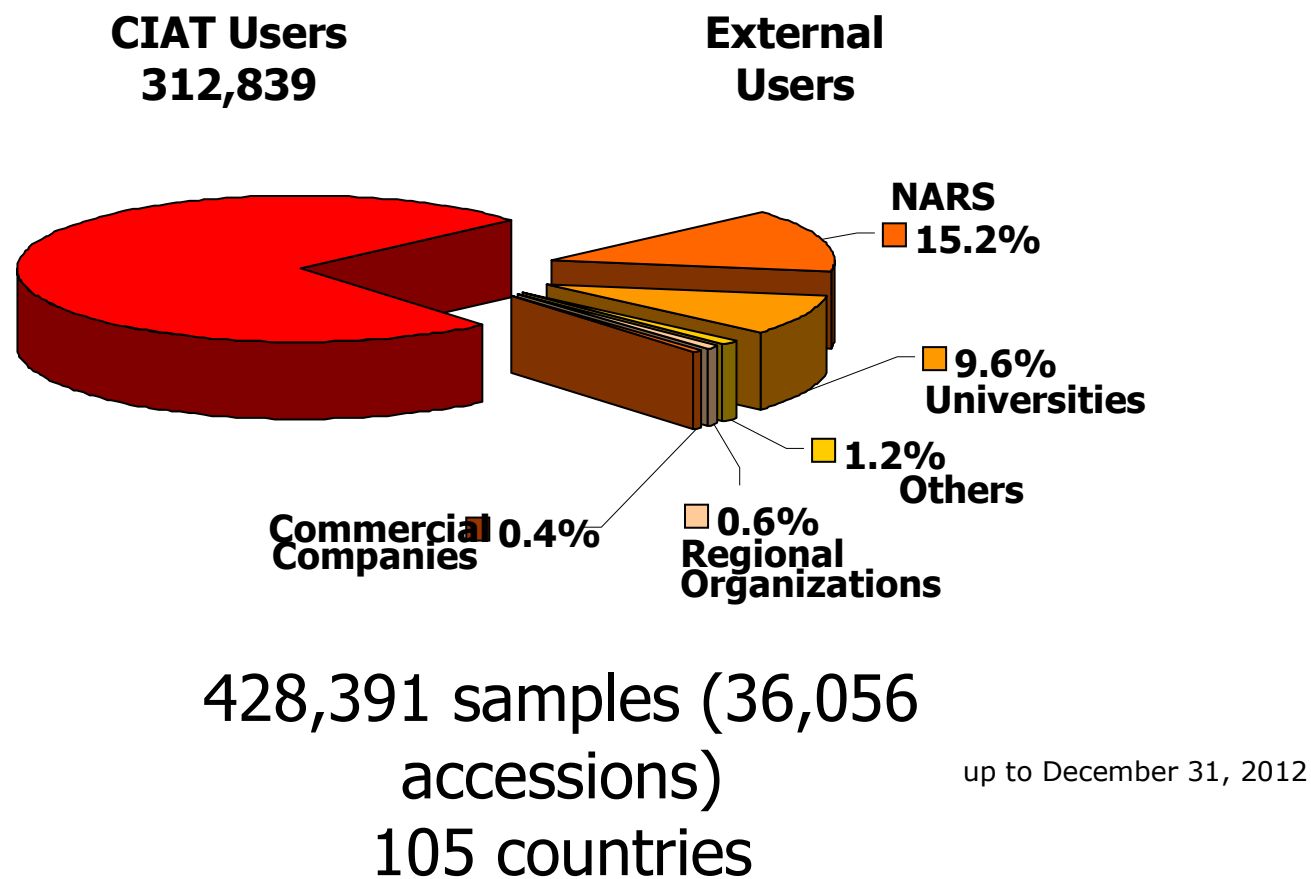


Figure 1. – Distribution of *Phaseolus* bean germplasm by the genebank at CIAT for the period of work 1973-2012.

6.2. Status of the *in situ* conservation of bean genetic resources

Conservation of *Phaseolus* genetic resources in original habitats in the Americas would have its role in this Strategy if evolutionary forces can continue to operate, so that facing new problems (e.g. a new disease or pest moved to the bean host because of climate change) traits of interest can be found. On the basis of points aforementioned in 3.1., such conservation *in situ* is particularly relevant for wild relatives and will thus be considered first.

In situ conservation of *Phaseolus* genetic resources is scarcely documented so far, especially when dealing with wild relatives (see also 6.3. below). Many populations of bean wild relatives can actually thrive in protected areas in the Americas, but without published records an assessment about which species and populations are currently conserved and where is uneasy. Without published inventories monitoring the success or failure of *in situ* conservation will be equally difficult. Looking at the situation in the field across the Americas southwards, perhaps the following comments can be made. In the NE USA, namely in Pennsylvania, *P. polystachyus* might be saved in Ohiopyle State Park (Debouck 2013e). In Florida, there seems to be one population of *P. smilacifolius*, true and rare species, out of risk at the Waccasassa Bay Preserve State Park (Debouck 2013e). The Sandhills Game Land in southern North Carolina harbors a few populations of *P. sinuatus* (Debouck 2013e), distinct from *P. polystachyus*, starting from its ecology (Radford et al. 1968). As rightly observed by Johnston

(1997), protection is overdue for the Edwards Plateau, Texas, home of the endemic *P. texensis*, for which several populations are known (Delgado-Salinas & Carr 2007). Many populations of wild beans are currently included in protected areas of Arizona and New Mexico. With some consideration for the buffer zones, it would be possible to even include type localities (Freitag & Debouck 2002; Standley 1910): for *P. grayanus*: an expansion of the Coronado National Forest to the east; for *P. parvulus*, an expansion of the Gila Wilderness Area to the south. But for *P. angustissimus* (“Río Grande above Dona Ana”) and var. *tenuifolius* (“near the copper mines and in Guadalupe Pass”), it might be too late given the fast growing urbanization in these areas.

A documented case about the presence of wild bean species is the biosphere reserve ‘Sierra de Manantlán’ in SE Jalisco in Mexico, with *P. albescens*, *P. coccineus*, *P. leptostachyus*, *P. lunatus*, *P. micranthus*, *P. pauciflorus*, *P. perplexus* and *P. vulgaris* (Vázquez-García et al. 1995). These populations could be considered ‘saved’ although wildfires affect the area frequently (Calderón-Aguilera et al. 2012). It is possible that ‘Rancho del Cielo’ in southern Tamaulipas, Mexico, harbours populations of wild *P. coccineus*, a few ‘*Digitati*’, and *P. glabellus* (Hernández-Xolocotzi et al. 1951), but the populations are not individually reported. The same may happen for a few populations of *P. marechalii* along the Mexican Neovolcanic Axis, but they are not documented individually (Salcedo-Castaño et al. 2009). The Parque Nacional Cascada de Basaseachic in Chihuahua (Cartron et al. 2005) is known to harbor populations of *P. ritensis* and of *P. parvulus* (Debouck 2013b and d, respectively). One population of *P. grayanus* has been sampled in the national park Cumbres de Majalca in Chihuahua, Mexico (Debouck 2013g). Across the Sea of Cortés, several islands have been declared as protected areas (Cartron et al. 2005), and populations of *P. filiformis* have been reported therein (Debouck 2013h). Other populations of *P. filiformis* are known to thrive within the national parks of Vizcaino and Pinacate (Cartron et al. 2005), in northern Baja California and Sonora, respectively (Debouck 2013h). The outlier population of *P. filiformis* in Durango is in the Biosphere Reserve of Mapimí (Debouck 2013h). The volcanoes west of Guatemala City – on paper a protected area - might have a few populations of wild *P. dumosus*, *P. vulgaris*, *P. xanthotrichus*, and the endemic *P. macrolepis*, but they need to be inventoried for effective protection. In Petén, in the Tikal national park, wild *P. lunatus* is known to be present, and the same seems to be true for other Mayan archaeological sites across the Peninsula of Yucatan (Debouck 2013e). Although Costa Rica has a significant part of its land declared as protected areas, the inventory up to the population level therein has not yet been published. While many populations are found outside protected areas (Araya-Villalobos et al. 2001), it is likely that protected areas such as Cerro Chiripó and Parque La Amistad because of its acreage and ecology (Matamoros-Delgado & Elizonda-Castillo 1996) harbour populations of *P. costaricensis*, *P. lunatus*, *P. talamancensis* and *P. tuerckheimii*. Similarly, populations of wild *lunatus* may thrive in the Parque Nacional Guanacaste (Debouck 2013e). For Panama, there is a protected area reported for Volcán Baru (Harcourt et al. 1996), from where populations of *P. costaricensis* and *P. tuerckheimii* have been reported (Debouck 2013f, and Salcedo-Castaño et al. 2011, respectively).

In Colombia, it seems likely that Parque Tairona harbours a few populations of *P. lunatus* (Debouck 2013e). In Ecuador, being the Galapagos a UNESCO World Heritage protected area, if the feral goats and cattle can be controlled (McMullen 1999), one would hope that some populations of the endemic *P. mollis* (Debouck 2013e) are effectively conserved *in situ*. But in mainland Ecuador, the current protected areas – i.e. Cayambe-Coca and Sangay (Suárez et al. 1996) - seem to protect populations of *P. dumosus* (likely feral and introduced) rather than the unique populations of wild *P. lunatus* and *P. vulgaris* on the Pacific slope of the Andes (Debouck 2013e,f, respectively; Debouck et al. 1989b). In Peru, the reserves of Cutervo and Macchu Picchu (Sagástegui-Alva et al. 2003; Suárez de Freitas et al. 1996) are harboring populations of *P. pachyrrhizoides* and *P. augusti*, respectively (Debouck

2013e), but the unique populations of wild *P. vulgaris* of NW Peru (Debouck et al. 1993; Kami et al. 1995; McClean et al. 2004) seem to be out of any protected area so far (Sagástegui-Alva et al. 2003). In Bolivia, the forests representing the northward extension of the subhumid Tucuman forest, where *P. augusti* and wild *P. vulgaris* are distributed (Freyre et al. 1996), are currently not considered in protected areas (Nagashiro et al. 1996). The protected area “Noel Kempff Mercado” in NE Bolivia could potentially harbor wild *P. lunatus* but this species has not been reported yet (Killeen 1998). In Argentina, it seems that some populations of wild *P. vulgaris* could be included in the proposed Aconquija National Park of Tucumán (Halloy 1997) and Lagunas de Yala of Jujuy (Debouck 2013f), while perhaps the most unique ones are endangered in the mountains just W of Cordoba City (Drewes 2008).

If it is true that several populations are already included in protected areas - yet not documented, there are others which may not be protected *in situ* at all. For some species that have adapted to difficult topographies and environments – to humans, *in situ* conservation might already be working. For example, *P. amblyosepalus* grows in the understory of pine forests in remote areas of the Sierra Madre Occidental of SE Sinaloa (Debouck 2013d), and the difficult access may *de facto* ensure some *in situ* conservation. The same may be true in the same mountainous range for *P. grayanus*, *P. reticulatus*, *P. sonorensis*, and possibly for the same reasons. Similarly, *P. pluriflorus* thrives in several lava beds ‘malpaís’ south and east of Mexico City (Debouck 2013d); such soil and topography makes urbanization or agriculture difficult. Unfortunately, the ecology of some *Phaseolus* species matches too well with the preferences of humans, making *in situ* conservation eventually awfully expensive because of the competition for the same increasingly scarce asset: land. It seems to be the case for *P. chiapasanus* (in the coffee growing areas of Mexico), *P. vulgaris* (in most Central American countries), or *P. lunatus* (on Pacific coastal areas from Nayarit down to Nicaragua). Things may not improve as many countries in the area because of a putative deficit in infrastructure and because of an immediate interest into free trade agreements, are willing to expand their road network putting more populations at risk with forest fragmentation (Calderón-Aguilera et al. 2012). This seems more relevant in Central American countries where the ecological niches for *Phaseolus* species given the lack of a longitude gradient are particularly narrow. And this threat seems more immediate and overwhelming as compared to the risks linked to climate change (Figure 2).

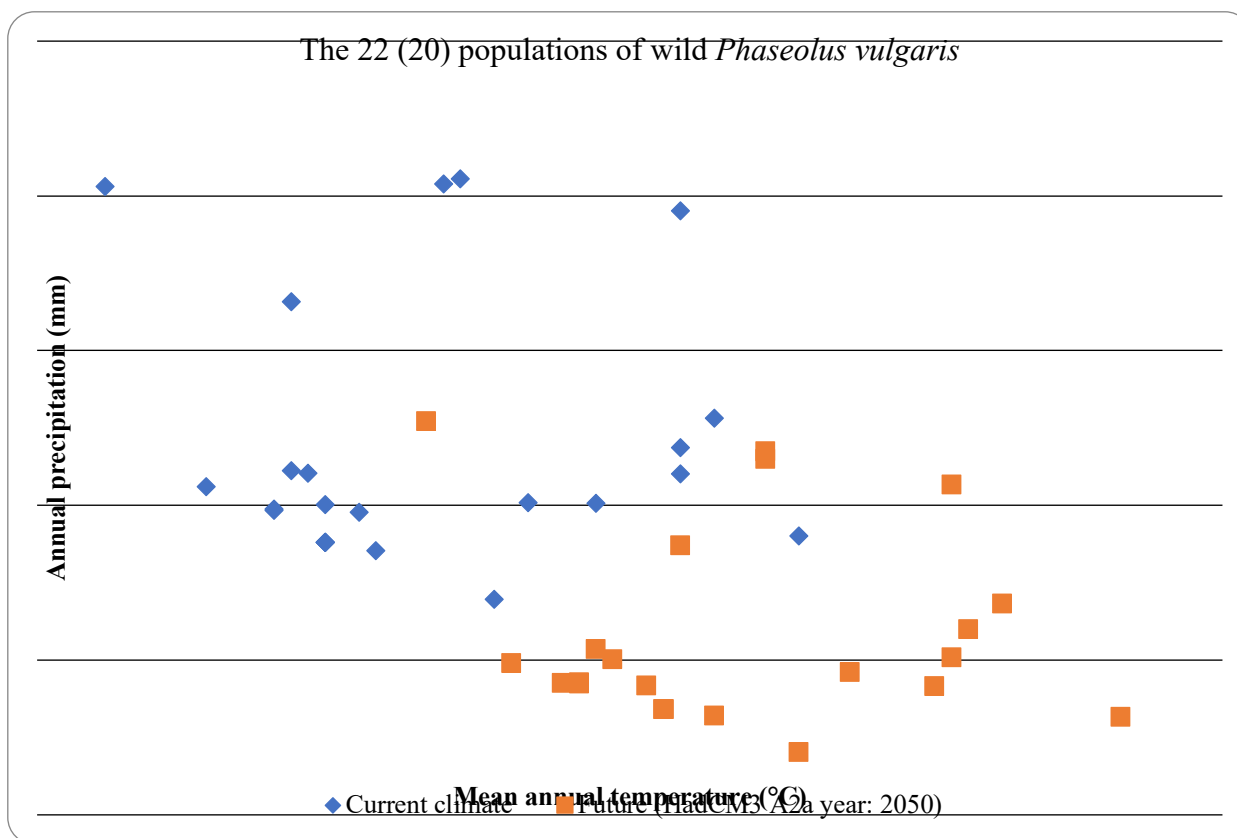


Figure 2. – Evolution of predicted temperature and rainfall from current conditions up to year 2050, for the sites of the 22 known populations (two endangered or extinct) of wild *Phaseolus vulgaris* L. in central Costa Rica.

One should keep in mind that when moving germplasm from the collection sites into the field multiplication plots of the genebank, germplasm accessions often face a variation in temperature of 1-2 °C or in available moisture; if these variations are kept to a minimum drift might not be too important. For wild *vulgaris* an increase of 1-2 °C and a decrease in moisture (across its range wild *P. vulgaris* often thrives in environments with 600-800 mm rainfall/ year) might not be lethal, while the destruction of the whole original habitat surely is! Change of land use in the Central Valley of Costa Rica seems to put several populations at risk of irreversible loss (Zamora 2010). Finally, one should keep in mind that contexts and markets may change the full picture almost overnight: habitats of *P. maculatus* or *P. rotundatus* in north-east Jalisco could have been considered at safe (because of rough topography, stony/ ‘malpaís’ soils and little rainfall) in the 1970s, while recent plantings of *Agave tequilana* have been expanding over the last decade in famed ‘non-productive’ lands !

An interesting parallel could be drawn with genetic resources of wild fish. In 2010, Paul Greenberg wrote: “Rather than eating into our principal as we have done for the last thousands years, by setting up a network of fisheries reserves we will in a sense put a portion of our ocean wealth into low-interest municipal bonds, an investment that if left alone will pay a steady, compounded interest over time.” (Greenberg, 2010, p. 247).

Box 10

In situ conservation of wild relatives of beans, although attractive on paper (because of the illusion that nobody has to pay), is not likely to work – to the extent needed if we continue with current behaviours. The inventory of all populations will not be completed before many populations will be extinct. Assessment of genetic uniqueness and potential value will not arrive on time in order to convince land owners to maintain the land under its original vegetation cover. Something should be attempted however, and a starting point might be in the inventory of *Phaseolus* species in protected areas already existing. This in turn will increase the value of such protected areas, with hope to emulate other landlords.

There would have been a golden justification for *in situ* conservation with the wild- weed- crop complexes (Beebe et al. 1997; Papa & Gepts 2003). One should note that the Phaseoli have active nectaries at the base of the floral disk (Webster et al. 1982), attracting heavy Hymenoptera (carpenter/ bumble-) bees which are responsible for cross pollination among landraces but also between landraces and wild forms of the respective Phaseoli species (Andersson & de Vicente 2010). Gene flow through pollen can occur in both ways, often asymmetrical, either towards the cultivated form (Singh et al. 1991) or towards the wild form (Chacón-Sánchez et al. 2005; Papa & Gepts 2003). The latter might be worth monitoring if the ‘bred’ genes affect fitness of wild populations (Gepts & Papa 2003; Papa et al. 2005). The former might explain some variability acquired by landraces of the bean crops in early (preceramic?) times, because if this still happens nowadays in remote places of tropical America where the two forms get into contact (Beebe et al. 1997; Martínez-Castillo et al. 2007) this gene flow is no longer significant for the evolution of the bean crops. Who would still be domesticating beans in the 2010s? Who would still have that patience?

Does on-farm conservation bring any help? Let us now see the situation of *in situ* conservation of cultivated materials or landraces. The few examples given in 5.1. clearly indicate that on-farm conservation of bean landraces is not working unless sustainable economic mechanisms are in place to pay for the conservation of higher diversity by farmers. A somewhat similar point was raised by Zeven (1996, p. 340) for the conservation of landraces in western Europe: “farmers will only continue to grow landraces when they are payed [sic!] to do so”. When there are specialty markets asking for specific landraces as in central Italy (Negri & Tosti 2002), it can work, but markets may change. If beans are used by the food processing industry, it is possible that interest for specific colors, color patterns and size will continue to fall down, causing little incentive for farmers to keep all that diversity on farm (Kaplan & Kaplan 1992). For on-farm conservation to be effective, one has to consider that landraces have each a sufficient population size to escape pests or disasters year after year (Brown 2000 indicated a “5,000 yardstick”), and on the other hand there should be unique and stable human selection pressures and practices in order to create and maintain such unique variants over time (Debouck et al. 1989a). The current production systems may not guarantee the demographic dimension nor the diversity and duration of such selective pressures. Finally, there is one more difficulty with the *in situ* conservation of landraces: who is monitoring which landraces are planted year after year, offering the alternate scenario of *ex situ* conservation if a farmer decides to discontinue the planting? In the case of wild beans *in situ*, the basic requirement will be to make sure that the original habitat with plenty of land is still there with as little modification as possible; it is obviously more complex and surely not static in the case of cultivated beans.

Box 11

To be meaningful *in situ* conservation of landraces would imply the continuity of original selection pressures by human cultures in original environments for centuries ahead (just as up to a recent past). We thus need plant (and human) demography, richness of bean mixtures, variety of selection pressures, and time for continuing evolution. Our modern bean production systems seem to not have that patience anymore!

6.3. What does not work properly now in conservation of bean genetic resources?

The Convention on Biological Diversity (1992) set a landmark in calling attention of the public and governments on the importance of biological diversity to sustain all human activities on the planet (see confirming reviews by Cardinale et al. 2012, Hooper et al. 2012), in claiming it as part of the assets of each country, and in establishing institutionally bodies to regulate its access and use. One would thus anticipate that countries as part of the expression of their sovereign rights would have a full list of the plant genetic resources within their borders, namely of bean landraces and crop wild relatives. Yet, since 1992 not much has been achieved and/ or updated in the very basic, such as inventories of *Phaseolus* species and populations for each country where we know the genus is part of the native flora (Table 12, from north to south, and then the Caribbean). For some countries (e.g. Guatemala, Honduras, Colombia, Venezuela, Paraguay), such inventories are overdue. Fortunately, there is a relatively recent compilation of species and populations (Freytag & Debouck 2002), with updates and estimates of geographic coordinates available in ‘Cahiers de phaséologie’ (Debouck 2013a, ...).

Table 12 – Compilation of last floristic inventories of *Phaseolus* species, with emphasis on wild forms/ species.

Countries with native <i>Phaseolus</i> genetic resources	Last or key compilation of <i>Phaseolus</i> species, sometimes with indications about localities	Comments
Canada	doubtful, conflicting information about the presence of the only likely species <i>polystachyus</i>	1
USA	“Vascular flora of the southeastern United States” Isely 1990; “Flora of New Mexico” Wootton & Standley 1915; “Arizona flora” Kearney & Peebles 1960; “Manual of the vascular plants of Texas” Correll & Johnston 1970; “Jepson manual – Higher plants of California” Isely 1993	2
Mexico	“Leguminosas de Coahuila” Carranza & Villareal 1997; “Los géneros de leguminosas del Norte de México” Estrada & Martínez 2003; “Systematics of the genus <i>Phaseolus</i> (Leguminosae) in North and Central America” Delgado-Salinas 1985; “Los parientes silvestres del frijol común en el Occidente de México” Lépez & Ramírez 2010	3
Guatemala	“Flora of Guatemala” Standley & Steyermark 1946	4
Honduras	none (!?)	5
Belize	“The forests and flora of British Honduras” Standley & Record 1936	6
El Salvador	“Lista Preliminar de Plantas de El Salvador” Calderón & Standley 1941	7
Nicaragua	“Flora de Nicaragua” W.D. Stevens et al. (eds.) 2001	8
Costa Rica	“Manual de plantas de Costa Rica” Zamora 2010	9
Panama	“Flora of Panama” Lackey & D’Arcy 1980	10
Colombia	“Catálogo ilustrado de las plantas de Cundinamarca” García & Forero 1968	11
Venezuela	“Catálogo de la Flora Venezolana” Pittier et al. 1945	12
Ecuador	“Catalogue of the vascular plants of Ecuador - Fabaceae” Neill et al. 1999	13

Peru	“Catalogue of the flowering plants and gymnosperms of Peru” Zarucchi 1993	14
Bolivia	“A catalogue of the ferns and flowering plants of Bolivia” Foster 1958	15
Brazil	“Studies in American Phaseolinae” Piper 1926	16
Paraguay	“Revisio specierum austro-americanarum generis Phaseoli L.” Hassler 1923	17
Argentina	“Catálogo de las plantas vasculares de la República Argentina” Hoc 1999	18
Cuba	“Flora de Cuba” Sauget & Liogier 1974	19
Dominican Rep.	“Catalogus Florae Domingensis” Moscoso 1943	20
Puerto Rico	“Flora of Puerto Rico” Liogier 1988	21
Jamaica	“Flora of Jamaica” Fawcett & Rendle 1920	22
Bermuda	“Flora of Bermuda” Britton 1918	23

Comments:

1: the only species ever reported as wild in Canada is *P. polystachyus*, and the problem arose because Authors were not reporting localities nor voucher specimens. Reporting present: Small 1903, Rydberg 1932, Sousa & Delgado 1993. Reporting absent: Lackey 1983, Oldham & Brinker 2009. See also discussion by Freytag & Debouck 2002.

2: since the ongoing project of ‘Flora of North America’ has not yet published the volume on Leguminosae, we have to refer to previous works. Isely (1990) rightly reported wild *P. polystachyus* and *P. sinuatus* as distinct species, but was wrong in concluding about *P. smilacifolius* as a hybrid between the former species. Wootton & Standley (1915) reported the expected species (*acutifolius*, *angustissimus*, *grayanus*, *maculatus*, *parvulus*), but not *filiformis* nor *ritensis*! Kearney & Peebles (1960) mentioned *acutifolius*, *angustissimus*, *grayanus*, *maculatus*, *parvulus*, *ritensis*, but no *leptostachyus*, and rightly raised the question of *wrightii* being distinct from *filiformis*. Correll & Johnston (1970) reported *acutifolius*, *angustissimus*, *maculatus* and *polystachyus*. About the later, they rightly picked the variant of the Edwards Plateau that would become *P. texensis*. They mentioned *wrightii* (= *filiformis*), but not *grayanus*. In the Jepson Manual (1993), Duane Isely rightly mentioned the sole population of the only species growing in California (*P. filiformis*).

3: the book by Carranza & Villareal (1997) rightly reported about *P. acutifolius*, *P. coccineus*, *P. filiformis*, *P. grayanus*, *P. maculatus*, *P. pedicellatus*, *P. plagiocilyx* and *P. zimapanensis*, but missed some Digitati. The book by Estrada & Martínez (2003) mentioned *P. maculatus* and *P. ritensis*, but missed many species from northern Mexico. The review by Delgado-Salinas (1985) remains an invaluable source of information; the reader might miss a list of specimens seen. The work by Lépiz & Ramírez (2010) reported about the presence of 17 valid taxa and location of some populations.

4: because of the publication date (1946!), there are synonymy problems (*anisotrichos*= *leptostachyus*; *formosus*= *coccineus*), but this work mentions rightly localities for wild *P. lunatus*, *P. macrolepis*, *P. tuerckheimii*, *P. viridis* and *P. xanthotrichus*. It did not pick up wild *P. vulgaris*, nor the wild relative of tepary, *P. parvifolius*. Yet, one can understand the reprinting of 1985!

5: searches in author’s library and specific web sites (e.g. MoBot) did not indicate a flora or catalogue of vascular plants for Honduras. The best source of data would thus be Freytag & Debouck (2002), and the updates of ‘Cahiers de Phaséologie’ (Debouck 2011).

6: this publication (1936!) indicated the presence of *P. lunatus* as wild and *P. vulgaris* as cultivated in Belize.

7: this work (1941!) basically reports three cultivated species (*coccineus*, *lunatus*, *vulgaris*) with a few varietal names.

8: the compilation of species (2001), with few herbarium specimens mentioned, by Delgado-Salinas, indicated two species (*P. tuerckheimii*, *P. xanthotrichus*) as possible.

9: this work (2010) reports about bean species found wild and cultivated in Costa Rica; the sole shortcoming is the absence of a list of all populations.

10: the Flora (1980) reported three species as wild (*P. coccineus* which was demonstrated later to be *P. costaricensis* [Freytag & Debouck 1996], *P. lunatus* and *P. tuerckheimii*) and *P. vulgaris* as cultivated.

11: this volume (1968) mentioned a few localities for *P. flavescens*, *P. formosus* as wild and *P. vulgaris* as cultivated. The true names for the former two are *dumosus* and *coccineus*, respectively, and refer here about feral populations.

12: this work (1945!) listed both *P. lunatus* and *P. vulgaris* as cultivated, and *multiflorus* (= *P. coccineus*) as ornamental; Schnee (1960) however indicated that *P. lunatus* could be spontaneous in Venezuela.

13: this work (1999) did not clear some synonyms (*multiflorus*= *coccineus*; *harmsianus*= *polyanthus*= *dumosus*, and *rimbachii*= *Dipogon lignosus*), but rightly recognized *P. augusti*, *P. mollis* and wild *P. lunatus* and wild *P. vulgaris*. It did not pick up that *P. rosei* is the wild Andean form of *P. lunatus* (Freytag & Debouck 2002). About *P. mollis* the WCMC (1991) probably rightly wrote ‘nt’, ‘neither rare nor threatened’ given the status of the Galapagos Islands as UNESCO Biosphere Reserve and national park of Ecuador.

14: this compilation (1993) rightly identified as wild *P. augusti*, *P. lunatus*, *P. pachyrrhizoides* and *P. polyanthus* (= *dumosus*), but did not mention wild *P. vulgaris* (strange enough given the work by Berglund-Brücher & Brücher 1976).

15: this work (1958) that is basically a list mentioned the presence of *P. augusti* and *P. bolivianus* (its synonym), but not wild *P. lunatus* nor *P. vulgaris* (see Freyre et al. 1996).

16: this former review of the genus (1926!) mentioned wild *P. lunatus* in Brazil but with no indications about localities (and not reported by Warming & Ferri 1973, but as cultivated). Although Debouck 2013e reports two populations of this taxon, this needs to be verified by additional field work.

17: this review (1923!) only reports about the presence of cultivated *P. multiflorus* (= *coccineus*), *P. lunatus* and *P. vulgaris*, and many more now considered belonging to other genera (see Delgado-Salinas et al. 2011).

18: the catalogue (1999) rightly mentioned wild *P. augusti*, *P. lunatus* and *P. vulgaris*, and many synonyms now classified into *Macroptilium*, *Ancistrotropis*, *Cochlianthus* and *Leptospron* (Delgado-Salinas et al. 2011).

19: this Flora (1946-53 reprinted in 1974) only reported *P. lunatus* as wild.

20: this work (1943) reported *P. lunatus* as wild and cultivated ('Pois de Souche', in Haiti), and *P. vulgaris* as cultivated and spontaneous after the cropping cycle. It also reported a *P. ricciardianus*, a spontaneous form of *vulgaris*; so far no true wild *P. vulgaris* has ever been reported from Hispaniola.

21: as expected this Flora (1988) reported *P. lunatus* as wild and cultivated, and cultivated *P. vulgaris*. Curiously enough, Liogier mentioned (*ibidem*, p. 194) the presence of *P. polystachyus* from the Rincón area, a record that had not been confirmed by any phaseologist so far!

22: the Authors in this Flora of 1920 mentioned *P. lunatus* and *P. vulgaris* both as spontaneous and cultivated, but *P. vulgaris* as wild form has never been confirmed from Jamaica. One should note that *P. dumosus* was listed as synonym of *P. vulgaris* (an indication that the Flora of Jamaica may need some updating).

23: Nathaniel Lord Britton reported the presence of wild *P. lignosus*, confirmed as endemic (Pettit et al. 2012).

A concrete outcome of the Convention on Biological Diversity has been in many countries the creation of ministries of environment/ competent authorities (Anonymous 1992: Art. 6.a, Art. 15.1; IUCN 1993). But being new governmental entities, there has been often a poor interface between the ministries of agriculture – development oriented - and those of environment – conservation oriented. And newness in this case often meant lack of technical capacity. A good example of it has been the regulation of access to genetic resources, even for the few listed in the Annex 1 of the International Treaty (FAO 2002: Art. 11, Art. 12). Even in order to remediate what countries need most: inventories of the genetic resources they have in order to put in practice their sovereign rights, botanists from national universities often have to go through cumbersome and lengthy processes (Ruíz 2008). Perhaps one logical way around would be that the biological assets including crop genetic resources and their wild relatives be under the sole control of . . . Treasury. Such a status might bring stability to a series of activities where duration and sustained efforts make the difference. As well noted by Jack Harlan (*ibidem* 1992, p. 240), crop failures happen putting highly socially diversified societies at risk, and curiously enough ministries of finances worry about taxes of current fiscal years, leaving the future food of peoples outside annual planning.

A second limitation at national level often relates to implementation schemes. Because for long bean breeding and genetic resources were in the hands of the same people, the latter was a second activity of the former, with two shortcomings. First, germplasm evaluations were often considered as selection activities, and materials not immediately meeting breeders' expectations were eliminated. The high proportion of white or cream seeded materials in some collections might be the result of such selections. Second, keeping genetic resources was often confused with keeping breeding lines. This can be seen in passport data, namely about origin, of many germplasm catalogs. Keeping large numbers of accessions was thought doing the job instead of making sure that the numbers meant effectively genetic diversity *per se*. The application of markers of molecular genetics has timely come to correct this major shortcoming, although not all curators have the means (financial resources, technical and human capacity) to use them routinely. Although this close association of bean breeding and genetic resources might present advantages at finding accessions to be quickly used in breeding

programs, it might not be desirable on the mid/ long-term because keeping the entire diversity, collecting additional sets, and documenting everything is a set of tasks in its own right.

The lack of large-scale germplasm evaluation is another limitation, and worse for effectiveness in finding useful traits, is limited to the national framework (understood along a set of bean germplasm of single geographic origin). Vavilov, in the 1920s responsible for a network of 400 experimental stations with 20,000 staff (Hawkes 1990, Reznick & Vavilov 1997) in one country – do we have today the equivalent while we have four additional billions people on board? -, understood early enough that the evaluation should be done at the crop (biological) level, not at the national level. An institution CIAT tried in the period 1976-1995 to follow that approach (CIAT 1973), with many useful traits disclosed (Hidalgo & Beebe 1997) and a very significant impact in breeding (Voyses 2000) unmatched to date.

Farmers often have little access to bean genetic resources because they do not know in most cases that bean genetic resources have been gathered in *ex situ* facilities. But when farmers know that, the access to genetic resources being done through genebank databases might not be an easy one. The reason lies in the language used by genebanks with standard descriptors (De la Cuadra et al. 2001), which is not straightforward towards many farmers. Genebank curators often complain about lack of understanding and interest by the public, being materialized in the form of meager and erratic annual funding, but conversely they should perhaps improve the accessibility of collections and data towards that very public they want to serve.

Investments in bean genetic resources as compared to needs remain low and quite variable from year to year. Most of it is from the public sector, approved annually and linked to the budgets of agricultural research. Little is coming from the private sector, but some grants on specific topics, not the continuing conservation work. The private sector (e.g. companies selling improved seed) usually works on snap beans, which represent quite a narrow niche in genetic resources. The return on investment by the public sector is however very significant (in this case CIAT genebank: Johnson et al. 2003) as compared to the cost (Koo et al. 2004).

The lack of good people now, but specially towards the future, is perhaps what worries more. Plant genetic resources can be best understood and put at work for food and the economic and cultural developments of human societies but through multidisciplinary approaches. Some of the scholars who most contributed to plant genetic resources (e.g. Vavilov, Harlan, Heiser) were biologists equally interested in humanities (anthropology, history, geography).

7. STRATEGY FOR THE CONSERVATION OF BEAN GENETIC RESOURCES

7.1. The rationale for a strategy

In an ideal world it might be convenient that a single entity takes care of everything in bean genetic resources, from the collecting through *ex situ* and *in situ* conservation to the distribution, even perhaps including some pre-breeding. But a convenient scenario may not mean a secure one, particularly in the long-term, namely if priorities of that single entity shift over time. An ideal world does not exist either because of national borders becoming stronger over the last five centuries, with pros perhaps related to implementation schemes and cons possibly related to flows of germplasm. As compared to thousands of years of evolution as “*res nullius*”, bean genetic resources evolve today in a national context. As noted by R. Leakey & R. Lewin (1995) and E.O. Wilson (2002), we are seeing the sixth extinction and have entered the critical one hundred years during which something can be saved or lost forever. Some may argue that the loss of bean genetic diversity does not matter because it will be re-created when needed by transgenesis. This argument may have a major flaw, because the bean genetic diversity still available today has been tested for millennia for many of the problems affecting the bean crops, and likely to affect them in the future. Transgenesis when possible and at which cost!, has been used to transfer paucigenic novel traits such as herbicide resistance (Aragão et al. 2002). As noted by Gepts (2002), genetic engineering will bring gain-of-function mutations for traits likely absent in the studied gene pool, without being a substitute for plant breeding. The conservation of that genetic diversity is therefore the sole insurance to have beans for food permanently.

At the extreme of the conservation chain, the Global Seed Vault in Svalbard maintains a safety back-up of bean genetic collections (from CIAT 30,574 accessions or 81% to date), and in order to perform well its role as safety back-up, it is understood that such bean genetic collections are safely maintained elsewhere (plus a couple of additional services). In other words, the Strategy will have to consider a couple of different actors with specific roles, perhaps not the 260 or so institutions (Table 11) that keep a collection of beans. Financially, such a high number might not be sustainable, while technically two to four reserve genebanks for example may suffice. Some level of coordination might be desirable too, so that duplication of efforts would be kept to the minimum or well approved before hand when some “duplication” is indeed desirable, namely in the area of safety back-ups. Coordination will also be necessary in order to make sure that there are no sets of germplasm ‘falling into the cracks’ or unavoidable tasks that are left unfinished. Last but not least mechanisms of control should be defined and implemented effectively so that the activities agreed upon by the few actors are carried out timely.

A Strategy for whom? Farmers and recently bean breeders, from the public sector in most cases for dry (common) bean (Johnson et al. 2003), and often from the private sector in the case of snap beans (Myers & Baggett 1999), have been the main users of bean genetic resources. Farmers, bean breeders and eventually the consumers are thus the first to benefit from the Strategy, and will likely and legitimately ask for the variability they need at any time now and in the future. Being the (common) bean a convenient biological model for *inter alia* genetic studies (Bassett 2007), university departments even high schools often use genebank collections (Dudnik et al. 2001). The Strategy is thus targeted at answering questions by curators of and scientists working on bean collections in order to meet timely such requests of the public.

7.2. The drives of the Strategy and major activities, and logical time sequence

Because of the overarching question set at the beginning, the Strategy is first of all focused on conservation, mostly *ex situ* conservation, given the unsolvable challenges of *in situ* conservation over the mid-/ long-term under current behaviours. And the boxes aforementioned have summed up some of the activities leading to efficient *ex situ* conservation. The following major activities will hopefully make *ex situ* conservation more relevant, biologically (the diversity useful to bean breeding and agronomy, and that is becoming extinct), and socially (the diversity that is likely to generate benefits to the society). The first drive deals with increasing knowledge without which conservation cannot be planned, with three sets of activities: inventories through collecting, information on seed storage behavior, and evaluation. Let us examine these into more detail.

7.2.1. Further collecting and acquisition

Collecting what is missing for conservation will be first because extinction does not help anybody nor does allow further activity by the actors. It would not make a lot of sense indeed that when eventually molecular tools to understand the bean genome are becoming available (Broughton et al. 2003; Porch et al. 2013; Schmutz et al. 2014), the different species representing all variations of this genome are extinct and not available! Collecting/ acquiring germplasm that is not yet documented/ conserved is somehow outside a time perspective – it should be done at any time, when the opportunity is there.

For cultivated *P. vulgaris* and from the Americas, given the replacement of landraces by modern varieties, it might be quite late to still find something not already present in genebanks, perhaps with some exceptions in the Colombian, Venezuelan and Peruvian Andes. For Lima bean, year-bean and tepary bean, there are places that would be worth visiting in Central America. Some non commercial cultivated types of Lima beans might still be worth collecting in Colombia, Venezuela, Peru, Paraguay and Brazil. The necessary checking (in order to avoid duplicates) with materials already existing *ex situ* will make this kind of exploration time consuming, but appropriate data and digital imagery on laptops taken to/ consulted from the exploration sites through internet may help. Germplasm of Lima beans from their expansion lands in Africa (Westphal 1974) and Asia (Baudoin 1988b, 1989) might still be under-represented in genebanks. With traditional agriculture being confronted with the opening of global markets, if it is to carry out this late collecting, it has to be done now (a need already stressed upon by Lyman in 1984!). The opening of global markets might also be misleading, with the introduction of bean varieties where in the past there were none: the case of the oasis of Siwas in western Egypt is a good example (Nabhan 2007).

As far as collecting of wild relatives is concerned, a gap analysis cannot be separated from some sort of breeding perspective, keeping in mind that there are five bean crops to take advantage of and to breed. Because of the founder effect that has been documented in four out of the five bean cultigens (Table 6), the immediate wild ancestors are an obvious priority, and the example of the bruchid resistance indicates that all populations should be sampled. Given the advances in the *ex situ* conservation, this means a significant additional collecting for the small seeded tropical wild form of Lima bean (which apparently includes two gene pools: Serrano-Serrano et al. 2010, 2012). For the other close wild relatives, it is more a geographic gap filling than the sampling of the entire range (Table 12). Populations to be sampled are the ones known to exist because of the information provided in ‘Cahiers de Phaséologie’ (Debouck 2013a,b,c, ...) and not yet present in genebanks. As it can be

seen in Table 13, the gap would be relatively small for wild *P. vulgaris* (namely in Oaxaca, Panama, Venezuela, Bolivia, and central western Argentina), although even in regions considered as well sampled such as western Mexico there are still gaps (Zizumbo et al. 2009). While wild *P. lunatus* has been relatively well sampled in Mexico (Andueza-Noh et al. 2013; Martínez-Castillo et al. 2014) and Costa Rica (Araya-Villalobos et al. 2001), Ecuador and Peru, there is substantial work to be done in lowland South America, from Venezuela down to Argentina, and in the Caribbean. Some collecting of wild Lima beans has been done in Cuba (Esquivel et al. 1993). Gap filling is still substantial in Venezuela for wild *P. lunatus*, weedy *P. dumosus* and wild *P. vulgaris* (Berlingeri & Crespo 2012). Wild teparies should be sampled towards the southeast, in Mexico and Central America. The sampling of wild *P. coccineus* has been irregular, while the range of wild *P. dumosus* that is much smaller has been already well sampled (with work pending in eastern Chiapas). The secondary gene pools of the five bean cultigens would need additional collecting work, possibly with the exceptions of *P. dumosus* and *P. costaricensis* in Guatemala and Costa Rica, respectively (Ramírez-Villegas et al. 2010; Araya-Villalobos et al. 2001). One should note that the gene pool of Lima bean is the largest in the genus, with a good representation of the secondary genepool only from the Andes (Ramírez-Villegas et al. 2010).

Table 13 – Sampling status for the close wild relatives of the five domesticated species of *Phaseolus* beans.

Status of *ex situ* and *in situ* conservation for bean wild relatives in Mesoamerica

Species	No. of populations		No. of accessions in genebanks	Gap as %		Populations in protected areas (%)	
	herb	hypo					
<i>acut</i>	127	(190)	153	---	(19)	8	(4.2)
<i>cocci</i>	410	(540)	150	63	(72)	10	(1.8)
<i>dumo</i>	11	(19)	9	18	(53)	2 ?!	(10.5)
<i>luna</i>	389	(600)	131	66	(78)	20	(3.3)
<i>vulg</i>	140	(420)	365	---	(13)	12	(2.8)

sources: Debouck 2010a,b,c; CIAT genebank; www.ciat.cgiar.org/urg, acces. Sept. 2010; IUCN 1996

As extinction is forever, at the time of establishing priorities for collecting, the regions where the rate of change in land use is the fastest should be considered first. In North and Central America, land close to quickly expanding cities (see Table 10) is the prime target for sampling. So should be considered: the urban corridor of New-York – Washington DC in the eastern USA for *P.*

polystachyus, many areas of western Florida for the same taxon, *P. smilacifolius* and *P. sinuatus* (Debouck 2013e). Some flat areas of Arizona and New Mexico with fast expanding urbanization might be sampled for *P. maculatus* (Debouck 2013b). Coastal areas even beaches in the Bermudas, the Caribbean, the Gulf of California, and the Pacific slope of Mexico are worth visiting for *P. lignosus*, *P. lunatus*, *P. filiformis*, and *P. lunatus* and *P. macvaughii*, respectively, because of the expansion of tourism resorts and harbours. As an example, the population of *P. macvaughii* Le Jolis *s.n.* found in October 1866 on “presqu’île Griffon” just beside Acapulco (and unicate in the herbarium of Genève; Debouck 2013c) might be at risk if not already gone; *P. macvaughii* has been found tolerant to salinity (Bayuelo-Jiménez et al. 2002). The surrounding areas of expanding cities such as Mexico City, Queretaro, Tuxtla Gutiérrez, and Quezaltenango are of value for wild *P. coccineus*. Land quickly converted to input-intensive horticulture is a risk for *P. maculatus* close to Tula or Puebla, *P. rotundatus* around Guadalajara, *P. leptostachyus* in the Chimaltenango area, *P. oligospermus* in the province of Cartago, and *P. augusti* in the Cochabamba valley. Free grazing by goats continues to be a threat in many parts of Durango, Zacatecas, Oaxaca, Apurimac and Chuquisaca for populations of *P. grayanus*, *P. venosus*, *P. oaxacanus*, *P. augusti* and *P. vulgaris* (Freyre et al. 1996), respectively, although most of the damage might have been done in the period 1525-1600.

With regard to species of sections of clade A (Table 2), the priority now is to have a representative of each species; this will allow the research community through advanced sequencing (see Schmutz et al. 2014) to understand genome changes and similarities as compared to the species of clade B where are the five cultigens. In this regard (Table 14), one can see that there is representation of the two species currently not assigned to any section. The two species of *Bracteati* known to date are represented (with 2 populations out of the 4 known for *P. talamancensis*). Out of the *Brevilegumeni*, *P. campanulatus* is so far not represented; *P. hygrophilus* is represented by one accession (the type!) for the two populations known (Salcedo-Castaño et al. 2011). In the *Digitati*, *P. neglectus* is missing. In the *Minkelersia*, out of nine species, only *P. pluriflorus* is represented and only by one accession. For the *Pedicellati*, six species out of nine are represented, namely the endemic to the Edwards Plateau, *P. texensis* (Delgado-Salinas & Carr 2007; Khoury et al. 2013). As already mentioned, there is no representative of the *Revoluti*, viz. *P. leptophyllus* (thought to be extinct: Delgado-Salinas et al. 2006). For the *Xanthotricha*, there is germplasm for four out of the six species of this section. On the other hand, Table 15 sums up the list of species currently not represented in CIAT genebank, and of potential for future breeding of Lima bean and common bean, respectively. The absence of *P. sinuatus* and *P. smilacifolius* from the SE USA is noteworthy (Khoury et al. 2013), while there are a couple of populations of the Andean secondary gene pool of Lima bean represented in CIAT genebank (Ramírez-Villegas et al. 2010).

Table 14 – Number of accessions currently maintained at CIAT for the different species of Clade A.

Sections of Clade A	Species	total accessions
Not assigned	<i>glabellus</i>	8
Not assigned	<i>microcarpus</i>	29
<i>Bracteati</i> Freytag	<i>macrolepis</i>	2
<i>Bracteati</i> Freytag	<i>talamancensis</i>	2
<i>Brevilegumeni</i> Freytag	<i>hygrophilus</i>	1
<i>Brevilegumeni</i> Freytag	<i>oligospermus</i>	13
<i>Brevilegumeni</i> Freytag	<i>tuerckheimii</i>	13
<i>Chiapasana</i> Delgado	<i>chiapasanus</i>	4
<i>Digitati</i> Freytag	<i>albiflorus</i>	6
<i>Digitati</i> Freytag	<i>albiviolaecus</i>	2
<i>Digitati</i> Freytag	<i>altimontanus</i>	1
<i>Minkellersia</i> (Mart. & Gal.) Maréchal, Mascherpa, Stainier	<i>pluriflorus</i>	1
<i>Pedicellati</i> (Benth.) Freytag	<i>esperanzae</i>	7
<i>Pedicellati</i> (Benth.) Freytag	<i>grayanus</i>	2
<i>Pedicellati</i> (Benth.) Freytag	<i>oaxacanus</i>	1
<i>Pedicellati</i> (Benth.) Freytag	<i>pedicellatus</i>	6
<i>Pedicellati</i> (Benth.) Freytag	<i>polymorphus</i>	1
<i>Pedicellati</i> (Benth.) Freytag	<i>texensis</i>	1
<i>Xanthotricha</i> Delgado	<i>hintonii</i>	4

<i>Xanthotricha</i> Delgado	<i>magnilobatus</i>	4
<i>Xanthotricha</i> Delgado	<i>xanthotrichus</i>	41
<i>Xanthotricha</i> Delgado	<i>zimapanensis</i>	8

Note: additional information can be found at <http://www.ciat.cgiar.org/urg>.

Table 15 – Species of sections related to Lima bean and common bean in clade B currently not represented in CIAT genebank.

Sections	Species
<i>Coriacei</i> Freytag	<i>reticulatus, venosus</i>
<i>Paniculati</i> Freytag	<i>albinervus, jaliscanus, juquilensis, maculatifolius, mollis, sinuatus, smilacifolius, sonorensis, viridis, xolocotzii</i>
<i>Phaseoli</i> DC	<i>persistentus</i>

Note: additional information can be found at <http://www.ciat.cgiar.org/urg>.

7.2.2. Research in seed conservation and breeding systems

Research in seed physiology is a prerequisite to the launching of large scale collecting because knowledge about seed storage behaviour is necessary before long-term conservation. “. . . *Phaseolus* sp., where seed storage presents relatively few problems” (Roos 1988, p. 31): germplasm of many (if not most) bean species can be conserved and distributed in the form of botanical seeds. The seeds can be dried down to 5% moisture content and be stored in sealed containers at -20°C, a norm for genebanks (FAO 1994; Walters 2004a,b). Hong and co-workers (1996) reported the orthodox behavior for four cultivated species of beans: *P. acutifolius*, *P. coccineus*, *P. lunatus* and *P. vulgaris*; however no wild species were included in this landmark compendium. Although with orthodox behavior (Ellis et al. 1990), there seem to be significant differences between accessions of cultivated common bean in storage (James et al. 1967; Roos 1984; Roos & Davidson 1992); an experimental approach to *ex situ* conservation is thus warranted.

Box 12

There is a consequence from the studies about seed physiology of the different bean species. Although most species in the genus have not been actually tested individually – and this seems an easy “*must*” in genebank research, one can assume an ‘orthodox’ behaviour in relation to dessication and storage at low temperature. *Ex situ* conservation in genebanks seems thus possible for most bean species, but preliminary testing for each species is needed.

Another line of research that cannot be ignored deals with breeding systems, because in view of *ex situ* conservation they rule the success of seed set and the genetic integrity of a particular accession. As early as 1858, Charles Darwin noted the importance of hymenoptera insects (e.g. bees, bumblebees, carpenter bees, etc) to get a good harvest of beans, in this case the scarlet runner (Darwin 1858). *P. coccineus* has indeed been reported as a cross pollinated species (Ibrahim & Coyne 1975; Kendall & Smith 1976; Sousa-Peña et al. 1996), although it is self compatible (Kendall & Smith 1976; Webster et al. 1980). The other species of *Phaseoli* seem all to be self-compatible (Kalin-Arroyo 1981), but with higher yield if visited by heavy insects, especially in the case of *P. dumosus* (Free 1966; Ibarra-Pérez et al. 1999; Schmit & Baudoin 1987). The reason lays apparently in the floral morphology of section *Phaseoli*: there are active floral nectaries on the floral disk between the corolla and the staminal tube (Webster et al. 1982), attracting heavy insects. In landing on the wings, because of a mechanical union between the wings and the base of the keel, the style terminated by the stigma is forced through the group of anthers, and pollen is deposited on the stigma (Delgado-Salinas 1985). Often, because of this mechanical movement, the stigma comes outside the tip of the keel, and pollen from other flowers stucked to the forefront of the visiting bee is deposited on the stigma. The diversity in floral morphology across the different species might be the result of a co-evolution with a diversity of pollinators; fair enough to mention the size and spatial position of standard, wings and keel between *P. chiapasanus* and *P. macvaughii* (see back cover of monograph by Freytag & Debouck 2002). As a practical consequence, accessions of most bean species although inbreeders and self-fertile plants, will cross with one another; in order to keep seed purity, blossom bagging, plant caging or distance planting is necessary (up to one mile for Lima beans: Ashworth 2002).

Box 13

There is a consequence from the studies about reproductive biology of the different bean species. No genetic self-incompatibility has been reported. It seems that all species are autogamous with varying degrees of outcrossing. In some species tripping seems a condition to get any seed at all. This particular biology has practical consequences for *ex situ* and *in situ* conservation (for example, hand pollination to get seeds and habitat idoneous for pollinator survival, respectively).

7.2.3. Further evaluation and documentation

Two essential elements for a continuing interest into the conservation are evaluation and documentation: there will be no point in conserving large collections if a substantial fraction has not been demonstrated of high value to the farmers, agronomists, breeders or biologists. Similarly, the society will rightly question the existence of large collections if there is no access through internet to the knowledge accumulated about them.

Evaluation should be a continuing effort. At CIAT it is because the entire cassava collection of 6,000 clones has been evaluated against whitefly that the resistance was found in one accession ECU72 (Bellotti 2002). In common bean, evaluation of the cultivated accessions against bruchids was already going into 5,600 with no resistance found (van Schoonhoven et al. 1981; van Schoonhoven & Cardona 1982) when at the suggestion of the writer the wild accessions were considered, and out of 170 accessions thirty were found resistant (van Schoonhoven et al. 1983). Another accession of wild *P. vulgaris* was found recently effective against the common bean weevil (Zaugg et al. 2013). These two examples would not make a plea for core collections: statistically there is no chance to pick up the accessions with the right trait. But it does not mean either that evaluation should remain static: the trait responsible for the resistance to bruchids – a different seed storage protein called arcelin – can be easily identified by SDS-PAGE electrophoresis (Kornegay et al. 1993; Zaugg et al. 2013), requiring less than two days instead of months of biological trials! Prospects exist to screen bean germplasm through gene based markers.

In contrast to the large scale evaluation for cultivated common bean (Hidalgo & Beebe 1997; Singh 2001) and to a lesser extent for Lima bean (Baudoin 1988b), wild germplasm has not been much evaluated, obviously first because of lack of large collections, perhaps with the exception of wild *P. vulgaris* namely for bruchid resistance (van Schoonhoven et al. 1983). The special agronomical handling of wild germplasm – acknowledged by Porch and co-workers (2013) - starting with seed scarification for an improved uniform germination has not helped either. Yet the little germplasm that has been evaluated has revealed very interesting traits (Table 9 *partim*) often absent in the cultivated germplasm. This is a clear indication that potential exists and that further evaluation and prebreeding with the secondary gene pools are worth trying. In the case of abiotic stresses (drought, salinity, frost), to some extent, geographic information systems (GIS) may guide to the very populations exposed to a specific constraint. For example, the population of *P. angustissimus* Barneby 1893 of the Yavapai County in Arizona might face freezing sub-zero temperatures in the period December-January, while the population Turner 4594 of Brewster Co. in Texas seems not exposed to it. Just as in the case of arcelin and bruchid resistance (Acosta-Gallegos et al. 1998), not all populations of a species may display uniformly the trait of interest, but sometimes they do: for instance, the hypogeal germination expressed by all individuals of many wild species (or in *P. coccineus*) may be interesting in eastern Africa for the recovery of seedlings after an attack of bean fly (Schmit & Baudoin 1987). Evaluation

methods evolve with the including of digital imagery and analysis (Guarino et al. 2002), yet multilocation trials are still rewarding for several agronomic traits (Krull & Borlaug 1970).

A bean common registry, with CIAT, INIFAP, USDA-Pullman and a couple of other collections, might be highly desirable. It would be a single site on the internet from which the databases of such bean collections could be consulted simultaneously, and where germplasm requests could be made to any of them. Any participating genebank would remain the sole owner of that information (passport, characterization, evaluation, genetic data, etc). It would also be the sole entity capable to make any change in the data at any time. A community of practice with genebank curators, bean breeders, agronomists, bean pathologists, etc, would define the bean descriptors, codification, and order of presentation, on the basis of existing sites (USDA-GRIN; CIAT at <http://www.ciat.cgiar.org/urg>).

7.2.4. Further promotion

The second drive deals with increased public awareness. This Strategy would be almost purposeless if the public is not aware of the bean collections and of the data that have added value to them. The effort to raise public awareness about bean genetic resources should however go much further, specially when the young public thinks that the beans on their plate are coming from the supermarket. That may be true but there is a long story behind that seed harvested from an improved variety.

7.2.5. Further education

The third drive includes activities in training and capacity building. If the idea of link genebanks has any appeal (see below), because the numbers of them will be much higher as compared to that of reserve genebanks, the number of professionals to be trained will be higher for the former. The kind of training will be different too: professionals in reserve genebanks likely should know about cryoconservation, while professionals in link genebanks should have education in rural anthropology.

7.3. Implementation of the Strategy, and funding mechanisms

People

Because the purpose of this strategy is: “What are the activities and resources required to safely conserve bean genetic resources in perpetuity?”, we need to consider the human resources, since not a single generation will be able to conserve these resources in perpetuity. Good people seems to become the most limiting factor, and the good people are overworked because they are good. Institutions should take a particular care in timely hiring staff to continue the work of those coming to retirement. An informal *Phaseolus* genetic resources network seems of order here, perhaps around the Bean Improvement Cooperative (BIC). The later is a “voluntary and informal organization to effect the exchange of information and materials”, based in the USA, and actively linking for over fifty years all professionals interested in bean breeding, agronomy and enhancement.

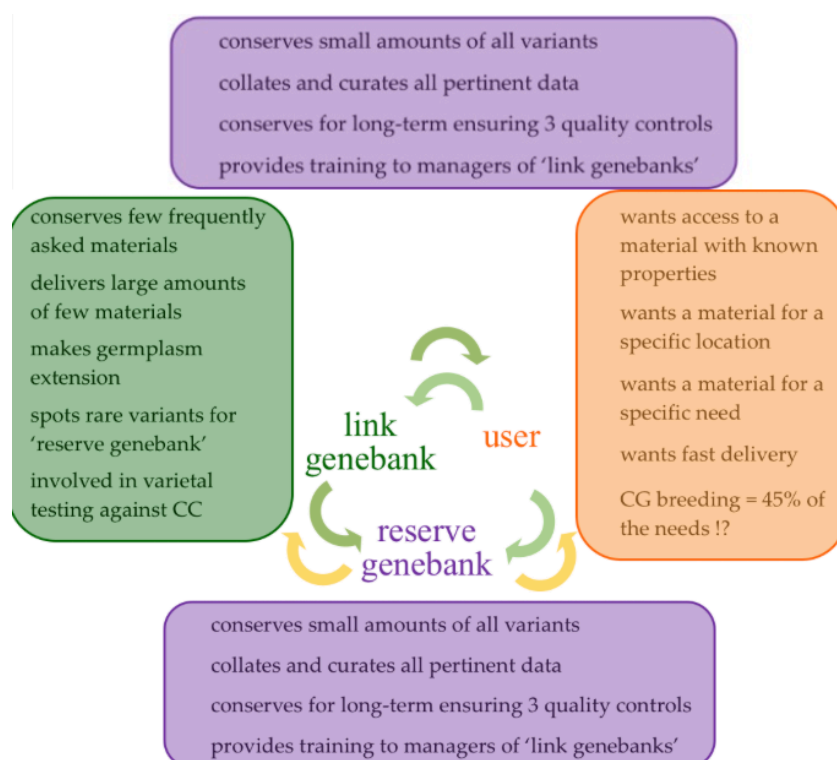
Institutions

As aforementioned, a total of more than 250 genebanks keeping genetic resources might not be economically sustainable and possibly difficult to implement due to lack of human resources in the mid/ long-term. In the following scheme (Figure 3) – proposed in view of the shortcomings noted by Don Marshall (1990, p. 386-388) and suggestions made by Paul Gepts (2006, p. 2288-2289), two kinds of genebanks serve the users community with complementary roles. The link genebanks which

can be at national or community level conserve the materials frequently asked by such users communities. They are ready to deliver large amounts of seed of fewer accessions; for example they can participate in the recovery of agricultures after hurricane or drought crisis as it happens from time to time in the Caribbean or Central America. The link genebanks work with rural extensionists to diversify the crop varieties planted by farmers, or to put back in farmers' hands extinct varieties, because of their contacts with the reserve genebanks. In that sense, the link genebanks are responsive to instant situations just as agricultures respond to climate change problems or new market opportunities. The link genebanks can also spot rare variants in view of their possible introduction and conservation into the reserve genebanks. Pending on the kind and volume of work with farmer communities, link genebanks adjust their operations. In terms of data, link genebanks mainly relay and translate in user friendly language the data obtained from the reserve genebanks; they will generate data in relation to the performance of germplasm in farmers' fields.

In this scheme (Fig. 3) the reserve genebanks are few and their prime responsibility is to conserve all bean variants of potential use (landraces, commercial varieties, wild species of primary and secondary gene pools). A very important role is the collation and verification of all relevant data (passport, characterization, evaluation, past and current uses, etc). In that sense, the reserve

Figure 3 – Interactions between users, link and reserve genebanks.



genebanks are gene libraries along three perspectives or levels: i) sequence variations causing gene variations or variable expressions (information at gene level), ii) genotypes with poor or good phenotypes (information at accession level), and iii) uses of such phenotypic variations by humans along history (information at crop level). This kind of work of curation of accessions/ data and expected service worldwide are long-term, with distribution of materials to users and link genebanks under strict quality controls (genetic, physiological and phytosanitary quality). Availability of accessions and data is permanent, even though volumes for distribution are small (to reduce risks associated with frequent regenerations). Another reason for smaller amounts as compared to the link genebanks is related to the costs of distribution (Koo et al. 2004; Schreinemachers et al. 2014). The reserve genebanks will make safety back-ups into the Global Svalbard Seed Vault (which is a vault not a genebank). The data collated and curated by the reserve genebanks can help to *in situ* conservation at farmers' level or in protected areas. Such data also address the question of coverage/ relevance of collections. In other words, it is the responsibility of the reserve genebanks to keep up with the advance in breeding, genomics, etc, and to document the extinction probabilities, so that germplasm is acquired/ collected in due time. The reserve genebanks carry out and/ or outsource research in bean seed physiology in order to extend periods between regenerations.

Financial resources and funding schemes

When they seem to be subject of commodization (Gepts 2004), it is perhaps appropriate to ask whom bean genetic resources belong to, assuming that the 'owner'(s) will take care of the full conservation costs. The owner would be willing to meet the full costs of the conservation because it is anticipated that these costs will be recovered by charging the user(s) at some time. Under this scenario, the charges are established by the owner(s) or by some market mechanisms (like a stock exchange of bean genes). Bean genetic resources and genes not being a finite resource like oil or coal, and because substitution is so often a way in biology, this scenario is not likely to work.

There might be two ways to look at this question. First, and after 1993 when the Convention on Biological Diversity (Anonymous 1992) became international law, bean genetic resources might be seen as the property of individual countries. This might be due to immediate interests, but it remains to be seen whether such a stand reflects interests in the mid- and long-term of the countries themselves on the one hand and of the bean crops on the other hand. We have seen above that domestication extends over centuries or millenia, sometimes outside the area where the initial events took place. For example, race 'Nueva Granada' of common bean (Singh et al. 1991) has its origin a long time ago in the central Andes (Chacón-Sánchez et al. 2005) today part of a country named Peru; however it has acquired unique characteristics during its migration to the northern Andes, ending in what is today Colombia and western Venezuela. Bolivia too seems to have benefited from this germplasm (Blair et al. 2012). Another example is provided by the small seeded Lima beans with an origin west of Isthmus of Tehuantepec in what is today western Mexico (Motta-Aldana et al. 2010; Serrano-Serrano et al. 2012). They had a significant development as a crop in the hands of the classic Mayan civilizations that inhabited the peninsula of Yucatan (Colunga-Garcíamarín & Zizumbo-Villareal 2004), today divided between three countries (Mexico, Belize, and Guatemala). So, today 'owner'(s) might be different from the previous one(s), and likely different from tomorrow one(s), because bean genetic resources develop in another time frame, surely longer than a century. The blocking of that evolution – "Darwin in the fridge" (Populer 1998) - and of the seed exchanges will turn the bean crops into 'living fossils',

and that is the risk with commodization where bean seeds are just another food item but no longer a genetic resource. One has to note that an endemic species such as *P. amblyosepalus* did not turn into a great bean crop but *P. lunatus* or *P. vulgaris* because they were crossing the Isthmus of Panama twice since the late Tertiary (Serrano-Serrano et al. 2010; Chacón-Sánchez et al. 2007, respectively). To make the point about the time dimension further, one can consider the case of another Phaseoleae: soybean, “one of the slowest crops to become established in North America” (Gilstrap 1961, p. 25). It was introduced into the USA at the end of the 19th century as a food item for oriental recipes, in the 1900-1930 it was harvested as a hay crop, and around World War II it was used as an oil and protein commodity for the food industry (Oldfield 1989; Sauer 1993). Only sixteen introductions – and five critically - contributed to the 136 cultivars released in the period 1939-1981, with an average annual genetic gain of 21 kg/ Ha (Specht & Williams 1984). And any soy breeder hungry for diversity continues to miss the loss of landraces collected in Asia in 1929-1931 (Sauer 1993), and surely the absence of soybean from Annex 1 of the International Treaty (FAO 2002) does not help!

Second, in view of the above, the owners may be willing to concentrate on wild species only, under the argument that these species in contrast to the cultivated materials harbour some unique genetic diversity. Evidence has been presented above that wild materials certainly have unique and valuable genes. The ‘problem’ for the owners is to sustain a long conservation and prebreeding effort without a firm insurance that these valuable genes will be used in a predictable future, because contexts of use regulated by market forces are largely unpredictable, as are the outcomes of scientific research public or private. An indicator of another priority mind set of the owners is reflected in the numbers of populations of wild *Phaseolus* species in protected areas (Table 13).

On the other hand, bean genetic resources might be seen as ‘international public goods’, even this recognition lies behind (Rands et al. 2010). It might be positive for Central American countries that Argentina produces large amounts of small seeded black and red beans of race ‘Mesoamerica’ so that these varieties can be available in Central America at affordable prices. It might be positive for Colombia that the countries of the Great Lakes in Africa consume beans of race ‘Nueva Granada’ so that genetic resources of *Coffea* growing there in native forest could be available to the Andean countries (in an amended Annex 1 of the International Treaty). Along this interpretation, we see that bean genetic resources benefit to users in the coming years and centuries in other places often far away from the original ones (Johnson et al. 2003). Bean genetic resources belong to future generations, and the conservation effort of today is basically to pass them a biological heritage as diverse as the one we inherit. Along this interpretation, it would be equally false to state that the initial developers/ domesticators have done all the work for free, while they have equally benefitted from their work and the one done by their predecessors. So, ‘international public goods’ might be the appropriate perspective because eventually bean genetic resources are to benefit to the highest number of people. If so, it is expected that it is the ‘international public’ that supports the conservation effort and that monitors its progresses. This monitoring role is important with respect to the “transgenerational power” (Wells 2010, p. 58), the capacity the current generation has to affect the food supply or scarcity for many generations in the future. Conversely, past generations could have restricted our food span, and they did not, so why should we?

Among the different possible scenarios for funding the conservation effort (several of them being discussed by Rubenstein et al. 2005), an endowment rooted in the United Nations system can perhaps be an appropriate funding mechanism, under international standards and periodical peer reviews. The point here is to ensure appropriate funding for the job to be done, and the quality in the execution. Now, it is expected that the countries who have genetic resources of *Phaseolus* beans invest into the

endowment fund for a few large consolidated efforts instead of the continuation of small duplicated works in isolation. Because it is time to stop “Privatizing gains and socializing losses” (Friedman 2009, p. 18), it is expected that such countries will contribute massively in order to warrant conservation activities in the long-term (i.e. centuries) and beyond instantaneous interests. In “Wild Solutions”, Beattie and Ehrlich (2004, p. 227) wrote: “This book shows why so many people have accepted that our most important capital is natural capital: biodiversity. To recapitulate one of our early themes, this is the capital of the real world. The currencies based on financial capital derive from the life-support systems and products generated by biodiversity”.

Conservation is paid through use: beside not being applicable to wild forms and species, this approach is applicable to only a small part of the total gene pool, practically the few commercial varieties in demand. Yes, but if that part is the one being preferred and evolving because it continues to be grown by farmers. The argument may be wrong. The matching of genotype-market-user preference might be completely outside the pest-pathogen context, the few being on the side of the former while the larger and the winner being on the side of the latter. It is far too dependent on local circumstances and on instantaneous, amnesic trends of markets. The popping beans give us a good example of the shortcomings of this approach: in the 1970-80s these landraces were in steep demographic decline in their Peruvian highland homelands; in the 2000-10s they are making a strong comeback with the booming of the *gourmet* food industry and tourism. From a strict economic viewpoint, the *ex situ* conservation of all popping bean accessions at CIAT has been amply justified. One should note that CIAT genebank did that collecting and conservation effort without being asked to do so and outside the priorities of the CIAT Bean Program at that time. This non-matching of priorities between the developers and the conservationists of germplasm is a recurrent limitation of the work of genebanks, and brings the following observation.

In spite of a continuous stewardship of crop germplasm collections almost since its foundation (Plucknett et al. 1987) – that should be commended, the CGIAR might still be seen – a glance at the budget distribution - as ‘development’ oriented. A net 40% invested in conservation today would give the right signal to human societies, towards sustainable development: development cannot be possible and sustained by eating the resources basis. In crop breeding one recent approach is called ‘allele mining’ and should be interpreted as combining brain and genetic resources to produce food and health from other renewable resources.

One thing is for sure the funding of genetic resources conservation is out of a charity context, because it is part of the asset of countries just as would be land or water resources. And if an endowment is an interesting scheme as already mentioned by Plucknett et al. (1987), then it is expected than countries of origin participate into the endowment. If we keep in mind the need for a collective insurance for food security, then countries with production and/ or consumption participate in the endowment.

7.4. Conditions to and indicators of success

The success of the Strategy is the progress of *Phaseolus* genetic resources, in terms of knowledge, conservation and sustainable use. Such progress will happen from deliberate and concerted actions of the actors, above all from the public sector, along some of the lines defined in this document. The private sector has a role, likely around some evaluation, the generation of new genetic diversity through breeding, and the distribution of some genetic resources through markets. This is important because through mechanisms such as the ones set in the International Treaty (FAO 2002), the private

sector can generate financial resources, even though these are modest (Rubenstein et al. 2005). The leading role will however be in hands of the public sector, because it is the one in charge of long-term interests of human societies.

Indicators of success of the Strategy apply from different perspectives. Increased knowledge about *Phaseolus* genetic resources is surely among the first, for example when a new species is described, or a new wild population is spotted and georeferenced, or an obscure landrace is authenticated. When an interesting trait is disclosed in an accession or the seed storage behavior of a bean species is defined, knowledge increases further. Everytime a landrace or a population of wild *Phaseolus* enters into a genebank, the conservation can be seen as strengthened. Because bean genetic resources have often to deal with scarcity of human talents, physical resources and time, managerial aspects and indicators will soon become important, either *in situ* or *ex situ* (Brown & Brubaker 2002). Relevance (do we conserve the *Phaseolus* genetic diversity that is/ will be used?), sustainability (are the proposed schemes robust enough to withstand periods over fifty years?), and irreversibility (are we carrying out today actions that will not be possible tomorrow?) will be some key aspects shaping technical indicators. As one can see, monitoring success is quickly turning global, not surprising for a global food resource. Monitoring is still complex in 2014, but becoming faster with the linking of genebank and herbarium databases, bibliographic databases.

8. Concluding remarks

“What are the activities and resources required to safely conserve bean genetic resources in perpetuity?”, was the initial question and the drive behind this strategy. From several considerations afore-mentioned, one may ask whether it is feasible and desirable to write a strategy “in perpetuity” or instead to ask the bean genetic resources community to revisit it periodically, say every five years, for example at the time of monitoring progresses and achievements. There are several reasons for not writing in stone in 2014 a strategy for bean genetic resources conservation, namely because in contrast to the major cereals the bean genetic resources are not fully known yet. Therefore, filling gaps in our knowledge basis (Box # 1 to 13), in representativity of *ex situ* collections and in the documentation of what is already conserved *ex situ* are obvious priorities.

Another reason is in the shifting of priorities in the evaluation of bean genetic resources: after the priorities set on pests and diseases (and before concluding), we see now a focus on nutritional aspects before another coming move into abiotic stresses related to climate change (Porch et al. 2013). That shift from the breeding programs is somehow expected because bean breeders must respond to the expectations by farmers and the society, with varieties better responding to current needs. Collectively however we would lose less time if evaluation could be complete and could anticipate such needs. In other words, evaluation should be seen as a continuing investment (as part of the “Societal insurance policy”: Gepts 2006).

A third set of reasons is this: breeders seem to have forgotten that there are five bean crops, so a much wider capital is available for food security, eco-efficient agriculture and healthy status of tropical soils. Jack R. Harlan (1992, p. 240-241) aptly noted that agricultural societies have long experienced crop failures, economical disasters and hunger, and that repeats are possible. The potato famine (Gray 1995) and the ruin of European wineries (Campbell 2005), both largely caused by genetic uniformity, are not so distant in our collective memory, unless technological progress turns us amnesic. There must be a comeback of the bean crops different from common bean, because our agricultural

environments are diverse. Another reason is the economic gain of ecological pre-adaptation; for example, does it cost less to increase seed size in tepary or to get a common bean truly drought resistant?

Bean genomics evolves fast in this decade, and could come with interesting answers to difficult questions, more than telling us that there are two gene pools in common bean. Clade A with genes currently intransferable to the bean cultigens might be a model to understand differences in gene regulation as compared to species in Clade B (e.g. why can *P. hygrophilus* thrive under 4,500 mm rainfall/ year and not *P. vulgaris* ?). Another important contribution could be in telling us the intimate differences between the species of Clade B, particularly the Phaseoli and the Paniculati, at the chromosome and gene levels. The same sequencing can then be applied to natural hybrids existing in the former section. Also expected is the information about genomes under stress, heat or drought for example, in order to understand closely why a tepary withstands better than common bean. Possibilities are great, in an additive, not exclusive mode.

Our knowledge about Mesoamerican bean genetic resources has advanced because of field work, of data accumulated from different disciplines, but also because of studies on other sets of the gene pools from other regions. The ‘gap analysis’ lead to the need of additional documentation of species and populations, of additional explorations of different regions, but also pinpoints to additional methodological developments. In this regard, and for *Phaseolus* beans, it is because of a track record of populations testified by herbarium specimens back to the early 1800s that GIS models can be established (Jones et al. 1997; Ramírez-Villegas et al. 2010). It is the long-term investment in different disciplines of biology (botany, ecology, genetics, ...) that allows taking advantage of recent advances in molecular genetics and informatics, and this success clearly invites us to continue to invest in these disciplines.

GIS tools combined with herbaria/ genebank accessions information have opened a new way of threat analysis and the planning of conservation. With satellite images, they allow a prediction about the location and speed of modification of land use. Who is generating and using that type of information is partly an unanswered question, because bean wild relatives (as for other crops as well) are falling between two groups of interest. On the one hand, agronomists consider them as wild plants just subject for botanical studies, and if found in the cultivated fields as weeds just worth an herbicide spray. On the other hand, botanists will find themselves lost in human made habitats as are the cultivated fields, deducing that not a single wild plant might still be growing there. That falling into the cracks might be reflected to the higher level up to the ministries, where MinAgrics will worry about expansion of cultivated fields under highest productivity, while MinEnvirons will carefully separate protected areas with double fencing. As early as 1952 Edgar Anderson alerted us that the plants most important for our food might be doubly ignored by botanists and ecologists. But through GIS tools and data at the population level as conservation units, there is a concrete and operational way to reconcile these two approaches in order to protect the biological heritage of countries that eventually is but one.

When people and agrobiodiversity will increasingly compete for the same land, it might be effective for the different plant genetic resources to join forces. North of Nicaragua, in the southern USA, Mexico and Central America, bean wild relatives often thrive in pine forest together with oaks, wild cucurbits, and many range species of the grass, legume, and sunflower families. The approach above-detailed when applied to many crop wild relatives including forest tree species may come up with a better definition of ‘hotspots’ (Myers et al. 2000), where something could be maintained *in situ* but

under a higher return for the land investment. True that the UNESCO Biosphere reserve ‘Sierra de Manantlán’ was triggered by the discovery of two wild relatives of maize, but the area once inventoried reveals an astonishing plant diversity (Vázquez-García et al. 1995) worth conserving for the Mexican society and next generations. The scenario can work if the authorities in charge of the land and *in situ* conservation can timely bring the specialists of the different plant genetic resources together. This pluridisciplinary approach involving plant taxonomy, ecology, GIS, population genetics, economics of conservation, land planning might not be completely utopian, as the levels of knowledge progress are not too unequal.

We have seen the importance of tropical American bean genetic resources in spite of insufficient collection and evaluation, for the tropical American region itself. The conversion of the potential of genetic resources into a success story through breeding lead to this contradiction (often verified in other crops: Jennings & Cock 1977): the extinction of landraces and the bean wild relatives in the homelands, and an increase planting in foreign lands with the repetition of the same success story. This situation may go up to the export of beans back to the original regions. This circle would invite the original regions to move into pre-breeding or at least to conserve more and to obtain returns for the transfer of documented traits. This is a bit the direction explored in the International Treaty on Plant Genetic Resources for Food and Agriculture. It might not be neither perfect nor satisfactory to all parties now because of divergent short-term interests, but on the long-term nobody gains in losing the Neotropical bean genetic resources!

In a lucid and farseeing essay Charley Heiser wrote: “To attempt to solve the world’s problems and to eliminate malnutrition the nations of the world need wise, able, foresighted, and honest leaders who have an understanding of ecological principles. Such leaders are now in short supply. And the problems aren’t the leaders’ alone. All of us must be involved.” (Heiser, 1990, p. 214).

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