GLOBAL STRATEGY FOR THE CONSERVATION AND USE OF PEA GENETIC RESOURCES

With support from

CROP TRUST

The International Treaty
ON PLANT GENETIC RESOURCES
FOR FOOD AND AGRICULTURE

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of Food
and Agriculture

COVER

Pisum sativum (garden pea) cv. "Carruthers Purple Podded". Photo: Petr Smykal

DISCLAIMER

This document, developed with the input of many experts, aims to provide a framework for the efficient conservation and effective use of globally important collections of pea genetic resources. The Global Crop Diversity Trust (the Crop Trust) provided support for this initiative and considers this document to be an important context for guiding the allocation of its resources. However, the Crop Trust does not take responsibility for the relevance, accuracy or completeness of the information in this document and does not commit to funding any of the priorities identified. This strategy document, dated 23 January 2023, is expected to continue to evolve and be updated as circumstances change and/or new information becomes available. Please direct any specific questions and/or comments to the strategy coordinator, Peter Giovannini (peter.giovannini@croptrust.org).

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The number of accessions presented in the text and tables of this strategy should be seen as the best estimates the authors could make at the time of writing based on the data available and the methods used, and not as a precise number. These figures can change depending on the sources of data and their completeness, and the assumptions made during the analyses.

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Pisum sativum flower. ICARDA Terbol station.
Photo: Michael Major for Crop Trust

1 SUMMARY

The plurality of genebanks that has built up around the world since the 1960s stands as a testament to the importance of long-term conservation of Plant Genetic Resources (PGR) for the global security of food and agriculture. The heterogeneous nature of their specific mandates, focus, size, funding and available resources is both a strength in terms of their individual institutional flexibility, and a weakness with respect to standardization of management and operational procedures. This lack of standardization presents particular challenges when it comes to collating and assessing their holdings and their ability to supply and support the varied user communities that are dependent on their materials and data. There was a high level of participation by *ex situ* collections in the *Pisum* Survey that was developed to feed information into this strategy, with the holdings of 14 of the responding institutions representing 73% of the estimated global *ex situ Pisum* collection. Significant efforts were made to cover as wide a range as possible of regions across the world where peas are grown, and were reasonably successful. One notable omission is that of the African continent, where none of the 14 institutions contacted responded.

XVII, 3. 106. Leguminosae.

453. Pisum sativum L. **Brech-Erbſe.**

Flora von Deutschland, Österreich und der Schweiz

Pisum sativum at Nordgen, Sweden.
Photo: Peter Giovannini for Crop Trust

2 THE STRATEGY DEVELOPMENT PROCESS

This strategy was launched in April 2020 as many countries around the word were in or preparing to enter lockdown measures due to the COVID-19 pandemic. A total of 86 institutions were contacted to participate in the *Pisum* Survey. A copy of the survey questionnaire is presented in Annex 1. A review of these institutions and past experience identified a number of regions in the world where engagement with previous international efforts of this type has been limited. Every effort was made to contact institutions in as many regions and countries as possible, irrespective of the size of collection, to try to engage and collate the widest set of data and knowledge base. This was especially important as the production areas for dry and vegetable (green) peas are significantly different. A total of 37 responses were obtained from institutions in 29 countries spread across a wide range of geographic regions. Details of the responding institutions are presented in Annex 2. Significant correspondence concerning institutional holdings and activities was also received from PHL060 and THA300 (see Annex 2 for a list of institution codes).

A series of online discussion groups was established to discuss taxonomy, descriptor lists and descriptor states, and genetic stocks. The outcomes of these discussion groups have fed into the development of this strategy.

The Global Crop Diversity Trust would like to acknowledge the contributions and efforts of the authors, all the individual respondents to the survey and various discussion groups that have been initiated in response to this strategy initiative.

Pisum sativum flower, ICARDA Terbol station.
Photo: Michael Major for Crop Trust

3 PEA (*PISUM SATIVUM* L.)

Pea is a globally important cool-season legume crop that is produced worldwide as both dried seeds or in fresh vegetable form (green peas), predominantly in temperate regions. The vast majority of peas cultivated around the world are classified as *Pisum sativum* L.

While this section is primarily focused on these forms, certain regions in Ethiopia uniquely cultivate landrace forms of *Pisum sativum* ssp. *abyssinicum* (or *Pisum abyssinicum* A. Braun, see Chapter 4.) The production of these landrace forms is limited to subsistence farmers mainly in the highland regions of Amahara and Tigray (Gebreegziabher and Tsegay 2016; Gebreegziabher and Tsegay 2018). This form is discussed in more detail in Section 3.2.

3.1 Pea Crop Types and Global Production

Peas as a commodity are utilized in a variety of different forms. They feature as both arable crops where the seeds are grown to maturity (dried seed) and in a range of vegetable crops where the immature seeds or edible podded types are harvested as fresh produce (Table 3.1).

In 2019 the primary global production of dried peas was 14.2 Mt. Compared with other temperate grain legumes, dried peas ranked second equal with lentils in terms of global production. Both were behind common beans, whose production amounted to 28.9

Table 3.1 Descriptions of arable and vegetable crop types of pea.

Arable Crop Type

- Field peas: The crop is grown to full maturity and harvested as dry seed, mostly for human consumption.
- Forage peas: The crop is cut as silage as a high-protein animal feed, and seeds are occasionally used for forage.

Vegetable Crop Types (green peas)

- Picking peas: Intact pods are sold fresh to consumers. Pods are picked when they are fully expanded just before they start to dry out. The developing seeds are in the phase of accumulating storage products but have not started to dry out.
- Snow peas or mangetout: Pods and seeds are eaten when they are very young, The pods are flat with thin walls.
- Snap peas or sugar snap peas: Edible pods are rounded with thick pod walls and seeds are further developed than in snow peas.
- Vining peas: Immature seeds are harvested midway through their development based on their sugar content.

Mt (FAOSTAT 2019). North America and Europe each accounted for 37% of the global dried pea production (5.2 Mt) and Asia accounted for 18% (2.6 Mt).

The global production of green peas in 2019 amounted to 21.7 Mt, second only to common beans at 27 Mt. They are the only temperate legume crop. Asia is the region with the largest production accounting for 89% (19.3 Mt) of the global total. Within Asia, production is higher in Eastern Asia (62%, 13.4 MT) than in Southern Asia (26%, 5.7 Mt). The second highest production region is Europe (1.2 Mt), followed by Africa (0.65 Mt), North America (0.27 Mt) and South America (0.21 Mt).

The top 10 producing countries for both dry and green peas are shown in Table 3.2. China, USA, India and France are the major producers of both forms of the crop.

A further analysis of global production and food supply based on annual average values drawn from FAOSTAT data between 2010 and 2014 was conducted by Khoury et al. (2021). That study focused on selected indicator metrics for a set of crops obtained from multiple data sources. A summary of the results of that analysis for pea and common bean (*Phaseolus*) is presented in Appendix 8. The data were compiled as part of a project funded by the ITPGRFA and the Crop Trust, led by the International Centre for Tropical Agriculture (CIAT). The analysis combined the data for dry pea and green pea production into a single figure. While useful, this figure masks the differences in production between the two crop types, and thus is harder to interpret. Revisiting the FAOSTAT data for dry and green pea global production from 2010 to 2019 shows that the production of both dry and green peas steadily increased over that period, with the production of dry peas increasing by 35.6% and that of green peas increasing by 36.5% (Figure 3.1).

Table 3.2 Top 10 producing countries for dry and green peas in 2019 (data from FAOSTAT 2019).

Country	Dry peas (Mt)	Country	Green peas (Mt)
Canada	4.2	China	13.4
Russia	2.4	India	5.6
China	1.5	France	0.3
USA	1	USA	0.23
India	0.8	Algeria	0.2
France	0.79	Egypt	0.17
Ukraine	0.57	Pakistan	0.17
Ethiopia	0.39	UK	0.15
Germany	0.23	Peru	0.13
Romania	0.22	Spain	0.13

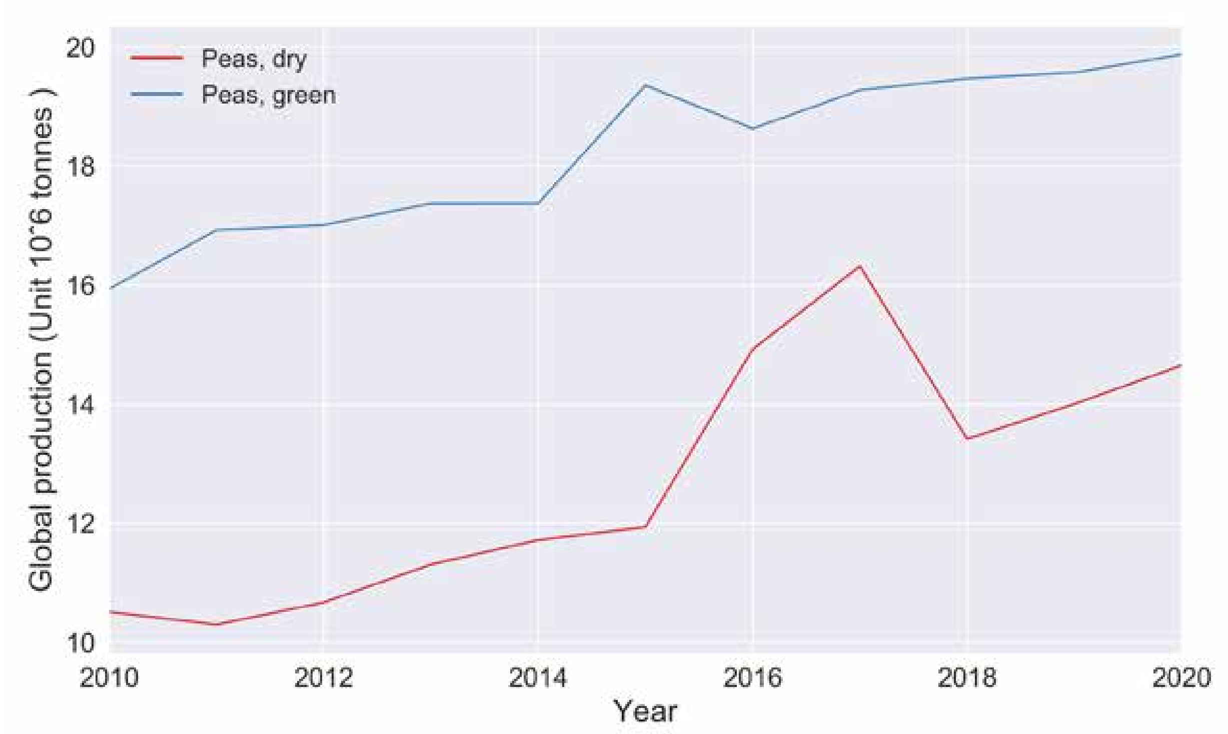

Figure 3.1. Global production of dry and green peas between 2010 and 2019 (FAOSTAT data).

These differences between the two crops and the fact that their major producing countries and regions are also different highlights the need for each crop to be analyzed and reported on separately. This will allow us to understand more fully the differences between the two markets and how they perform.

3.2 Additional Niches and Emerging Markets for Pea Products

Along with the main established markets for peas for human and animal consumption, several other uses for peas and derived components have emerged in recent years. These new uses offer opportunities for improvement through breeding and selection, and are generating new requirements for germplasm screening and use for novel allelic variation to improve the functional properties of seeds.

Pea seeds show wide variations in size, shape and seed coat patterning. These variations have been exploited by selection and breeding over the centuries to produce a number of distinct market types with strong regional identities. These include the small-seeded petite pois-type pea produced in France and the large-seeded marrowfat-type pea produced in England. Another example is the round-seeded marbled-seed-coat type referred to as maple pea, which is the type preferred by anglers and pigeon fanciers in the UK.

Because of their functional properties, peas and other grain legumes have an important and growing role in food formulation and processing. These properties include their solubility, water- and fat-binding capacity and foam production, making them suitable for use in baked products, extruded products, soups, and ready-to-eat snacks. Such applications have become possible because seed components can be separated after milling by wet and dry fractionation and air classification processes. These steps allow the extraction and purification of pea protein, as well as the denser starch and lipid fractions (Pelgrom et al. 2013; Pelgrom et al. 2015).

The dramatic increase in the development of functional foods and their appearance in supermarkets is another important development in the use of the pea crop. This has been driven in part by the move to source more sustainable sources of plant protein (Sandberg 2011; Lu et al. 2020). It has also been helped by the growing gluten-free market, which has provided a viable market for yellow and green pea flour. As a non-dairy alternative, pea milk using pea protein isolate is another product that has recently come to the market, again targeting the sustainable use of plant protein to provide a product for lactose-intolerant consumers. In Japan, extruded peas are a popular snack food (R. Redden, personal communication).

Peas can also affect diet and health because they attenuate postprandial glycemia and insulinemia, thereby helping to manage type 2 diabetes (Bahadoran and Mirmiran 2015). Recent studies including clinical trials found that wrinkled-seeded peas with higher contents of 'resistant starch' break down more slowly in the body, and help to prevent 'sugar spikes' where blood sugar levels rise sharply after a meal (Petropoulou et al. 2020). Thus, flour from wrinkled-seeded peas has potential uses in commonly consumed processed foods such as biscuits. If the consumption of such functional ingredients could prevent 'sugar spikes' over the long term, it could reduce the risk of diabetes (Delamare et al., 2020).

There has been increased cultivation of crop plants in domestic urban situations as a result of the global recession in 2007 and the promotion of gardening and home-grown vegetables for wellbeing. This has prompted vegetable breeders to screen germplasm for characteristics that were not previously considered as important, such as more attractive and distinctive foliage and a more compact plant habit. While small in themselves, these markets are driving the search for novel morphological variations for use as parental stocks by plant breeders, and also introduce more people to eating peas, thus potentially increasing pea consumption (Shinnmay 2017).

3.3 Cultivated Dekoko peas in Ethiopia

The pea cultivated in the Amhara and Tigray regions of Ethiopia is the Dekoko type (minute size). This morphologically distinct form of cultivated pea has long intrigued taxonomists and geneticists. It is favored for human consumption when cooked and is used in ceremonial meals (festival food), so it commands a premium price. The high price has helped to maintain its cultivation. Its early flowering is also valued as a drought avoidance mechanism, whereby the harvest is more assured, albeit at lower yields. Despite this, cultivation of Dekoko peas has drastically declined as a result of drought and political disruption to traditional farming during the mid-1970s and 1980s (Butler 2002).

Within the past 10 years, however, there has been a considerable renewal of interest in this neglected crop within the Ethiopian research community. This has resulted in a range of research activities, including new collections of Dekoko germplasm, characterization studies aimed at crop improvement and extending the areas of cultivation (Tsegay and Gebreegziabher 2019; Yirga and Tsegay 2013). These studies also report on the use of these peas for soil improvement and as a green manure or cover crop (Gebreegziabher & Tsegay, 2016).

Pisum sativum, Naturalis Biodiversity Center

4 *PISUM* TAXONOMY AND DIVERSITY

4.1 Taxonomy and diversity

The garden pea (*Pisum sativum* L.) belongs to the Fabaceae (Leguminosae) plant family, the third largest flowering plant family with around 760 genera and approximately 19,500 species. *Papilionoideae* is the largest subfamily, with around 476 genera and close to 14,000 species (Lewis et al. 2005). The largest group of papilionoids is the Hologalegina clade, with nearly 4,000 species in 75 genera. This group includes the large galegoid tribes (Galegeae, Fabeae and Trifolieae). Tribe Fabeae Rchb. currently consists of five genera: *Lathyrus* (grasspea/sweet pea) (about 160 species); *Lens* (lentils) (four species); *Pisum* (peas) (two to three species); *Vicia* (vetches) (about 160–250 species) and the monospecific genus *Vavilovia* (Smýkal et al. 2011; Schaefer et al. 2012; Mikič et al. 2013; Smýkal et al. 2017). The Fabeae tribe is considered one of the youngest groups of legumes (Kupicha 1981; Steele and Wojciechowski 2003; Wojciechowski et al. 2004; Lock and Maxted 2005). Bayesian molecular clock and ancestral range analyses suggest a crown age of 23–16 million years ago (Mya), in the mid-Miocene (Lavin et al. 2005; Schaefer et al. 2012). The Fabeae tribe is considered to be monophyletic, but is nested within the non-monophyletic tribe Trifolieae.

The phylogenetic relationships of *Pisum* within the tribe Fabeae have been explored by Schaefer et al. (2012). They reported that *P. sativum* s. l. (including *Pisum elatius* M. Bieb. and *Pisum humile* Mill.) is sister to *Pisum fulvum* Sibth. & Sm., and both are sisters to *V. formosa* (Stev.) Fed. The tribe is morphologically characterized by mostly paripinnate, often tendrilled leaves and a pubescent style (or pollen brush) (Smýkal et al. 2011). The genus *Pisum* is distinguished morphologically from the related genera *Lathyrus* and *Vavilovia* by the presence of large, leafy stipules, which are semi-amplexicaul.

The genus *Pisum* L., which was originally considered to be distinct from *Lathyrus* L. (Linnaeus 1753), has recently been included in the *Lathyrus*/*Vicia* complex (Schaefer et al. 2012) to achieve monophyly. Interestingly, Lamarck (1778), who was aware of Linnaeus's description, designated pea as *Lathyrus oleraceus* Lam., the name that might eventually be returned to after generic re-circumscription of the tribe (Smýkal et al. 2015). This assignment was used recently in a legume monograph by Coulot and Rabaut (2016).

Despite the fact that *Pisum* is a small genus and has been used as a genetic model system ever since the work of Mendel (1866), its taxonomy is still debated. The Kew database recognizes two distinct *Pisum* species, *P. fulvum* Sibth. & Smith and *P. sativum* L. Whereas *P. fulvum* is listed as a monophyletic species without any synonyms, *P. sativum* has 17 synonyms (Hellwig et al. 2022).

Common pea is a diverse species. This is true for its cultivated forms, due to conscious and unconscious selection in different directions corresponding to the variety of use; and its wild forms, due to their existence as local populations with limited genetic exchange because of geographical isolation and the predominance of self-pollination. Populations of wild pea (*P. sativum* subsp. *elatius* and *P. sativum* subsp. h*umile,* as recognized by Ladizinsky and Abbo (2015) are mostly small and restricted, and are scattered broadly across the Mediterranean basin from Portugal in the west to Iran in the east and from Hungary in the north to Tunisia, Morocco and Jordan in the south. The greatest diversity of wild peas is in the Near East (Turkey, Syria, Israel), the center of pea diversity (Smýkal et al. 2017a; Coyne et al. 2020). The distribution of *P. fulvum* Sibth. & Sm. is restricted to the Middle East (Ladizinsky and Abbo 2015; Smýkal et al. 2017a; Hellwig et al. 2021a). As a direct result of broad phenotypic diversity, many different Latin names at different ranks have been proposed for various forms of pea (Ellis 2011).

The classification of *Pisum* L., based on morphology and karyology, has changed over time. It was once considered to be a genus with five species (Govorov 1937; Makasheva 1979) and then as a monospecific genus (Lamprecht 1966; Marx 1977). Later, Davis (1970) and Kupicha (1981) recognized two species, *P. fulvum* Sibth. & Sm. and *P. sativum* L., and did not consider *P. abyssinicum* A.Br. as a species. The nomenclature of the group has remained complex, and numerous names have been proposed for wild relatives of pea. The taxonomic status of *P. abyssinicum* has been discussed often, and its status has varied from subspecies (*P. sativum* subsp. *abyssinicum* (A.Br.) Berger) to species (Maxted and Ambrose 2001; Vershinin et al. 2003; Jing et al. 2007; Smýkal et al. 2011; Smýkal et al. 2015; Trněný et al. 2018).

Another taxon that Maxted and Ambrose (2001) suggested should be included in *Pisum* is *Vavilovia formosa* (Stev.) Fed., first described as *Orobus formosus* Stev and sometimes referred to as *Pisum formosum* (Stev.) Alef. More than a century after its discovery, it was upgraded to a separate genus in the tribe Fabeae, as the monospecific genus *Vavilovia* Fed. (Fedorov 1952). Based on recent molecular analyses (Schaefer et al. 2012; Smýkal et al. 2017b), it is still considered to be a distinct genus (Smýkal et al. 2013; Mikič et al. 2013).

Pisum taxonomical classification

Wild representatives of *P. sativum* were traditionally (Ben-Ze'ev and Zohary 1973) subdivided into two large groups: subsp. *elatius*, tall mesophylic plants of the maquis (dense thickets of shrubs and low trees) and forested river banks of the Mediterranean; and 'subsp. *humile*' or '*syriacum*', small xerophytic plants growing in steppe-like communities in the Near East. The differences between the two subspecies were mostly quantitative and reflected adaptations to different habitats (Ladizinsky and Abbo 2015). In a study by Ben-Ze'ev and Zohary (1973), the two karyological classes coincided only partially with morphological characters, indicating that the two groups are polyphyletic. This led Townsend (1968) and Davis (1970) (see Table 4.1) to consider all wild forms of *P. sativum* as belonging to the same subspecies under the priority name *P. sativum sensu lato.* In the review by Yarnell (1962), *P. humile* and *P. sativum* were considered to be conspecific, even though they might have different chromosomal inversions and translocations. Recently, Ladizinsky and Abbo (2015) recognized two species: *P. fulvum* Sm. and *P. sativum* L., with the latter divided into three subspecies: the domesticated pea subsp. *sativum* and two wild forms, subsp. *elatius* (M. Bieb.) Asch. & Graebn. and subsp. *humile* (Holmboe) Greuter, Matthäs & Risse. The classification of *Pisum* L. based on morphology and karyology clearly delineates two

Table 4.1 Taxonomy of *Pisum* after Davis (1970).

Pisum sativum L.	
Pisum sativum subsp. *sativum*	
	var. *sativum*
	var. *arvense* (L.) Pair
Pisum sativum subsp. *elatius* (M. Bieb) Achers. & Graebn.	
	var. *elatius* (M. Bieb) Alef
	var. *pumilio* Meikle (syn *P. humile* Boiss. & Noë)
	var. *brevipedunculatum* Davis & Meikle
Pisum fulvum Sibth. & Sm.	

species, *P. fulvum* Sibth. & Sm. and *P. sativum* L. (Davis 1970; Kupicha 1981). *P. sativum* has been further divided into three taxa recognized either as subspecies or species: *P. elatius* Bieb. (Bieberstein 1808), *P. humile* Boiss. & Noë and *P. syriacum* Boiss. & Noe. (Makasheva 1979). The type specimens of the species described by Bieberstein are preserved at the Botanical Institute, St. Petersburg, while the type specimens of species described by Boissier are preserved at the Geneva Herbarium.

P. elatius M. Bieb. was first described at the rank of species in 1808, and first reduced in rank to a subspecies by Schmalhausen (1895), although many authors ascribe the down-ranking to Ascherson and Graebner (1910). *P. humile* was described by Boissier and Noë (1856) but that name is illegitimate because it is a later homonym of *P. humile* Miller (1768), a form of cultivated pea. Berger (1928) downgraded the rank of the taxon to that of subspecies and gave it a new name: *P. sativum* subsp. *syriacum* A. Berger, but its status was again raised to species by Lehmann (1954) as *Pisum syriacum* (A. Berger). C.O. Lehm., although this nomenclatural change remained unsupported.

Ben-Ze´ev and Zohary (1973) suggested that there are two wild populations of *Pisum*: *P. sativum* subsp. *elatius* Bieb. and *P. humile* Boiss & Noë (= *P. syriacum* (A. Berger) C.O. Lehm.). These two wild groups were described as being morphologically, ecologically and genetically distinct. According to Ben-Ze'ev and Zohary (1973), the two taxa differ in their internode length and the size of peduncles, pods and flowers. Makasheva (1979) characterized these differences numerically:

- plant height 80–250 vs. 20–130 cm,
- 6 *vs.* 4 sympodial bundles in the upper part of the plant,
- flowers 2–3.5 *vs.* 1.3–1.8 cm, and
- pods 5.8–8 *vs.* <5 cm long.

All these differences are, however, quantitative and might simply represent adaptations to two different habitats. Similarly, Ladizinsky and Abbo (2015) supported the division of wild pea into two groups: subsp. *elatius* and subsp. *humile*. They went further than Ben-Ze´ev and Zohary (1973) and recognized two varieties of subsp. *humile*, a "southern" and a "northern" form, based on geographic distribution. They delimited the southern form as subsp. *humile* var. *humile* (Boiss et Noë) Ladizinsky, and the northern form as subsp. *humile* var. *syriacum* (A. Berger) Ladizinsky.

Most cultivated peas are traditionally attributed to *P. sativum* subsp. *sativum*, and are recognized on the basis of characters resulting from domestication, namely, non-dehiscing pods and seeds without a rough testa. Some authors continue to recognize other subspecies, such as

- *P. sativum* subsp. *asiaticum,* a vague aggregate of forms from Egypt to Central Asia,
- *P. sativum* subsp. *transcaucasicum,* a vetch-like fodder crop from Transcaucasia, and
- *P. sativum* subsp. *jomardii* from Egypt, based on Govorov and Makasheva nomenclature (Govorov 1937; Makasheva 1979; Kosterin and Bogdanova 2008).

Thus, the actual diversity of wild forms of *P. sativum*, as well as the associated taxonomy, has a confusing history.

After considering the available data, we propose the following classification of *Pisum*.

For cultivated pea:

- *Pisum sativum* L. described by Linnaeus (Sp. Pl. 2: 727. 1753) is based on cultivated pea and should be used solely for cultivated materials (Sp. Pl. 2: 727. 1753);

Table 4.2 Taxonomy of *Pisum* after Maxted and Ambrose (2001).

Pisum sativum L.	
Pisum sativum subsp. *sativum*	
	var. *sativum*
	var. *arvense* (L.) Pair
Pisum sativum subsp. *elatius* (M. Bieb) Achers. & Graebn.	
	var. *elatius* (M. Bieb) Alef
	var. *pumilio* Meikle
Pisum fulvum Sibth. & Sm.	
Pisum abyssinicum A. Braun	
Vavilovia formosa (previously *Pisum formosum*)	

- *Pisum abyssinicum* A. Braun (Flora 24 (1, no. 17): 269–270. 1841) should be used for Ethiopian cultivated pea.

For wild pea:

- *Pisum elatius* Bieb. (Fl. Taur.-Caucas. 2: 151. 1808) in the broader sense;
- *Pisum fulvum* Sm. (Fl. Graec. Prodr. 2(1): 62. 1813 ; Fl. Graec. (Sibthorp). 7(2): 79, t. 688. 1832).

This essentially corresponds to the classification used by Maxted and Ambrose (2001) (Table 4.2), and Ellis (2011), except that *P. elatius* as the progenitor of the crop is ranked at the species status instead of the subspecies status. In this strategy document, we will use the classification proposed above. Furthermore, we recommend that the classification system used is clearly stated when entering passport data in a database. The classification system can be recorded in the REMARKS field of the multi-crop passport descriptors (MCPD).

Pea domestication

Pea belongs to the most ancient set of cultivated plants from the Near East domestication center. It is still an important crop that is used widely as a grain, a vegetable and animal fodder (Smýkal et al. 2013 Smýkal et al. 2015). Domesticated about 10,000 years ago (De Candolle, 1884; Vavilov 1951; Kislev and Bar-Yosef 1988; Smartt 1990; Ambrose 1995; Zohary and Hopf 2000; Abbo et al. 2010), pea, among other grain legumes, accompanied cereals and formed an important part of the diet of early civilizations in the Middle East and Mediterranean. These regions are also the area of origin and initial domestication of pea. Cultivation of pea spread from the Fertile Crescent to present-day Russia, and westwards through the Danube valley (Smýkal et al. 2013; Smýkal et al. 2015) into Europe and to ancient Greece and Rome, which further facilitated its spread to northern and western Europe. In parallel, pea cultivation moved eastward to Iran (then Persia), India and China (Makesheva 1973; Chimwamurombe and Khulbe 2011). The domestication of pea has been experimentally tested, both to determine the genetic basis of the pathway from the wild plant to the cultivated crop (Weeden 2007) , as well as to better understand wild pea harvesting (Abbo et al. 2008). In pea, explosive pod dehiscence and seed dormancy (hard seededness) were probably the greatest barriers to domestication (Smartt 1990; Abbo et al. 2014). Based on morphological and genetic studies, *P. sativum* subsp. *humile, P. sativum* subsp. *elatius* and *P. fulvum* were identified as wild germplasm in that they display traits such as dehiscent pods and seed dormancy (thick testa). These traits are necessary for survival in the wild (Hradilová et al. 2019) but are undesirable in a domesticated annual crop. In contrast, *P. sativum* subsp. *sativum,* including the varieties *arvense, transcaucasicum* and *asiaticum*, generally display indehiscent pods and little seed dormancy, and therefore are considered to be the result of domestication. *P. abyssinicum* also bears indehiscent pods, produces moderately large seeds and lacks seed dormancy (Weeden 2007; Ellis 2011; Weeden 2018).

Genetic diversity held in germplasm collections

The genetic diversity of the *Pisum* genus has been traditionally assessed morphologically (Lehman 1954) and on the basis of seed proteins (Waines 1975), flavonoids (Harborne 1971; Pate 1975), allozymes (Hoey et al. 1996) and chloroplast DNA polymorphisms (Palmer et al. 1985). All these studies separated *P. fulvum* as a distinct species and *P. sativum* as an aggregate of *P. humile, P. elatius* and *P. sativum*. Members of the *Pisum* genus contain the flavonoid phytoalexin pisatin, as do members of the genus *Lathyrus*, but not members of the genus *Vicia* (Bisby et al. 1994), which contain wyerone instead. Serological studies of *Pisum* taxa by Kloz (1963) indicated close relationships among all the studied taxa, except for *P. fulvum* and *P. abyssinicum*. He was possibly the first to indicate that *P. abyssinicum* might have originated from hybridization between *P. elatius* and *P. fulvum*. This was also suggested by retrotransposon-based diversity analyses (Ellis et al. 1998; Vershinin et al. 2003; Jing et al. 2010) and clearly shown in a study using a genome-wide approach. Independently of the taxonomic status assigned, wild peas comprise a broad continuum of forms (Jing et al. 2012) and there are varying degrees of reproductive isolation among representatives of wild and cultivated peas (Ben-Ze'ev and Zohary 1973; Bogdanova and Berdnikov 2001; Bogdanova and Kosterin 2006; Yadrikhinskiy and Bogdanova 2011; Bogdanova et al. 2014).

More recently, molecular analyses of pea diversity preserved in germplasm collections have been conducted using various methods, including amplified fragment length polymorphism (AFLP) (Ellis et al. 1998; Tar'an et al. 2005), retrotransposon-based insertion polymorphism (RBIP) (Smýkal et al. 2008; Jing et al. 2010; Jing et al. 2012), sequence-specific amplification polymorphism (SSAP) (Pearce et al. 2000; Vershinin et al. 2003), microsatellite (Ford et al. 2002; Baranger et al. 2004; Smýkal et al. 2008; Zong et al. 2009; Kwon et al. 2012), and gene sequence analyses (Jing et al. 2007; Zaytseva et al. 2012; Burstin et al. 2015; Tayeh et al. 2015a; Tayeh et al. 2015b). The largest sample set analyzed so far was dominated by cultivated types and only about 140 were wild (Jing et al. 2010).

Biogeographical studies on the genus *Pisum* were conducted by Kosterin and Bogdanova (2008) and Kosterin et al. (2010) using a combination of mitochondrial, chloroplast and nuclear *SCA* (seed albumin) genes. Although these analyses were carefully conducted and interpreted, results based on three genes cannot fully reflect the diversity pattern, as individual genes might have different evolutionary trajectories (Jing et al. 2007).

Worldwide, there are approximately 100,000 pea accessions stored in various genebanks, of which around 58,000 might be unique (Smýkal et al. 2013 and Chapter 5 of this document). There are 25 large collections preserving pea diversity, together holding around 76,000 accessions. A further estimated 26,000 accessions are distributed over about 140 collections worldwide (see Chapter 5 and Smýkal et al. 2013). There has been no international genetic resource center for pea since 2000. Previously, the International Center for Agricultural Research in Dry Areas (ICARDA) in Aleppo, Syria played that role. The inventory made in 2013 (Smýkal et al. 2013) identified 98,947 accessions distributed over 28 genebanks. These accessions included landraces (38%), commercial cultivars (34%), mutant or genetic stocks (5%) and breeding lines (13%). Of the 98,947 accessions, only 1,876 (2%) were wild pea relatives (Smýkal et al. 2013; Smýkal et al. 2015). Of these, there were 706 accessions of *P. fulvum*, 624 accessions of *P. s.* subsp. *elatius*, 1562 accessions of *P.s.* subsp. *sativum* (syn. *P. humile/syriacum*) and 540 accessions of *P. abyssinicum*, although various levels of specimen duplication and misidentification exist (Smýkal et al. 2013). The main germplasm collections are held by:

- National Research Institute for Agriculture, Food and Environment (INRAE), France (8,839 accessions in addition to over 9,000 lines of TILLING mutants;
- Australian Grains Genebank (AGG; formerly Australian Temperate Field Crops Collection, 7,432 accessions);
- Vavilov Institute, Russia (8,203 accessions, of which 69 are wild *P. elatius*);
- US Department of Agriculture (USDA) (6,827 accessions);
- ICARDA (6,105 accessions);
- Leibniz Institute of Plant Genetics and Crop Plant Research, Germany (5,343 accessions);
- Instituto di Genetica Vegetale Italy (4,558 accessions);
- Institute of Crop Sciences, China (3,837 accessions);
- National Bureau of Plant Genetic Resources (NBPGR), India (3,609 accessions); and
- John Innes Centre, UK (3,006 accessions, of which 418 are wild pea accessions) (Coyne et al. 2020).

Several main germplasm collections have been subjected to molecular analyses to reveal their genetic diversity and structure. Retrotransposon-based insertional polymorphism analysis of 3020 accessions (92% of the complete collection) in the John Innes *Pisum* germplasm collection showed that most of the genetic diversity in the *Pisum* genus exists in wild species and landraces (as opposed to cultivars) (Jing et al. 2010). There is also evidence of substantial introgressions in the *Pisum* species and subspecies group, which have extensively distributed alleles through this genus (Jing et al. 2010). The USDA assembled the Pea Single Plant Plus Collection, consisting of 431 *P. sativum* accessions showing morphological, geographic and taxonomic diversity. This collection was subjected to genome-wide genotyping to reveal its genetic structure. A group of accessions from Central Asia appeared to be nearly as diverse as *P. fulvum* and *P. elatius* (Holdsworth et al. 2017). Analysis of the Australian germplasm revealed a distinct group of accessions of Chinese origin (Zong et al. 2008; Zong et al. 2009; Wu et al. 2017), and this was confirmed in composite analyses of 4,429 accessions from the John Innes Center, Czech, USDA, and Australian collections (Smýkal et al. 2011). Pavan et al. (2022) pointed out that because of inter-fertility between wild and cultivated peas, the 'boundary' between these two groups is not clear cut. These results showed that despite the wide diversity captured in the historically cultivated germplasm, relatively few genotypes with a high degree of relatedness have been used as parents in modern pea breeding programs, leading to the narrow genetic base of the cultivated germplasm (Ellis 2011; Jing et al. 2010; Jing et al. 2012; Smýkal et al. 2011).

Wild pea diversity analysis

Most of the published diversity studies have used materials stored in germplasm collections. However, such materials could not properly capture the genetic diversity at the collection site and provided only limited opportunities to relate genetic diversity to the environment. Moreover, studies using germplasm samples were typically biased towards cultivated pea. Some exceptions are the studies of Smýkal et al. (2017a) and Trněný et al. (2018), in which a large number of wild samples covering a wide distribution range were analyzed. A few recent studies have sampled wild pea materials from their habitat (Smýkal et al. 2018; Hellwig et al. 2021a; Hellwig et al. 2021b; Hellwig et al. 2022) to explore the relationship between genetic diversity, geography and environment. The genetic structure was assessed on 187 individuals of *P. elatius* from 14 populations collected in north-western part of the Fertile Crescent. Low heterozygosity was detected, and the estimated selfing rate in wild pea natural populations supported a mixed mating system and predominant self-pollination within the species. The recorded genetic diversity was correlated with geographic but not environmental (climatic) background factors extracted from available databases. Moreover, niche modelling under future climate projections revealed that the suitable area for this species will decline, highlighting the need for further collections and *ex situ* conservation (Smýkal et al. 2018; Coyne et al. 2020). Besides other anthropogenic factors, climate change should be considered as one of the reasons for the decline of this species. From a long-term perspective, a reduction in genetic variation could be expected to lower the adaptability of a population and increase the risk of its extinction. The heterogeneity found within populations, including those of self-pollinated species, highlights the importance of proper sampling strategies for germplasm collections to capture and preserve genetic diversity. Currently, the wild pea accessions held *ex situ* originate from a limited number of individuals, and are maintained as a disproportional bulk that is prone to genetic erosion.

A similar analysis of 81 samples of *P. elatius* across the environmental gradient of Israel showed association of diversity with latitude and temperature (Hellwing et al. 2021), and suggested there was a genetic bottleneck during the last glacial period, followed by population recovery and range expansion eastward to Turkey. Sampling of 15 populations of *P. fulvum* from natural habitats in Israel combined with genotyping-by-sequencing analyses revealed a strong genetic bottleneck during the last glacial period and only limited patterns of isolation by distance and environment, which explained 13%–18% of the genetic variation (Hellwig et al. 2021a). Restriction site-associated DNA sequencing (RAD-seq) of 494 samples revealed five distinct groups with a notable geographic pattern (Hellwig et al. 2022).

Status of Ethiopian pea (*P. abyssinicum*)

P. abyssinicum was first described (Braun 1841) at a species rank. The type specimen, BR0000006255831, was collected in 1840 by W.H. Schimper and is stored at the herbarium of the National Botanic Garden of Belgium (BR). Ethiopian pea (*P. abyssinicum*), also known as Dekoko ('minute-seeded' in Amharic) is considered endemic to Ethiopia and southern Yemen (Butler 2003; Gebreslassie and Abraha 2016).

Early studies on sequence variations in the ITS region (Saar and Polans 2000; Polans and Saar 2002) and the histone H1 subtype 5 gene (Zaytseva et al. 2012b) supported a possible hybrid origin of *P. abyssinicum*. A possible hybrid origin of *P. abyssinicum* was also suggested in several other studies (Vershinin et al. 2003; Jing et al. 2007; Jing et al. 2010; Ellis 2011; Smýkal et al. 2011; Zaytseva et al. 2012), which positioned *P. abyssinicum* between wild *P. elatius* and *P. fulvum*. Those studies detected a strong reduction in diversity as a result of a bottleneck, and proposed that this was likely related to a recent single-origin hybridization.

The issue was revisited by Weeden (2018), who analyzed 54 gene sequences in a set of 76 cultivated pea (*P. sativum* subsp. *sativum*), two wild pea (*P. elatius*), 11 *P. fulvum*, and one *P.s.* subsp. *abyssinicum* samples. The results revealed a close relationship among the three *P. sativum* subspecies, and did not support the hypothesis that *P.s.* subsp. *abyssinicum* was formed by hybridization between one of the *P. sativum* subspecies and *P. fulvum*. The results of that study supported its status as a distinct subspecies, *P. sativum* subsp. *abyssinicum*. It qualifies for species status on the basis of its phenotype (early flowering and strongly serrate leaflets) and biological isolation (see Warkentin et al. 2015). The presence of indehiscent pods, moderately large seeds and a lack of seed dormancy indicate that it is a domesticated taxon.

The intriguing question is whether it was domesticated independently. An independent domestication of Ethiopian (*P. abyssinicum*) pea has been proposed by several authors (Vershinin et al. 2003; Jing et al. 2010; Polans and Moreno 2009; Ellis 2011) and is supported by the results of chromosomal translocation analyses (Ben-Ze'ev and Zohary 1973; Conicella and Errico 1990). The progeny of crosses between *P. abyssinicum* and cultivated *P. sativum* did not show any segregation in domestication traits, suggesting that identical loci/genes are involved (Holden 2009). This question can be solved when all of the genes involved in pea domestication have been identified (Weeden 2007). A careful hybridization study was conducted by Holden (2009) and significant segregation distortion was found to be biased in favor of maternal alleles in both populations. This may represent partial reproductive isolation between *P. abyssinicum* and *P. sativum*. Evidence of separate domestication was inferred from the fixation of early domestication traits at separate loci in the two species. In summary, the observed transgressive segregation of domestication traits (seed weight and seed number) in wide crosses suggests that these taxa do not share a domestication history (Holden 2009).

The independent domestication of this species was also suggested by the genome-wide analysis conducted by Trněný et al. (2018). Their results indicated that *P. abyssinicum* originates from another *P. elatius* pool rather than *P. sativum*. An independent genetic origin of *P. abyssinicum* was also supported by the results of a RAD-seq analysis (Hellwig et al. 2022).

P. abyssinicum has been used as a bridge between *P. fulvum* and *P. sativum* because it crosses reasonably well with both (Warkentin et al. 2015). Several studies detected narrow genetic diversity within *P. abys-*

sinicum (Ellis et al. 1998; Vershinin et al. 2003; Jing et al. 2010; Smýkal et al. 2011).

Another often-discussed group of peas are the so-called Afghan types or *P. sativum* subsp. *asiaticum* (Govorov) as defined by Govorov (1937) and Makasheva (1979). These authors further subdivided this group into 34 varieties and convarieties, based largely on geographical origin and seed characters. These pea types have rarely been included in published analyses, except those of Ta'ran et al. (2005) and Jing et al. (2010), where they formed a separate cluster. This group distinction is further supported by the requirement of specific *Rhizobium* strains (Young and Matthews 1982) due to *sym2* mutant recessive allele of nodulation factor (Lie *et al.* 1984).

Regardless of what taxonomic system is the most accurate or best fit for purpose, when estimating the number of accessions conserved *ex situ* for each taxon there is a need to harmonize the taxonomic labels used across institutions and also within institutions over time. Therefore, a *Pisum* taxon dictionary was compiled to standardize taxonomic labels in the data from Genesys and the World Information Early Warning System for Plant Genetic Resources for Food and Agriculture (WIEWS) (See Annex 3) in a consistent way, and using only accepted taxon labels. The dictionary was compiled by automatically matching taxa recorded in passport data against GRIN Taxonomy (GRIN Global 2022), or against GBIF Backbone taxonomy (GBIF 2022) if no match was found in GRIN taxonomy. Finally, the results were checked manually and reviewed by experts. The automatic matching was completed using the API of the Global Names Resolver using a Python custom script. GRIN Taxonomy (Table 4.3) was used as the primary backbone for this standardization as it is widely used as a reference for cultivated plants and their wild relatives.

Table 4.3 *Pisum* taxa recognized according to GRIN-taxonomy. Source (USDA GRIN-Global, date of access: 1/04/2022).

Name	Synonym of
Pisum abyssinicum A. Braun	
Pisum abyssinicum A. Braun var. *vacilaianum* ined.	*Pisum abyssinicum* A. Braun
Pisum arvense L.	*Pisum sativum* L. subsp. *sativum* var. *arvense* (L.) Poir.
Pisum arvense L. subsp. *arvense*	*Pisum sativum* L. subsp. *sativum* var. *arvense* (L.) Poir.
Pisum arvense L. subsp. *humile* Holmboe	*Pisum sativum* L. subsp. *elatius* (M. Bieb.) Asch. & Graebn. var. *pumilio* Meikle
Pisum arvense L. var. *arvense*	*Pisum sativum* L. subsp. *sativum* var. *arvense* (L.) Poir.
Pisum arvense L. var. *hibernicum* A. F. Schwarz	*Pisum sativum* L. subsp. *sativum*
Pisum arvense L. var. *vernale*	*Pisum sativum* L. subsp. *sativum*
Pisum commune Clavaud	*Pisum sativum* L. subsp. *sativum*
Pisum elatius M. Bieb.	*Pisum sativum* L. subsp. *elatius* (M. Bieb.) Asch. & Graebn. var. *elatius* (M. Bieb.) Alef.
Pisum formosum (Steven) Alef.	*Vavilovia formosa* (Steven) Fed.
Pisum fulvum Sm.	
Pisum fulvum Sm. var. *amphicarpum* Warb. & Eig	*Pisum fulvum* Sm.
Pisum fulvum Sm. var. *fulvum*	*Pisum fulvum* Sm.
Pisum humile Boiss. & Noë	*Pisum sativum* L. subsp. *elatius* (M. Bieb.) Asch. & Graebn. var. *pumilio* Meikle
Pisum jomardii Schrank	*Pisum sativum* L. subsp. *jomardii* (Schrank) Kosterin
Pisum macrocarpum (Ser.) Sturtev.	*Pisum sativum* L. subsp. *sativum* var. *macrocarpum* Ser.
Pisum maritimum L.	*Lathyrus japonicus* Willd. subsp. *maritimus* (L.) P. W. Ball
Pisum maritimum L. var. *glabrum* Ser.	*Lathyrus japonicus* Willd. subsp. *maritimus* (L.) P. W. Ball
Pisum maritimum L. var. *maritimum*	*Lathyrus japonicus* Willd. subsp. *maritimus* (L.) P. W. Ball
Pisum ochrus L.	*Lathyrus ochrus* (L.) DC.
Pisum pumilio (Meikle) Greuter	*Pisum sativum* L. subsp. *elatius* (M. Bieb.) Asch. & Graebn. var. *pumilio* Meikle
Pisum saccharatum (Ser.) hort. ex Rchb.	*Pisum sativum* L. subsp. *sativum* var. *macrocarpum* Ser.
Pisum sativum L.	
Pisum sativum L. subsp. *abyssinicum* (A. Braun) Govorov	*Pisum abyssinicum* A. Braun
Pisum sativum L. subsp. *asiaticum* Govorov	
Pisum sativum L. subsp. commune (Clavaud) Govorov	*Pisum sativum* L. subsp. *sativum*

4.2 Threats

In a European assessment for the International Union for Conservation of Nature (IUCN) Red List conducted in 2010, *Pisum* was classified as of ‘Least Concern’ (Osborne 2011) based on a review of herbaria and *ex situ* records in the European Search Catalogue for Plant Genetic Resources (EURISCO). The assessment included a reference to *P. sativum* var. *arvense* in the wild as being endangered in Slovakia (Eliáš et al. 2007) and *P. elatius* as endangered in Switzerland in 2002 (Moser et al. 2002). However, neither of those species is listed in the updated Red List synthesis status report of threatened species of 2010 (Cordillot and Klaus 2011).

Table 4.3 (continued) *Pisum* taxa recognized according to GRIN-taxonomy. Source (USDA GRIN-Global, date of access: 1/04/2022).

Name	Synonym of
Pisum sativum L. subsp. *elatius* (M. Bieb.) Asch. & Graebn.	
Pisum sativum L. subsp. *elatius* (M. Bieb.) Asch. & Graebn. var. *brevipedunculatum* P. H. Davis & Meikle	
Pisum sativum L. subsp. *elatius* (M. Bieb.) Asch. & Graebn. var. *elatius* (M. Bieb.) Alef.	
Pisum sativum L. subsp. *elatius* (M. Bieb.) Asch. & Graebn. var. *pumilio* Meikle	
Pisum sativum L. subsp. *hortense* (Neilr.) Asch. & Graebn.	*Pisum sativum* L. subsp. *sativum* var. *sativum*
Pisum sativum L. subsp. *humile* (Holmboe) Greuter et al.	*Pisum sativum* L. subsp. *elatius* (M. Bieb.) Asch. & Graebn. var. *pumilio* Meikle
Pisum sativum L. subsp. *jomardii* (Schrank) Kosterin	
Pisum sativum L. subsp. *pumilio* (Meikle) Ponert	*Pisum sativum* L. subsp. *elatius* (M. Bieb.) Asch. & Graebn. var. *pumilio* Meikle
Pisum sativum L. subsp. *sativum*	
Pisum sativum L. subsp. *sativum* var. *arvense* (L.) Poir.	
Pisum sativum L. subsp. *sativum* var. *macrocarpum* Ser.	
Pisum sativum L. subsp. *sativum* var. *sativum*	
Pisum sativum L. subsp. *syriacum* A. Berger	*Pisum sativum* L. subsp. *elatius* (M. Bieb.) Asch. & Graebn. var. *pumilio* Meikle
Pisum sativum L. subsp. *tibetanicum* ined.	*Pisum sativum* L.
Pisum sativum L. subsp. *transcaucasicum* Govorov	
Pisum sativum L. var.-gr. *axiphium* Alef.	*Pisum sativum* L. subsp. *sativum* var. *macrocarpum* Ser.
Pisum sativum L. var.-gr. *medullare* Alef.	*Pisum sativum* L. subsp. *sativum* var. *sativum*
Pisum sativum L. var.-gr. *speciosum* Alef.	*Pisum sativum* L. subsp. *sativum* var. *sativum*
Pisum sativum L. var. *hibernicum* Alef.	*Pisum sativum* L. subsp. *sativum* var. *sativum*
Pisum sativum L. var. *hortense* Neilr.	*Pisum sativum* L. subsp. *sativum* var. *sativum*
Pisum sativum L. var. *saccharatum* Ser.	*Pisum sativum* L. subsp. *sativum* var. *macrocarpum* Ser.
Pisum sativum L. var. *speciosum* (Alef.) Makasheva	*Pisum sativum* L. subsp. *sativum* var. *sativum*
Pisum spp.	
Pisum syriacum (A. Berger) C. O. Lehm.	*Pisum sativum* L. subsp. *elatius* (M. Bieb.) Asch. & Graebn. var. *pumilio* Meikle
Pisum transcaucasicum (Govorov) Stankov	*Pisum sativum* L. subsp. *transcaucasicum* Govorov

A Dutch variety of *Pisum sativum* ssp. *arvense* called Kapucijner. Photo: Phacelias/Wikimedia

5

OVERVIEW OF *PISUM SATIVUM* COLLECTIONS

Globally there are over 130 institutions holding **Pisum** ***germplasm. These vary in size and focus and provide a wide diversity of opportunities for user engagement.***

A total of 133 institutes holding *Pisum* germplasm were identified from information extracted from WIEWS, Genesys and community knowledge. The details of all these organizations are shown in Annex 5. These institutions constituted a number of categories from CGIAR and regional genebanks to national governmental, parastatal and non-governmental organizations, including community seed banks and seed saver organizations. Some institutions have more than one type of storage facility (long-, medium- and short-term). In total, these institutions manage a total of 95 long-term, 48 medium-term and 32 short-term facilities. A subset of 106 institutions with either long- or medium-term storage facilities identified as either genebanks or community seed banks were invited to complete the *Pisum* Survey developed to obtain information for this strategy (Annex 1). The wide range of geographic regions underlines the pan-global utility of *Pisum* as a crop in one form or another (Table 5.1).

Collections are maintained for a variety of reasons: 89.2% of survey respondents listed their primary objective as long-term conservation, 64.9% cited working collection, 40.5% cited breeding collection, and 27% cited reference collection. Many listed more than one objective (Table 5.2), with seven institutes combining long-term conservation, working, breeding and reference collection objectives. Long-term conservation and breeding were cited as primary objectives for nine collections.

Two collections listed their primary objectives as working and breeding collections (ESP009 & ESP109). The primary objectives listed by the survey respondents are shown in Annex 7.

5.1 Source and Uniqueness of Collections

The *Pisum* holdings in different collections each have their own history and composition depending on their mission and operational mandate. The survey asked about the origin of materials in collections, and the responses revealed a range of different compositions. Some collections are entirely based on materials originating from their own country (LVA009 and TUR001). In other cases, 100% of the collection consists of materials introduced from abroad, for example, BRA001, which acts as a base collection (Figure 5.1). Fourteen of the 32 collections reported that >50% of their accessions were originally collected from within their own country.

Table 5.1 Institutions with either long- or medium-term genebanks with *Pisum* holdings, listed by region. Institutes with both long- and medium-term facilities were counted as long-term. Figures shown in the table were derived from data in Annex 7. Numbers in red indicate institutions that responded to the *Pisum* Survey.

	Region	Institutional Status	Long Term	Medium Term
Africa				
(14 Genebanks)	Northern Africa	Governmental	4	1
	Eastern Africa	Governmental	5	
		Parastatal	2	
		Regional	1	
		CGIAR	1	
	Southern Africa	Governmental		1
Americas				
(18 Genebanks)	North America	Governmental	6 (2)	
		Non- Governmental	1 (1)	
	Central America	Governmental	2	
		Parastatal	1	
	South America	Governmental	6 (2)	1 (1)
		Private		1
Caribbean (1 Genebank)		Governmental	1	
Asia				
(22 Genebanks)	Eastern Asia	Governmental	3 (2)	
		Regional	1 (1)	
	South-Eastern Asia	Governmental	2	1
	Southern Asia	Governmental	4 (1)	
	Western Asia	Governmental	5 (1)	5
		GCGIAR	1 (1)	
Australia & New Zealand (2 Genebanks)		Governmental	1 (1)	1
Europe				
(49 Genebanks)	Northern Europe	Governmental	9 (5)	
		Regional	1 (1)	
		Non-Governmental	1 (1)	
	Eastern Europe	Governmental	11 (7)	
		Parastatal	1	
	Southern Europe	Governmental	14 (5)	2 (1)
	Western Europe	Governmental	8 (3)	
		Non-Governmental	2 (1)	
		Private	1	

Table 5.2 Primary objective combinations as listed by the survey respondents.

<table>
<tr><th>Long Term Cons.</th><th>Working Collection</th><th>Breeding Collection</th><th>Reference Collection</th><th>Heritage</th></tr>
<tr><td>33</td><td></td><td>1</td><td>1</td><td>1</td></tr>
<tr><td></td><td colspan="2">2</td><td></td><td></td></tr>
<tr><td colspan="2">9</td><td></td><td></td><td></td></tr>
<tr><td colspan="3">3</td><td></td><td></td></tr>
<tr><td colspan="4">7</td><td></td></tr>
</table>

When asked to what extent they considered the *Pisum* accessions in their collection to be unique and not duplicated extensively elsewhere (excluding safety duplication), two collections (LVA009 and RUS255) considered their holdings to be totally unique. The remaining 31 respondents considered their collection to be mostly (39.4%) or partially unique (51.5%). The qualifying comments backing up the assessments (Table 5.3) generally focused on their broad diversity while others focused on their coverage of national diversity, frequently coupled with evaluation data.

5.2 Size and Composition of Collections

The number of pea accessions across the 133 institutions in the global review (Annex 5) totaled 73,030 when considering only data from Genesys and WIEWS, and 102,917 when including additional data from the survey (i.e., when values for the same genebank differed between the survey and Genesys/WIEWS, the value reported in the survey was used to derive this estimate).

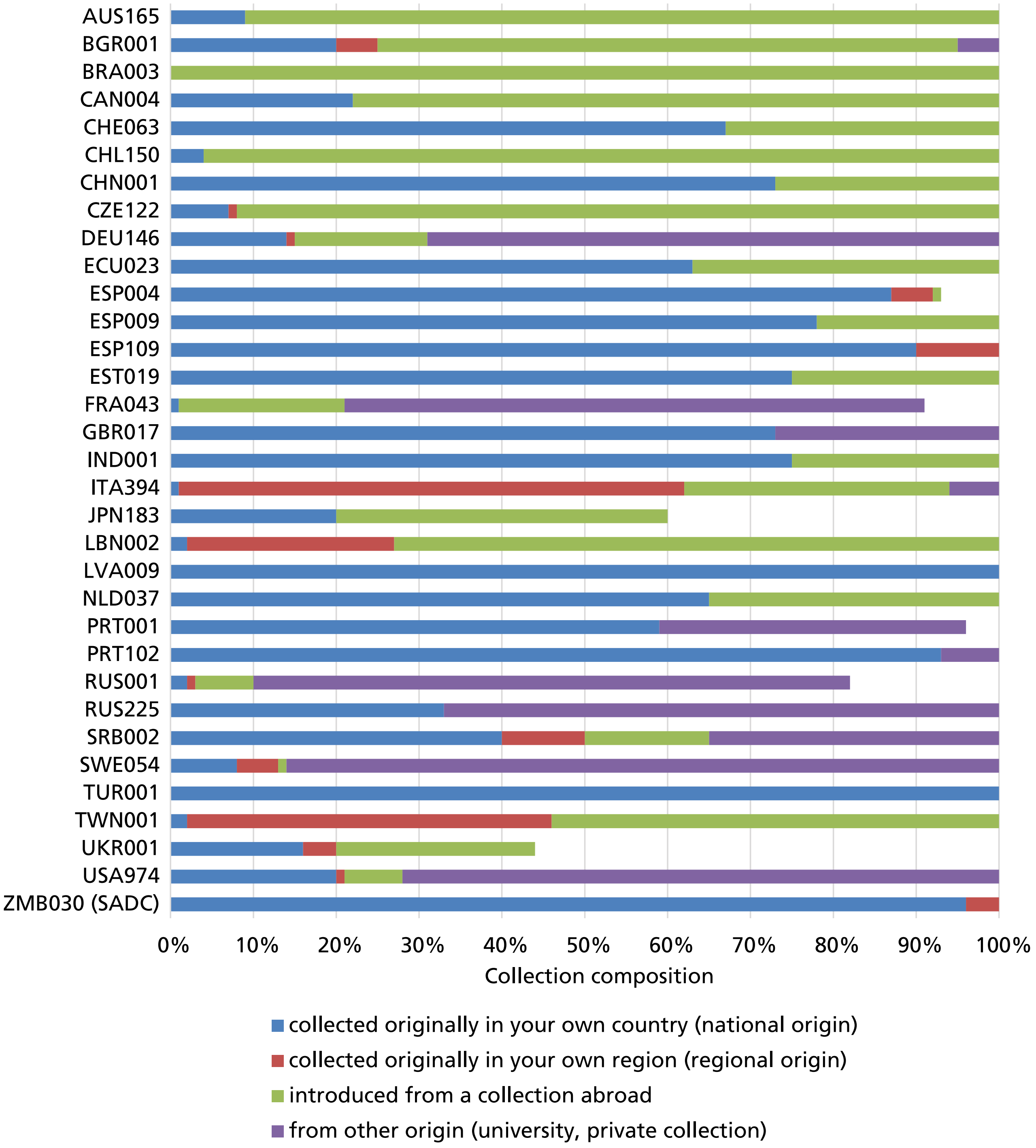

Figure 5.1. Percentage composition of collections based on origin of materials. Three genebanks have total values of less than 100% as some of the questions were not answered (missing values).

The size of the collections varied greatly, with 25 institutions reporting holdings of more than 1000 accessions, seven institutions reporting holdings of 501–999 accessions, 23 with 101–500 accessions, 11 with 50–100 accessions, and 72 with fewer than 50 accessions. On a numerical basis, seven collections (FRA043, RUS001, AUS165, CHN001, USA022, LBN002 and DEU146) held 51.2% of the combined total.

The collections that responded to the global survey held 83% of the total number of accessions globally (where the total was estimated from survey data combined with Genesys and WIEWS data).

The largest 13 collections among those responding to the survey held 70.8% of the total accessions in the combined dataset (WIEWS, Genesys). The collections

Table 5.3. Qualifying comments about the uniqueness of collections.

Collection	Response
AUS165	Diversity of species, origin and improvement status of germplasm.
BGR001	Winter resistant, high protein content, pest and disease resistance.
CAN004	Canadian material.
CHE063	Old varieties with a Swiss background conserved with a network of volunteers.
CHL150	International and National Material, Basis for Improvement Program.
CHN001	Diversity.
CZE122	Old national landraces, Czech cultivars.
DEU146	Very diverse collection from around 80 countries of origin.
ECU023	Ecuadorian accessions and the rest materials from other 15 countries.
ESP004	Includes mainly accessions collected in Spain, from a wide diversity of environmental conditions, for food and feed.
ESP009	Collection from the northwest of the Iberian Peninsula, where currently this crop is underutilized.
ESP109	Spanish landraces.
EST019	Accessions adapted to local conditions.
FRA043	Includes wild, cultivated and mutant accessions and is regenerated under glasshouse conditions with no risk of cross-pollination.
GBR017	Heritage cultivars that are not widely or commercially available (not listed on the National list or EU common catalogue).
GBR165	High degree of characterization and high level of uniformity in accessions.
GBR247	The collection is broad based and comprises a wide range of wild and semi-cultivated material in addition to landraces and cultivars from many regions around the world.
IND001	A mix of collections from 24 states of India and introduced varieties from 34 countries.
ITA394	A core subset of 230 landrace accessions from nearly all historical growing countries and about 500 improved genotypes have been GBS genotyped and phenotyped for performance in various environments.
JPN183	Japanese landraces.
LBN002	Remarkable genetic diversity and the presence of wild relatives.
LVA009	All accessions are of Latvian origin.
NLD037	25% are landraces collected in E. Africa, Pakistan and India.
POL003	Type lines for genes, old cultivars, genotype and taxonomy characterized.
PRT001	The majority of the collection consists of traditional varieties from Portugal.
PRT102	Most of the accessions are landraces (old cultivars).
RUS001	It is the eldest in Europe, has many unique accessions including old landraces no longer existing in nature, material from centres of origin, different mutations.
RUS255	These are confirmed wild peas originated from natural populations in different parts of their range.
SRB002	Winter hardiness, grain and forage yields, earliness.
SWE054	The collection contains several unique Nordic landraces as well as old cultivars. In addition, it includes the special collection "*Pisum* genetic stock" donated by the former Swedish breeding institute Weibullsholm. This worldwide collection consists of breeding material (including numerous mutants), cultivars, landraces and species as well as type lines for different genes.
TUR001	All of the collection collected from Turkey.
TWN001	Big diversity.
UKR001	The most value of our collection is landraces and Ukrainian old breeding varieties presence.
USA022	We ship to most countries in the world, average distribution 4371 seed packets of peas annually.
USA974	The collection is all open-pollinated and many heirloom varieties

Table 5.4 Summary of the collections globally based on data from databases (Genesys and WIEWS) and complemented with data from the survey. W: Wild; L: Landraces; IV: Improved varieties ; GS: Genetic stocks; BR: Breeding and research lines; U: Unknown; O_S: Other (from survey); Total_DB: Total from databases; Total_S: Total survey; Total_DB_S: total integrating information from survey and databases; CO: country represented in collection (based on Genesys and WIEWS data); CU: cumulative number of accessions; PER: percentage of the total number of accessions.

Institute	W	L	IV	GS	BR	U	O_S	Total DB	Total S	Total DB_S	CO	CU	PER
FRA043	158	237	1897	151	1200	1660	7800	611	13103	13103	1	13103	12.73
RUS001	56	2645	3176	0	740	1642			8302	8259	#N/A	21362	8.02
USA022	262	3000	2426	712	505	0		6319	6905	6905	95	28267	6.71
CHN001	103	5945	136	500	246	0			6884	6884	#N/A	35151	6.69
AUS165	71	2451	942	63	1082	1782		7575	6391	6391	100	41542	6.21
LBN002	242	1008	713	34	183	3944		4596	6124	6124	90	47666	5.95
DEU146	60	1545	3077	24	348	343		5359	5397	5397	81	53063	5.24
IND001	2	167	103	5	667	67	1879	4415	4424	4415	13	57478	4.29
GBR247	481	605	1085	1039	411	0		3562	3621	3621	39	61099	3.52
GBR165	0	6	3064	300	176	0		3298	3546	3546	1	64645	3.45
POL003	120	170	1180	680	640	161		3156	2951	2951	56	67596	2.87
UKR001	1	351	1675	0	776	0		2305	2803	2803	73	70399	2.72
SWE054	0	143	188	1970	106	28		2414	2435	2435	47	72834	2.37
GBR016	0	0	35	0	2006	75		2116		2116	1	74950	2.06
ITA394	0	675	75	0	1260	0		1225	2010	2010	52	76960	1.95
ETH085	0	1798	0	0	0	88		1886		1857	4	78817	1.80
ESP109	24	375	0	0	0	0	1405	977	1804	1804	32	80621	1.75
ITA436	0	0	0	0	0	1716		1716		1716	68	82337	1.67
CAN004	1	377	706	1	383	10		616	1478	1478	5	83815	1.44
PAK001	0	152	15	0	1306	0		1502		1473	58	85288	1.43
CZE122	84	12	1264	0	70	4		2437	1434	1434	47	86722	1.39
BGR001	2	200	400	100	500	171	10	1749	1383	1383	31	88105	1.34
HUN003	0	91	37	0	4	1089		1221		1221	25	89326	1.19
USA974	0	0	1125	0	0	0		1125		1125	3	90451	1.09
BRA003	2	0	0	0	0	0		1080	1076	1076	5	91527	1.05
NLD037	13	350	510	0	86	51		1014	1010	1010	49	92537	0.98
BRA012	0	0	0	0	0	958		958		958	3	93495	0.93
CHL150	0	0	0	0	914	0		1054	916	916	18	94411	0.89
USA962	0	2	2	0	707	1		712		712	10	95123	0.69
ESP004	12	572	73	0	10	41		708	708	708	12	95831	0.69
SVK001	0	9	336	0	201	0		548		548	22	96379	0.53
BLR011	0	14	712	0	59	0		786		518	52	96897	0.50
PRT001	0	389	0	0	70	0		478	477	477	43	97374	0.46
COL017	0	0	0	0	0	460		460		460	1	97834	0.45
SRB002	6	30	49	0	267	48			400	400	#N/A	98234	0.39
JPN183	5	115	20	0	0	211		347	351	351	1	98585	0.34
LSO015	0	0	0	0	0	307		307		307	1	98892	0.30
MNG030	0	8	253	0	45	0		306		306	23	99198	0.30
ECU023	0	0	0	0	0	253		253	253	253	1	99451	0.25
TWN001	0	188	0	0	0	0		195	188	188	14	99639	0.18
MDA010	0	24	145	0	0	0		169		169	20	99808	0.16
ZMB030	0	167	0	0	0	2		169		169	3	99977	0.16
BGD003	0	39	8	0	118	0		165		165	1	100142	0.16
COL029	0	0	0	0	0	160		160		160	1	100302	0.16

Institute	W	L	IV	GS	BR	U	O_S	Total DB	Total S	Total DB_S	CO	CU	PER
ARG1350	0	85	68	0	0	0		153		153	2	100455	0.15
UKR009	0	14	68	0	31	34		147		147	28	100602	0.14
GBR017	0	30	0	0	0	0	108	140	138	138	17	100740	0.13
MAR088	4	30	0	0	0	97		131		131	12	100871	0.13
ROM081								130		130	5		0.13
ROM007	0	114	9	0	4	0		127		127	6	101128	0.12
ETH013	0	123	3	0	0	0		126		126	24	101254	0.12
GBR004	100	0	0	0	0	3		103		103	12	101357	0.10
TJK027	0	58	0	0	33	0		91		91	2	101448	0.09
AUT001	0	3	77	0	5	1		86		86	9	101534	0.08
BLR016	0	0	56	0	20	0		76		76	11	101610	0.07
BOL317	0	76	0	0	0	0		76		76	12	101686	0.07
AUT046	0	0	0	0	0	74		74		74	16	101760	0.07
CUB014	0	0	6	0	66	0		72		72	3	101832	0.07
LVA009	0	9	14	0	28	10		61	61	61	2	101893	0.06
ARM059	0	0	0	0	0	47		57		57	6	101950	0.06
CHE063	2	55	0	0	0	0			57	57	#N/A	102007	0.06
EGY087	0	52	0	0	0	0		52		52	1	102059	0.05
AZE015	10	1	29	5	3	2		50		50	4	102109	0.05
CHE001	0	0	0	0	0	45		45		45	2	102154	0.04
PRT102	1	35	7	0	0	0		85	43	43	4	102197	0.04
ERI003	1	41	0	0	0	0		42		42	1	102239	0.04
ESP009	0	29	2	0	0	11		42		42	3	102281	0.04
UGA132	0	33	0	0	0	0		33		33	1	102314	0.03
ALB026	0	0	0	0	9	22		31		31	3	102345	0.03
GRC005	0	1	5	0	23	0		29		29	1	102374	0.03
ISR002	18	0	0	0	0	11		29		29	1	102403	0.03
LTU001	0	0	2	1	23	0		26		26	1	102429	0.03
TZA016	0	27	0	0	0	6		33		25	2	102454	0.02
ROM008	0	0	3	0	21	0		24		24	1	102478	0.02
TUR034	6	18	0	0	0	0		24		24	1	102502	0.02
LBY006	0	8	9	0	5	1		23		23	5	102525	0.02
CYP004	6	6	0	0	0	10		22		22	1	102547	0.02
RUS255	21	0	0	0	0	0			21	21	#N/A	102568	0.02
ESP172	0	18	0	0	0	1		19		19	1	102587	0.02
UZB006	0	0	1	0	0	18		19		19	7	102606	0.02
LKA036	0	1	5	0	0	11		17		17	6	102623	0.02
ARM005	0	0	0	0	0	16		16		16	2	102639	0.02
ESP027	0	15	0	0	0	1		16		16	2	102655	0.02
EST019	0	4	67	0	152	0		223		15	5	102670	0.01
ITA363	0	11	0	0	4	0		15		15	1	102685	0.01
ZMB048	0	15	0	0	0	0		15		15	1	102700	0.01
AZE005	0	0	8	0	6	0		14		14	8	102714	0.01
ZAF062	0	14	0	0	0	0		14		14	1	102728	0.01
LBN020	13	0	0	0	0	0		13		13	1	102741	0.01
MEX208	0	13	0	0	0	0		13		13	1		0.01
TUR001	0	196	0	0	0	0		196	12	12	1	102766	0.01
HRV044	0	11	0	0	0	0		11		11	1	102777	0.01

Institute	W	L	IV	GS	BR	U	O_S	Total DB	Total S	Total DB_S	CO	CU	PER
SDN002	0	11	0	0	0	0		11		11	1	102788	0.01
HRV053	0	0	9	0	0	0		9		9	5	102797	0.01
KGZ040	0	0	7	0	0	0		7		7	2	102804	0.01
BIH309	0	2	0	0	4	0		6		6	#N/A	102810	0.01
TUN029	0	4	0	0	0	2		6		6	1	102816	0.01
HRV021	0	2	1	0	2	0		5		5	1	102821	0.00
KEN212	0	1	0	0	0	4		5		5	2	102826	0.00
MWI041	0	4	1	0	0	0		5		5	1	102831	0.00
AUT005	0	1	0	0	0	3		4		4	2	102835	0.00
BEL002	0	0	0	0	0	4		4		4	1	102839	0.00
BLR026	0	0	0	0	4	0		4		4	1	102843	0.00
DEU627	0	0	4	0	0	0		4		4	2	102847	0.00
JOR015	1	3	0	0	0	0		4		4	1	102851	0.00
JOR105	0	2	0	0	0	0		4		4	1	102855	0.00
ROM055	0	4	0	0	0	0		4		4	3	102859	0.00
AUT047	0	2	1	0	0	0		3		3	3	102862	0.00
DEU005	0	0	3	0	0	0		3		3	2	102865	0.00
DEU628	0	0	3	0	0	0		3		3	1	102868	0.00
GEO013	0	3	0	0	0	0		3		3	1	102871	0.00
MKD001	0	2	1	0	0	0		3		3	2	102874	0.00
NPL069	0	3	0	0	0	0		3		3	1	102877	0.00
SVN019	0	3	0	0	0	0		3		3	2		0.00
THA300	0	1	0	0	2	0		3		3	1	102883	0.00
USA995	0	0	3	0	0	0		3		3	2	102886	0.00
ARM010	0	0	0	0	0	2		2		2	1	102888	0.00
AUT025	1	0	1	0	0	0		2		2	2	102890	0.00
CUB284	0	0	2	0	0	0		2		2	2	102892	0.00
ESP026	0	2	0	0	0	0		2		2	1	102894	0.00
GBR006	0	0	2	0	0	0		2		2	2	102896	0.00
ROM019	0	0	1	0	1	0		2		2	1	102898	0.00
ROM021	0	0	2	0	0	0		2		2	1	102900	0.00
ROM023	0	2	0	0	0	0		2		2	1	102902	0.00
USA971	0	2	0	0	0	0		2		2	1	102904	0.00
AZE003	0	0	0	0	1	0		1		1	1	102905	0.00
AZE014	0	0	1	0	0	0		1		1	1	102906	0.00
BGD028	0	1	0	0	0	0		1		1	1	102907	0.00
BLR019	0	0	0	0	1	0		1		1	1	102908	0.00
ECU167	1	0	0	0	0	0		1		1	1	102909	0.00
GEO001	0	1	0	0	0	0		1		1	1	102910	0.00
HRV050	0	1	0	0	0	0		1		1	1	102911	0.00
ITA368	0	1	0	0	0	0		1		1	1	102912	0.00
MEX006	0	1	0	0	0	0		1		1	1	102913	0.00
MEX194	0	1	0	0	0	0		1		1	1	102914	0.00
MEX263	0	1	0	0	0	0		1		1	1	102915	0.00
MMR015	0	1	0	0	0	0		1		1	1	102916	0.00
NZL001	0	0	0	0	0	1		1		1	1	102917	0.00
Total								**73030**	**86706**	**102917**			

and the proportion of the total held are as follows: FRA043 (12.7%), RUS001 (8.0%), CHN001 (6.7%), AUS165 (6.2%), USA022 (6.7%), LBN002 (6.0%), DEU146 (5.2%), IND001 4.3%, GBR247 (3.5 %), (%), GBR165 (3.4%), POL003 (2.9%), UKR001 (2.7%) and SWE054 (2.4%).

The composition of collections based on sample status was highly variable, reflecting their different mandates (Table 5.4). GBR247 had the largest number of wild species accessions (481) followed by USA022 (262), LBN002 (242), FRA043 (158) and POL003 (120). The RUS255 and TUR001 collections, although small, exclusively comprised wild species accessions (21 and 12 respectively). More than 1000 accessions of landraces were held by CHN001 (5945), USA022 (3000), RUS001 (2645), AUS146(2451), DEU (1545) and LBN002 (1008). Landraces formed the majority of the holdings in a number of collections (CHE063, ESP004, ESP009, GBR017, PRT001 and TWN001). Four collections reported holdings of more than 1000 obsolete improved cultivars: DEU146 (3051), GBR165 (2199), USA022 (2000) and CZE122 (1264).

Four collections reported holdings of more than 1000 improved cultivars: RUS001 (2699), UKR001 (1675), FRA043 (1383) and GBR247 (1085). Other large collections of obsolete and improved cultivars include statu-

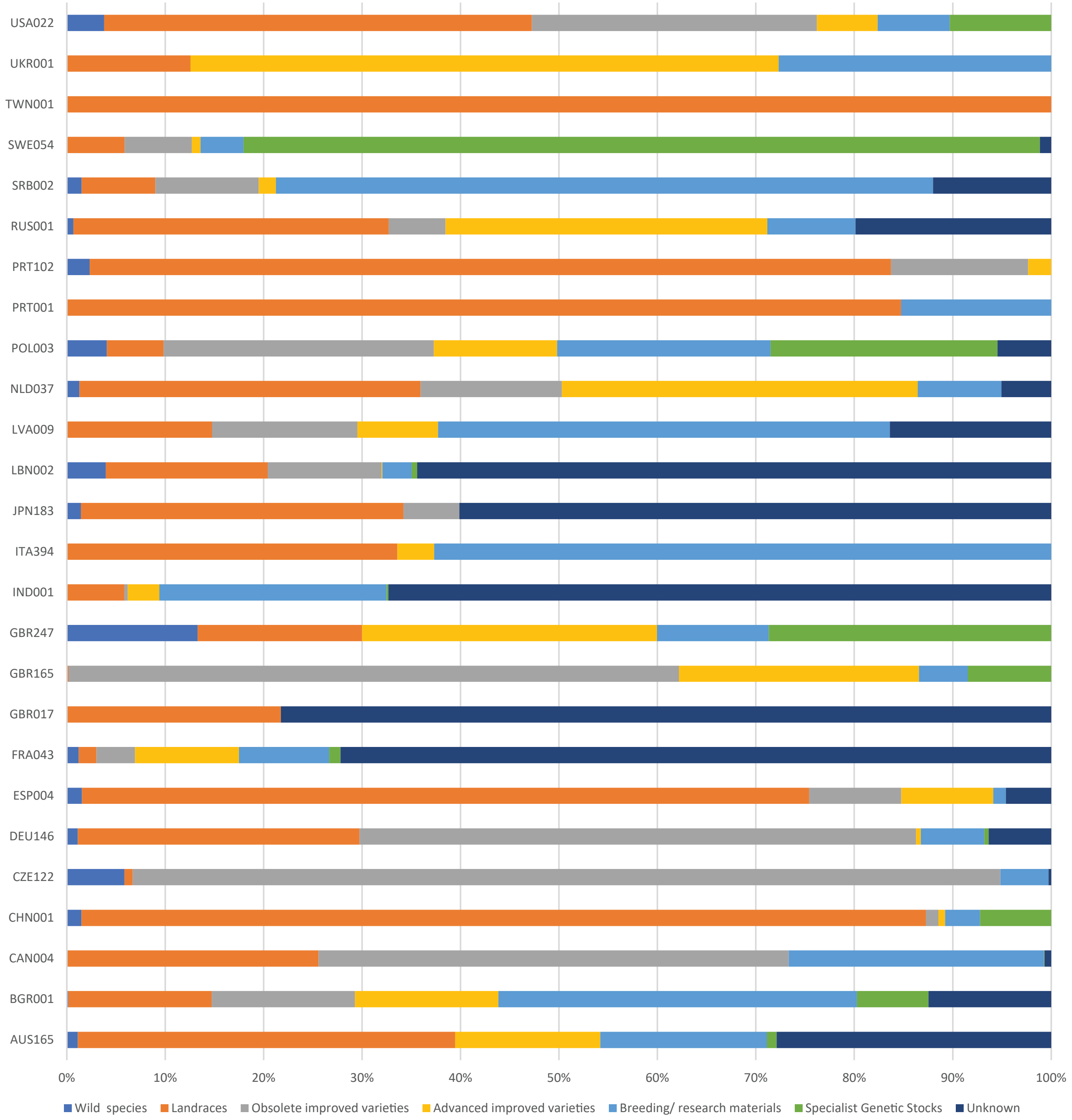

Figure 5.2. Relative composition of collections in terms of sample status, based on survey responses.

tory collections underpinning cultivar registration and plant breeder rights such as GBR165 (3298 accessions) and large specialist seed saver organizations such as USA1174 (1195).

Collections reporting large holdings of breeding/research materials included ITA394 (1260), FRA043 (1200) and AUS165 (1082). This class of materials formed the majority of holdings in two collections: CHL150 (914) and EST019 (152).

Specialist genetic stocks of peas were held by SWE054 (1970), GBR247 (1039), USA022 (712) and POL003 (680). Further details about genetic stocks are reported in Section 7.4.

A total of 10421 accessions were reported as 'unknown' sample status by 17 collections. It is not known whether this is because their status is actually unknown or because that information is yet to be processed.

A graphical presentation of the relative composition of each collection based on sample status shows these findings more clearly (Figure 5.2), including the high proportion of wild species in RUS255, TUR001 and BRA003. The figure also highlights which particular components are highly represented in individual collections.

The percentage representation, in terms of sample status, was totaled across the 34 collections who responded to the survey. Landraces formed the largest proportion (29%), followed by obsolete improved cultivars (17%), and then breeding/research lines and advanced cultivars, each at 14% (Figure 5.3). Wild related species accounted for 2%, specialist genetic stocks accounted for 7%, and materials with 'unknown' status accounted for 17%.

Comparison of current collection totals with earlier published data highlighted one collection (FRA043) with a significant increase in the number of accessions (Table 5.5). Other collections showed more modest expansion (UKR001, POL003, RUS001 and CZE122) while the remainder were either static (NLD037 and HUN003) or showed some contraction (BGR001, DEU146 and SWE056).

5.3 Crop Wild Relatives in Ex Situ Collections

Details of *Pisum* taxa including crop wild relatives (CWR) extracted from 91 *ex situ* collections from Genesys, WIEWS and USDA-GRIN are presented in previous sections of this document. This section focuses on detailing *Pisum* CWR holdings in specific collections. The caveat to this data is that it does not take into account duplication of accessions between collections. Establishing the extent of duplication is not possible without further research, including molecular fingerprinting.

Twenty-two collections responded to the survey with details of *Pisum* CWR holdings, amounting to 1006

Table 5.5. Percentage change in number of accessions from 2008 to 2020 held in 14 collections (2008 data from Ambrose (2008), 2013 data from Smýkal et al. (2013), 2020 data from the *Pisum* Survey).

Inst. Code	2008	2013	2020
BGR001	1415	2100	1383
CZE122	1273	1326	1434
DEU146	5505	5343	5361
FRA043	1891	8839	13000
GBR247	3496	3567	3621
HUN003	1188	1205	1221
NLD037	1001	1002	1010
POL003	2321	2894	2951
RUS001	7235	6792	8302
SWE054	2710	2849	2390
UKR001	1671	1671	2305

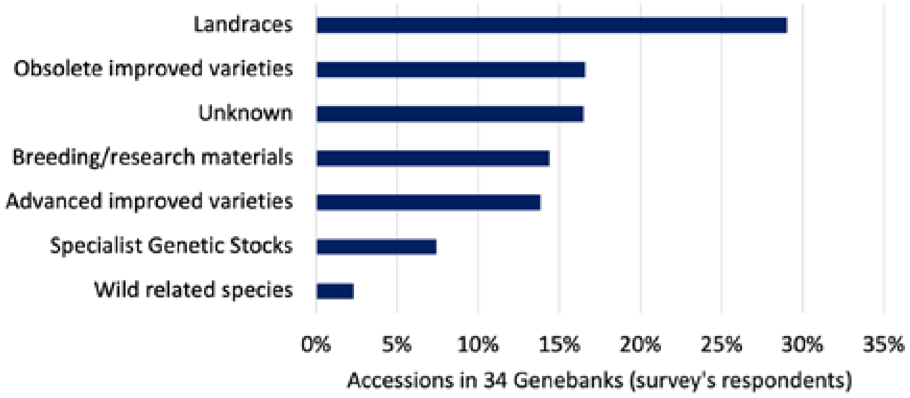

Figure 5.3. Percentage of different sample types totaled across 34 collections who responded to the survey.

accessions in total. The most populous CWR holdings were of *P. sativum* ssp. *elatius* var. *elatius* with 416 accessions held across 20 collections (Table 5.6). *P. fulvum* was the second most populous with 298 accessions held across 15 collections. There were 222 accessions of *P. abyssinicum* held across 14 collections. The data shown in Table 5.6 suggest that relatively few collections hold significant numbers of *Pisum* CWRs, but all of them have good storage facilities (Annex 6) and high levels of safety duplication (Table 8.4). Therefore, these materials are not considered to be at risk.

Table 5.7 shows the estimated number of accessions of several taxa based on data from databases (Genesys and WIEWS) and data obtained through the survey, as well as the estimates of Smýkal et al. (2013). The numbers of accessions of *P. sativum* and *P. elatius*

Table 5.6 CWR holdings in collections responding to the *Pisum* Survey.

Institute code	*Pisum fulvum*	*Pisum abyssinicum*	*Pisum sativum* spp. *elatius* var *elatius*	*Pisum sativum* ssp. *elatius* var. *pumilio*	*Pisum sativum* ssp. *elatius* var. brevipedunculatum	Total
USA022	36	20	122	27	0	205
GBR247	81	35	78			194
AUS165	53	24	28	10		115
DEU146	14	44	35			93
FRA043	30	22	33	1		86
LBN002	33	16	25	2		76
POL003	5	26	24			55
CHN001	5	6	15	17	3	46
SWE054	4	16	6	5	0	31
ESP109	19	2	1	0	0	22
RUS255	6		2	13		21
RUS001	5	4	11			20
TUR001			11		1	12
ESP004			10[1]			10
SRB002	5	3	1	0	0	9
GBR165	0	2	5	0	0	7
UKR001	1	1	3	0	0	5
NLD037		1		1		2
CHE063			2			2
BGR001			2			2
BRA003	0	0	2	0	0	2
CAN004	1					1
Total	298	222	416	76	4	1016

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[1] Only identified at subspecies level.

Table 5.7 Estimated number of accessions per taxa based on data from databases and survey responses; *when data from databases and survey were inconsistent we used data obtained through survey; ** estimated by subtracting the number of wild *Pisum* accessions and P. *abyssinicum* accessions reported from the total number of *Pisum* accessions reported ; *** no data available to assess how many *Pisum* accessions are still not identified at species level; in these cases the estimated number of *Pisum sativum* L. accessions includes *Pisum* sp. accessions.

Taxa	Smýkal et al. 2013	Databases 2022	Survey 2020	Databases corrected* and integrated with survey data
Pisum fulvum Sibth. & Sm.	706	409	298	332
Pisum abyssinicum A. Braun	540	176	222	238
Pisum sativum subsp. *elatius* (M. Bieb) Achers. & Graebn. (including var. *pumilio* and var. *elatius*)	624	456	496	579
Pisum sativum L.	97077**	68924	86939**	101768**
Pisum sp.	***	3065	***	***
Total	98947	73030	87955	102917

estimated by Smýkal et al. (2013) were similar to those obtained by combining Genesys/WIEWS data from 2022 with data from the survey. However, the estimates for the number of accessions of *P. fulvum* and *P. abyssinicum* were quite different from those of Smýkal et al. (2013). It is unclear whether this reflects an actual change in collections, or low accuracy of data used to make estimates. It is possible that a significant number of accessions still require precise taxonomic identification. For example, 3065 accessions were recorded as *Pisum* sp. in the Genesys/WIEWS data, but 15693 of these *Pisum* sp. were from DEU146, and are now recorded as *P. sativum* in the DEU146 database.

5.4 Specialist Resources

Headline: There are a number of specialist collections of* Pisum *reflecting the rich history of genetic studies on pea from Mendel to the present day.

A number of institutions maintain subsets of specialist resources within their collections. Most notable for peas are six collections of genetic stocks (Table 5.8). That work was initiated in the first decade of the 1900s by geneticists working in Sweden, and their legacy has been carried forward to the present day in a number of centers. The collections include mutation stocks and reference lines into which mutations have been introgressed. Some have been repeatedly backcrossed into particular backgrounds to develop near isogenic stocks. A further class of specialist genetic stocks are recombinant inbred lines developed by multiple generations of selfing of F_2 individuals for mapping purposes. Some of these may be based on multiple marker stocks to help establish or refine linkage groups, or are the result of wide crosses to assist with alignment of genetic and physical maps. These reference stocks have underpinned an enormous body of research into the development of genetic maps, as well as numerous aspects of plant, pod and seed development, seed quality traits, disease resistance and crop improvement. They have also played a crucial role in dissecting the complex developmental pathways and regulation of nodulation and nitrogen fixation.

This category of stocks was greatly expanded in the 1960s through induced mutagenesis programs. The use of mutagenesis for inducing novel allelic variation (EMS) and deletions (gamma-ray) has been crucial for research on *Pisum* genetics, but there are significant challenges in terms of managing mutant collections. By their very nature, mutations frequently have deleterious as well as pleiotropic effects that affect overall plant vigor, growth and fertility. Consequently, mutants cannot be reliably grown outside and require additional management and hands-on intervention. The building up of knowledge and experience of their often complex and subtle phenotypes can take a number of growing cycles. This requires a degree of continuity of core dedicated staffing to acquire a working knowledge of their behavior in order to maintain them and to be able to advise others as to their characteristics. The retirement of a number of specialists working on *Pisum* genetic stocks has highlighted the problem of maintaining community knowledge in this important area of germplasm management.

A further specialist collection established by USA022 is a mini core of the USDA collection based on single plant selections.

Recommendation: *Establish a network of interest among key curators of pea mutation stocks to share expertise and management advice. This will help address the issue of maintaining a working knowledge base and expertise for these important resources going forward.*

Table 5.8 Specialist *Pisum* germplasm resources and associated websites.

Inst. Code	Resource	Website
FRA043	EMS TILLING Population (4,817 M2)	Forward & reverse genetics tool
GRB247	Genetic Stocks	*Pisum* Gene List
NORGEN	Genetic Stocks (3,755)	SESTO
POL003	Genetic Stocks	
USA962	Genetic Stocks (712)	G.A. Marx Pea Genetic Stock Centre (Listed in Genesys)
USA022	Single Plant Collection (431)	Mini Core of USDA Collection based on morphological, geographic, and taxonomic diversity. SNP and Fasta sequenced


Pisum sativum flower. ICARDA Terbol station.
Photo: Michael Major for Crop Trust

6 GAPS IN *EX SITU* COLLECTIONS

6.1 Spatial Gap Analysis: Pea CWR and Landraces

A gap analysis of *Pisum* was conducted based on 728 unique geo-referenced records compiled from four datasets:

- Global Biodiversity Information Facility,
- Global Database of *Cicer, Lathyrus, Lens, Medicago, Pisum* and *Vicia* Wild Relatives (ICARDA, Syria),
- additional data from the collections of Nigel Maxted and Ali Shehadeh, and
- ecogeographic surveys of food and forage legumes.

In that study, a complementarity analysis identified the location of a priority hotspot for *P. fulvum* and *P. elatius* species diversity in the Osmaniye province in Turkey (Maxted et al. 2012).

In work conducted by CIAT for the CGIAR Genebank Platform (CGIAR Genebank Platform 2020), Ramirez Villegas et al. (2020) developed a new methodology to assess gaps in geographical coverage for landraces conserved *ex situ*. The methodology was based on modeling the potential geographic distribution of a crop's landraces and comparing this with the geographical coverage of accessions conserved *ex situ*. Gaps were differentiated in three categories: low probability gaps (gap found with one approach), medium probability gaps (gap found with two approaches), high probability gaps (gaps found with three approaches). More details on the three different approaches (cost distance, networking, environmental distance) are described in Ramirez-Villegas et al. (2020) and Ramirez-Villegas et al. (2022).

The analysis for pea found that landraces in collections with accessible and georeferenced data held in Genesys covered about 60% of the geographic area where landraces are expected to be found based on their distribution model (Figure 6.1).

The area outputs obtained using the three different models are shown in Figure 6.2. Metrics of the results of the landrace gap analysis conducted by CIAT, grouped by country, are presented in Annex 4. According to this analysis, the countries with the largest gap areas are France, China, Turkey, Norway, Finland, Italy, Iran and the UK.

The issues described for passport data in the previous section apply equally well to this section. Specifically, the main limitation of this analysis is that only a small proportion of the global *Pisum* accessions conserved *ex situ* have coordinate data (e.g., 8% of the *Pisum* accessions recorded in Genesys have this information) and the accessions lacking this information could not be included in this analysis.

6.2 Pea Diversity Tree Analysis

An assembly of *Pisum* passport data from 91 genebanks was compiled using data from Genesys (Genesys 2022) and WIEWS (WIEWS 2022) databases (hereinafter, this dataset is referred to as the combined

WIEWS/Genesys dataset), and the previously described taxon dictionary was used to standardize taxon labels.

The WIEWS/Genesys dataset was then used to review taxon coverage by 'country of origin'. Supplementary Table 1 summarizes the results of this analysis. Because of the heterogeneous nature of the completeness of passport data in terms of biological status, it was necessary to choose among different assumptions to conduct this analysis. Specifically, for accessions with a validated taxon of cultivated pea and country of origin, when the biological status was unknown (cultivars and breeding lines having been excluded if known), they were assumed to be landraces. A variation of the same analysis was also run where only accessions explicitly recorded as landraces were counted as such. However, the results of that analysis did not match as well with the known situation for many countries, so the results are not reported here. The numbers of accessions from each collection are shown in Table 5.4.

A pea diversity tree developed as part of the CGIAR Genebank Platform was updated during the development of this strategy. A diversity tree is a stratification of a genepool into groups and subgroups. This concept has its origin in a paper published by van Treuren et al. (2009). The Crop Trust has adopted this idea as an additional tool to visualize, analyze and understand the coverage of a crop genepool in *ex situ* conservation. Accession data from Genesys and WIEWS have been mapped to the groups in the pea diversity tree (PDT 2020), which is based on both expert opinion and literature and stratifies the genepool by countries of origin and cultivation, to identify the level of coverage and possible gaps in *ex situ* collections of wild and landrace accessions (Table 6.1). The pea diversity tree is shown on the pea page at Genesys.

Because many assumptions were made in preparing this dataset, the analysis comes with a significant warning as to accuracy in terms of absolute numbers. A further note of caution is that the aggregate numbers against each taxon by country of origin do not take into account the question of putative duplicate accessions. There are likely to be many duplicates among such a large number of genebanks as a result of high levels of exchange of *Pisum* germplasm among institutions from the 1960s through to the 1980's.

Nevertheless, this is the first time a survey of *ex situ* pea collection data on this scale has been possible, and it enables an estimate of baseline coverage to be established. Improvements to passport and provenance data on the basis of the recommendations in this review should allow for more accurate estimates to be made in the future.

Another limitation of this pea diversity tree analysis is that a stratification by country does not correct for the different areas of the countries, and more specifically, for the areas where pea landraces are grown. To correct for this bias, we also divided the number of accessions by the potential landrace distribution area for each country as estimated by Ramirez-Villegas et al. (2020) (see Section 6.1). Therefore, to identify gaps, we looked both at the absolute number of accessions in each end group in the diversity tree and the number of accessions per 1000 km^2 of potential distribution area (Table 6.1).

Landraces

Africa: In East Africa, Malawi is a gap and Kenya is poorly represented. South Africa is also poorly represented. The latter also ranked relatively high (34th) for gap area in the spatial analysis (Annex 4).

Americas: Colombia is less well represented than other countries in this region. In terms of accessions per potential distribution area, Mexico also seems under-represented. Accordingly, Mexico ranked relatively high (19th) for gap area in the spatial analysis (Annex 4).

Asia: In the Caucasus area, Azerbaijan is not well represented, with only 10 accessions. In Central Asia, there are only nine accessions from Turkmenistan. The pea diversity tree distinguished four different macroregions in China, but only a small proportion of the accessions collected in China have coordinate data, so it was not possible to assess how well each of these four macroregions is covered. In the spatial analysis, China ranked second when countries were ranked by gap area, but at the country level, the number of total and relative number of accessions were not among the lowest values. The discrepancy between the results of the two analyses could be because of biased sampling within the country, or because some accessions are listed in databases without coordinate data, and therefore they could not be included in the spatial analysis. In South Asia, 55 accessions from Iran were listed in the WIEWS-Genesys dataset, but Iran appeared to be under-represented in terms of the number of accessions per potential distribution area. Iran was also among the countries with the biggest gap area (see Section 6.1). According to the diversity tree analysis, Southeast Asia is not well represented in *ex situ* collections, with a small number of accessions from Indonesia, Philippines and Vietnam and no accessions from Cambodia.

In the Middle East cluster, Iraq, Israel, Jordan and Lebanon and Palestine have a low number of accessions and Iraq also has a relatively low number of accessions per potential area.

Table 6.1 Total number of accessions for landrace groups in the pea diversity tree based on data[1] from a review of 133 ex situ collections. The potential distribution area in each country, which was used to calculate the number of accessions per 1000 km^2 of potential distribution area, is from the spatial analysis (described in 5.1) conducted by Ramirez-Villegas et al. (2020).

Cluster	Landrace end-Group in pea diversity tree	Accessions	Accessions per 1000 km^2 of potential distribution area*
East Africa			
	Ethiopia	3819	313.47
	Kenya	4	10.47
	Malawi	0	0
	Tanzania	32	48.48
	Uganda	47	435.19
	Zambia	33	647.06
	Other East Africa	85	n/a
South Africa			
	South Africa	22	8.07
Central America			
	Mexico	74	7.44
South America			
	Argentina	120	197.04
	Bolivia	102	42.03
	Chile	80	25.20
	Colombia	24	8.50
	Peru	62	20.40
Others America	586		
Caucasus			
	Armenia	46	33.38
	Azerbaijan	10	3.07
	Georgia	410	98.53
Central Asia			
	Kazakhstan	87	131.02
	Tajikistan	364	77.45
	Turkmenistan	9	107.14
	Uzbekistan	93	15.23
	Others Central Asia	49	n/a
China	Unknown	765	
	All China	810	16.86
	East and South China	14	n/a
	Inner Mongolia	1	n/a
	NE and NW China	23	n/a
	Shaa’nxi	7	n/a
East Asia			
	Japan	59	36.67
	Korea, Democratic People’s republic	15	105.663
	Korea, Republic of (South Korea)	16	32.06

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[1] Accessions with biological status as landraces and unknown status were considered as landraces for this estimate.

Cluster	Landrace end-Group in pea diversity tree	Accessions	Accessions per 1000 km² of potential distribution area*
	Others East Asia	55	
South Asia			
	Afghanistan	689	49.82
	India	4495	304.60
	Iran	55	2.47
	Nepal	261	53.88
	Pakistan	343	66.25
	Others South Asia	69	n/a
South Eastern Asia			
	Cambodia	0	0
	Indonesia	10	28.65
	Philippines	1	40
	Vietnam	3	32.97
Europe			
	Belarus	37	4.26
	Bulgaria	471	133.05
	North Macedonia	9	5.84
	Romania	422	27.11
	Serbia	14	3.21
	Slovenia	1	0.77
	Denmark	85	24.65
	Estonia	15	4.53
	Finland	108	5.63
	Latvia	76	32.00
	Lithuania	19	14.74
	Norway	18	0.83
	Sweden	864	39.61
	UK	796	48.64
East Mediterranean			
	Albania	66	38.69
	Bosnia and Herzegovina	0	0
	Croatia	35	11.45
	Egypt	95	39.32
	Greece	465	60.95
	Libya	31	9.87
	Montenegro	1	1.18
	Turkey	837	18.38
	Others East Med	35	
West Mediterranean			
	Algeria	72	11.31
	Italy	499	28.98
	Morocco	157	19.45
	Portugal	476	90.36

Cluster	Landrace end-Group in pea diversity tree	Accessions	Accessions per 1000 km² of potential distribution area*
	Spain	968	31.45
	France	468	12.69
	Tunisia	46	33.95
Rest of Europe	Rest of Europe	3640	n/a
Middle East			
	Iraq	8	4.42
	Israel	26	27.75
	Jordan	18	14.43
	Lebanon	11	20.00
	Palestine	10	32.47
	Syria	204	37.77
	Others Middle East	34	n/a
Russia	Russia	1377	90.49

Europe: In North Europe, Estonia, Lithuania and Norway are underrepresented in terms of the absolute number of accessions. Finland is underrepresented in terms of the number of accessions per potential distribution area. Norway and Finland are also among the countries with the biggest gap area (see Section 6.1). North Macedonia, Serbia, Slovenia, Bosnia and Herzegovina, and Montenegro are also underrepresented both in terms of absolute and relative number of accessions (accessions/potential area). This is at least partly because these countries were part of the former Yugoslavia and many collections have not been able to prioritize the revision of passport data to reflect recent country changes. According to the diversity tree analysis, the west Mediterranean is well represented compared with other areas. However, Italy ranked 6th among countries with the largest gap area in the spatial analysis.

CWRs

The focus on reviewing the diversity of *Pisum* CWR using molecular markers in recent years has resulted in the careful sourcing and verification of accessions of *P. fulvum* and *P. elatius* from a wide range of *ex situ* collections (Smýkal et al. 2017; Bogdanova et al. 2021). These included a significant number of accessions that were not available in WIEWS or Genesys, or that had incorrect passport data in these databases. Therefore, we used the information from Genesys, WIEWS and Smýkal et al. (2017) to gain more accurate estimates of the number of accessions of *P. fulvum* and *P. elatius* (see Table 6.2)

This analysis clearly highlights the low representation of *P. fulvum* from Turkey and low coverage of *P. elatius* from North Africa, Iran and Jordan. The numbers from France, Portugal, and the Balkans are also considered low, based on the current knowledge of the distribution of CWR in these countries.

When interpreting the results of the gap analyses for pea conducted using the diversity tree and spatial analysis methods, it is useful to keep in mind the advantages and limitations of each method. The diversity tree approach has the advantage that it can include accessions without coordinate data when groups in the tree are at the national level or regional level, but its limitations are that it misses more fine-grained geographical gaps and does not normalize groups according to objective criteria. The spatial analysis provides a more fine-grained output but cannot include accessions without geographical coordinates, so it can overestimate gaps when a large proportion of accessions conserved in genebanks lack this information. Therefore, caution is needed when interpreting the results of these analyses.

***Recommendations**: Further collecting of cultivated pea should prioritize landraces from Azerbaijan, Turkmenistan in the Caucasus; Southeast Asia; Iran in western Asia; South Africa, Kenya, and Malawi in Africa; Iraq, Israel, Jordan, Lebanon and Palestine in the Middle East; and Estonia, Lithuania, Finland, Norway and Belarus in Europe. Further collecting of* P. elatius *should prioritize North Africa, Iran and Jordan. Further collecting of* P. fulvum *should prioritize Turkey.*

Passport data is a key attribute of *ex situ* accessions in terms of taxon identity and provenance. While passport data for recent accessions are more complete, those for accessions collected in earlier times remain a significant problem, as reported by a number of survey respondents (see Section 9, Table 9.1). With stretched resources, uploading and reviewing historical passport data are not a high priority when set against urgent regeneration and distribution issues. Nevertheless, to improve the quality of efforts to identify coverage and gaps in future studies, it would be useful to improve the quality of passport records and update them to reflect current national jurisdictions while preserving the original data entered when the accession was collected. Key countries to focus on would be those in the former Czechoslovakia and Yugoslavia.

Recommendations: *Amend passport records to reflect current national jurisdictions while preserving the original data entered when the accession was collected. This will help to improve the quality of identifying coverage and gaps in future studies.*

Recent studies on CWR have identified significant numbers of accessions for which the records are not yet uploaded into regional or global PGR portals. Action should be taken to upload such data to central portals to enable better estimates of germplasm coverage and to identify gaps in collections to guide further collection efforts.

Table 6.2 Number of accessions of *P. elatius* from countries in Asia, Europe, the Middle East, North Africa and Russia, and of *P. fulvum* from the countries in the Middle East.

Pisum elatius		**Total**
Asia		
	Armenia	27
	Azerbaijan	20
	Georgia	10
	Iran	6
	Central Turkey	12
	West Turkey	6
	East Turkey	16
	Turkey no coordinates	
	Turkey total	114
Europe		
	Balkans	11
	Cyprus	22
	France	2
	Greece	11
	Italy	13
	Portugal	3
	Spain	23
Middle East		
	Israel	47
	Turkey	6
	Jordan	2
	Lebanon	20
	Palestine	5
	Syria	8
North Africa		
	Algeria	4
	Morocco	2
	Tunisia	2
	Others	7
Russia		32
Pisum fulvum		
	Israel	155
	Jordan	21
	Lebanon	16
	Palestine	41
	Syria	41
	Turkey	6

ICARDA long-term storage genebank at Terbol station. Photo: Michael Major for Crop Trust

7 STORAGE FACILITIES

Seed storage facilities reported in the *Pisum* Survey ranged from ambient storage through to long-term facilities. Twenty-six institutions (74.3%) had long-term (at or below -18°C) storage facilities as either their primary or secondary facility (Annex 6). This rose to 83% when three further institutions (FRA043, RUS001 and UKR001) that listed freezers as their third storage facility were included. A further four institutions reported having good medium-term storage facilities (GBR247, ESP009, ESP109 and SRB002).

Twenty-eight institutions (80%) reported 100% of their holdings as being in either long- or medium-term storage facilities (Table 7.1). Two institutions (GBR017 and RUS255) reported no long- or medium-term storage facility, although they reported safety duplication of 86% and 57% of their collections, respectively, at other sites (Table 8.4).

The majority of the collections that responded to the *Pisum* Survey hold all or a majority of their *Pisum* collection in long-term storage at -18°C – -20°C. More variation was reported in the regulation of relative humidity and in the packing materials used. Paper bags should be replaced with laminated aluminum foil bags or hermetic glass jars.

Table 7.1. Percentage of institute holdings held in long-, medium- or short-term seed storage facilities as reported in the *Pisum* Survey.

Institute Code	Long-term	Medium-term	Short-term
AUS165	83%	17%	0%
BGR001	60%	35%	5%
BRA003	100%	0%	0%
CAN004	100%	100%	
CHE063	10%	90%	
CHL150	100%	100%	4%
CHN001	100%	80%	0%
CZE122	100%		
DEU146	100%		20%
ECU023	100%		
ESP004	75%	96%	
ESP009		100%	
ESP109		20%	100%
EST019	100%		
FRA043	10%	100%	100%
GBR017			100%
GBR247	0%	100%	0%
IND001	94%	6%	
ITA394	100%	30%	
JPN183	70%		100%
LBN002	87%	100%	
LVA009	100%		
NLD037	100%		
POL003	100%		
PRT001	44%	56%	
PRT102	100%		100%
RUS001	15%	94%	99%
RUS255	0%	0%	100%
SRB002		85%	15%
SWE054	100%		
TUR001	100%	100%	
TWN001	94%	100%	0%
UKR001	37%	15%	47%
USA022	68%	100%	
USA974	100%		

Pea diversity. Photo: Petr Smykal

8 COLLECTIONS AND RISK MANAGEMENT

The majority of* Pisum *collections are experiencing significant operational challenges in many aspects of their important work.

The operational framework for maintaining any *ex situ* collection consists of a number of components, including the estate and facilities, staffing levels, information systems, regeneration requirements and facilities, and safety duplication. The survey asked respondents to report on any major limitations they faced that impacted on the management of their collections. Thirty-one respondents (81.5%) cited major limitations relating to finances, facilities or staffing (Figure 8.1). These findings are unfortunately not new, and are in line with those reported by Engelmann and Engels (2002).

The majority of respondents cited limitations in more than one area and three respondents cited limitations in all three areas (CHL150, SRB002 and SWE004). The largest proportion of respondents reported limitations in the areas of funding (54.8%) followed by staffing (51.6%) and facilities (29%). In some cases, these limitations are reducing the effectiveness of operations. For example, financial restrictions in Ecuador have stopped all pea research and only *ex situ* conservation is ongoing at ECU023. A lack of political support in the Czech Republic has resulted in financial and staffing shortages at CZE122, and UKR001 reported problems associated with inadequate funding and staff shortages.

At AUS165, staff shortages, partly due to the retirement of their experienced pulse crop curator, have created problems in maintaining the regenera-

Figure 8.1. Venn diagram showing major limitations to collection management as reported by the survey respondents.

tion capacity, characterizing the materials, and the uploading of hard-copy data into computer systems.

Limitations at the operational level were reported in several areas (Table 8.1), the most frequent being the lack of evaluation data (29%). One collection (FRA043) reported that this was due to time and cost limitations for full material characterization under natural growing conditions. Reduced regeneration capacity, through either staff shortages or limited field and glasshouse space, was cited as a major limitation by 22.6% of responding institutes. Information systems were cited as limitations in 16.1% of cases.

Information systems were reported as a major problem area by BGR001. Another respondent, CAN004, reported that it has been upgrading from GRIN-Canada to GRIN-Global since 2013 because of IT support problems. The uploading of historical datasets was reported as a problem at AUS165, CAN004, ESP109, and SWE054. Disease and pest management were operational limitations in 9.7% of cases, and at CHN001 this was due to budget constraints. SWE054 reported difficulties in seed health testing and cleaning of virus-infected material, and the same problems exist at USA022 because of a lack of virus testing infrastructure. Two collections (NLD037 and USA974) cited their aging stocks as a concern with respect to germination and associated regeneration issues.

A follow-up question on funding for routine operations and maintenance asked for an assessment of the current situation and a forward three-year forecast. Of the five respondents stating that current funding was good, four stated that they did not envisage any change while one stated that they anticipated a decline in funding within three years (Table 8.2). Of the 11 respondents stating that they had adequate funding, six anticipated improvements within three years while the remaining five expected no change. Of the seven respondents stating that their funding was inadequate, three expected improvements over the coming three years and the other four expected no change.

Table 8.1 Major operational limitations reported as a percentage of survey respondents (n=31).

Operational Limitation	%	Institute Code
Stock levels	6.5%	CHE063, CHL003
Evaluation	29.0%	AUS165, ESP004, FRA043, IND001, ITA394, NLD037, RUS001, TUR001, USA974
Characterization	19.4%	AUS165, BGR001, ECU023, ESP004, IND001, TUR001
Regeneration Capacity	22.6%	AUS165, EST019, FRA043, ITA394, NLD037, TUR001, USA974
Information Systems & Historical Data	16.1%	AUS165, BGR001, CAN004, ESP109, SWE054
Molecular Characterization	6.5%	ECU023, RUS001
Disease & Pest Management	9.7%	CHN001, SWE054, USA022
Germination (Age of Seed)	6.5%	NLD037, USA974

8.1 Quality Management Procedures

Some genebank operations are better covered by management systems and/or written procedures and protocols than others

Written Standard Operating Procedures are desirable for all collections for effective and transparent running, both from the organization's perspective and for the confidence of external users. The remit, crop focus, location and resources make each collection effectively unique, and there is no single management model that would encompass or fit all of them. The development of standards for various genebank operations has been ongoing since the 1960s. Handbooks setting out guidelines and templates of procedures have been developed and periodically updated for a whole range of genebank operations to assist genebanks to develop their own bespoke versions (Engels and Visser 2003; Rao et al. 2006; FAO 2014). Interactive toolkits are also available for some aspects of seed conservation (e.g., the CWR Toolkit [Magos et al., 2017]) . The heterogeneous landscape across the genebank community has been the subject of considerable debate for many years, and has been perceived as a block to more extensive sharing and collaboration among collections. It has also been perceived by various parties to reduce the confidence of some external users.

The European Genebank Integrated System (AEGIS), a virtual genebank system developed by the European Cooperative Programme for Plant Genetic Resources (ECPGR), has a downloadable template for the preparation of operational manuals for genebanks based on a set of policies, processes and quality procedures known as AQUAS.

Table 8.2 Current and three-year forecasts for funding for routine operations and maintenance.

	Current Situation		
Three-year Forecast	Good (1)	Adequate (2)	Not Sufficient (3)
	5	11	7
Static	4	5	4
Improves		6	3
Declines	1		

All of the survey respondents reported that they have written procedures for storage and maintenance, but the percentage of institutes with written procedures for other operations varied from 44–94% (Figure 8.2). A few collections have gone as far as developing quality management systems (QMS) and have obtained ISO9001 certification (DEU146, NLD037).

Recommendation: ***Further improve the management systems or written procedures and protocols to cover all routine operations in genebanks.***

8.2 Urgent Regeneration Requirements

Many collections maintain regeneration programs to refresh and multiply their stocks, with an aim to produce seed lots for safety duplication and to replenish or replace stocks in base collections. Regeneration issues were mentioned by 23% of survey respondents as being an area of collection management with major limitations (Table 8.1). This was further qualified as being due to insufficient funding to cover costs, inadequate field and/or glasshouse space and a lack of specialist staff.

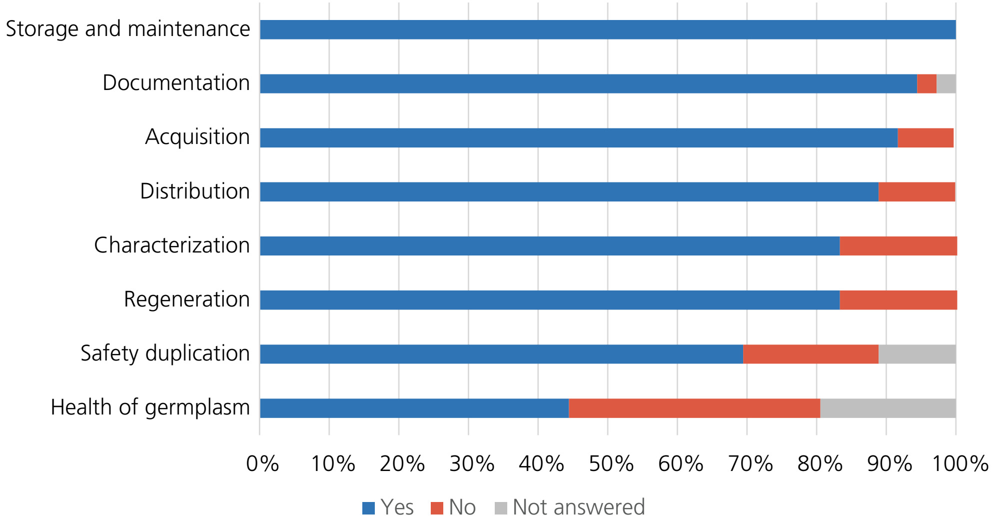

Figure 8.2 Percentage of institutes reporting that they have established a genebank management system or written procedures and protocols for the listed routine operations.

Table 8.3 Percentage of collections by category requiring urgent regeneration, as reported by the survey respondents. Figures in parentheses indicate the actual number of accessions.

Institute code	Wild species	Landraces	Obsolete improved varieties	Advanced improved varieties	Breeding research materials	Unknown	Other
AUS165	100 (77)	2		2	0	2	
BGR001		10					
BRA003							9
CAN004	0	5	5	5	5	5	
CHE063		15					
CHL150					100 (916)		
CZE122	0	0	5		0		
ECU023						100 (253)	
ESP009		20			10		
FRA043					50 (600)		50 (830)
LBN002	1	2	1	0	1	8	
NLD037	0	1	1	1	0	0	
RUS001	90 (50)	0	0	0	0	0	
RUS255	20						
SWE054	22	2	6	0	14	10	
TUR001	70	60					
TWN001		6					
UKR001		2		3	3		
USA974							69 (877)

When asked to indicate the proportion of the collection by category that required urgent regeneration (apart from the normal routine regeneration), 19 respondents reported that urgent regeneration was required (Table 8.3), although the scale of the problem varied significantly between collections. The most serious need was at CHL150 and ECU023, where their entire collections required urgent regeneration with no funds currently available to undertake this action. FRA043 reported 1430 accessions requiring urgent regeneration and USA974 reported that 69% of their collection, or 877 accessions, required urgent regeneration because of seed aging. The categories of germplasm that were most consistently flagged as requiring urgent regeneration were landraces and wild species. Wild species were reported as a particular problem by AUS165, TUR001 and RUS001.

8.3 Safety Duplication

The duplication of a genetically identical sub-sample of the accession to mitigate the risk of its partial or total loss because of natural or man-made catastrophes should be an objective of all *ex situ* collections. Safety duplicates (SDs) are genetically identical to those in the base collection and are referred to as the secondary most original sample (Engels and Visser 2003). Safety duplicates are deposited in a base collection at a different location, preferably in another country and generally under a 'black box' arrangement.

Of all the survey respondents, 75% reported that they have safety duplication arrangements with at least one other site, with 28% reporting that they use two sites and 5% reporting that they use three sites (Table 8.4). Of the institutes with such arrangements, 46% use the Svalbard Global Seed Vault (SGSV) as either their primary safety duplication site (BGR001, CAN004, DEU146 and GBR247), secondary safety duplication site (AUS165, EST019, NLD037, RUS001, SWE054, TWN001, USA022 and USA974) or tertiary safety duplication site (LBN002). Safety duplication sites other than the SGSV were evenly divided between national and international institutions. The responding institutes that currently have no safety duplication arrangements in place are BRA001, CHN001, ECU023, ESP004, FRA043, IND001, JPN183, POL003, PRT102 and UKR001. The situation at UKR001 is of particular concern as 47% (1281 accessions) of their collection is only maintained in short-term seed storage facilities (Table 8.1).

The majority of safety duplicates (61%) are in the form of black box depositions. The safety duplicates of four collections (CHE063, ESP009, RUS001 and USA022) have been fully integrated into the host site and a fifth (RUS255) is working towards being fully integrated.

From the data provided, the proportion of holdings currently safeguarded as safety duplicates at primary sites is about 30% (25,835 of a total of 86,706 accessions). Similarly, the number of accessions recorded as being safety duplicated in the Genesys-WIEWS dataset is 20,092, which is about 28% of the 73,030 records in this dataset.

The secondary safety duplication sites account for an estimated 10% of total holdings (including the SGSV when this is used as a secondary safety duplication site). The figures for primary and secondary safety duplication site holdings cannot be added together, because in some cases the same materials are backed up as second safety duplication sets. SWE054 reported a total of 77% of their active collection as being duplicated in their base collection or safety duplication collection and 92% as duplicated in their base collection in Denmark.

Five collections (CAN004, CHL150, DEU146, GBR247 and NLD037) reported safety duplication levels of 100% of their holdings. Three collections reported safety duplication levels of between 80% and 92% (EST019, GBR017 and SWE054) and two others reported safety duplication levels of between 60% and 70% (RUS001 and USA022).

The number of safety duplicates of accessions reported in the *Pisum* Survey in 2020 as being deposited in the SGSV was 17,326, which is close to the value of 17,140 determined in June 2022 by searching the Seed Portal of the SGSV. The number of *Pisum* accessions recorded as being deposited in SGSV in the combined Genesys-WIEWS dataset was significantly lower at just 7,211 accessions. This may mean that the FAO/Bioversity Multi-Crop Passport Descriptors field for duplication site (DUPLSITE in Genesys and 'Genebank(s) holding safety duplications - code' in WIEWS) is significantly underpopulated in the uploaded data. On the basis of the estimated figures for *Pisum* accessions at the global level (Table 5.4) and the number of *Pisum* accessions recorded in the Seed Portal of the SGSV, we can estimate that about 17% of global *Pisum* accessions are backed up at the SGSV.

Recommendations: *Significant progress in the safety duplication of collection holdings has already been achieved. Until we have more information about unintended duplication within and among genebanks (see section below on rationalization of global* Pisum *collections), safety duplication should be increased to cover the largest proportion of potentially unique accessions conserved* ex situ *as possible. This could be done through safety duplication at the SGSV and also through collaboration with the genebanks identified as holding key* Pisum *collections, as these already have infrastructure and processes in place for long-*

term conservation. It is especially important to backup collections that have no safety duplication, including BRA003, CHN001, ECU023, ESP004[1]*, FRA043, IND001, JPN183, POL003, PRT102 and UKR001.*

Collections are encouraged to further populate the DUPLSITE field when data are uploaded to data portals such as EURISCO and Genesys. This will improve the monitoring and reporting of safety duplication levels in collections and the value of this as a responsive metric for monitoring and risk management of PGRFA.

Emphasizing the importance of populating the DUPLSITE to genebank curators would help improve the granularity of data associated with safety duplication down to the accession level.

8.4 Current and Future Assessment of Conservation

Collection holders were asked for their current assessment of different aspects of PGRFA conservation, the robustness of their operations and service delivery (Table 8.5), and their expectations for the same issues in three years' time (Table 8.6). The current level of funding for routine operations and maintenance was stated by 23% of respondents as not sufficient, while 50% considered funding levels to be adequate. The future expectation on this question was more positive, with 42% responding that future funding prospects were either good or adequate. Only 15% did not see funding prospects improving. The five genebanks responding that that funding was currently inadequate and not expected to improve were CHL150, ESP009, BGR001, ECU023 and UKR001.

The responses to the question about current retention of trained staff were evenly spread among good, adequate, and not sufficient. Again, many respondents expressed a degree of optimism for the future, responding with good or adequate scores. Close to a third (32%) of respondents scored the current situation as not sufficient, while 21% expected that the situation would not be sufficient in the future.

The majority of respondents (53%) felt there was an adequate or moderate interest in PGRFA conservation, which is likely to have a bearing on support for *ex situ* conservation efforts. Only 15% of respondents gave high or good scores about the current interest in PGRFA conservation, but one-third (33.3%) of respondents felt that this area would improve in the future.

On the question as to whether the current genetic variability in their collection matched the needs of users and breeders, the majority of respondents (52.3%) gave high or good scores for the current situation. One institution responded that the level of genetic variability was insufficient (IND001) although their future expectation was scored as adequate. Overall, there were more adequate and good scores for this situation in the future.

When asked about current access to germplasm information, 44.1% of respondents gave high or good

Table 8.4 Data on primary, secondary, and tertiary safety duplication (SD) sites obtained in the *Pisum* Survey. (SGSV = Svalbard Global Seed Vault. N/S = data not supplied, N/A = not applicable.)

Primary SD site		**Secondary SD site**					**3rd site**
INSTCODE	**Name of institute maintaining your safety duplicates**	**Type of storage**	**% of collection**	**site 2 Name of institute**	**site 2 Nature of storage**	**site 2% of collection**	
AUS165	Department of Primary Industries New South Wales	Black box	42.4	SGSV	Black box	40	
BGR001	Svalbard Global Seed Vault	Black box	0.7	N/A			
BRA003	-		0				
CAN004	Svalbard Global Seed Vault	Black box	48.6%	N/A			
CHE063	National Swiss Genebank	Black box	42.1	N/A			
CHL150	Base Bank INIA	Black box	100	N/A			
CZE122	Research Institute of Plant Production, Piešťany, Slovakia	Black box	5.5	N/A			
DEU146	Svalbard Global Seed Vault	SGSV regulations	37.6	N/A			

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[1] Recently, Spain has started sending different materials to Svalbard, including *Pisum* accessions.

	Primary SD site	Secondary SD site					3rd site	
INSTCODE	Name of institute maintaining your safety duplicates	Type of storage	% of collection	site 2 Name of institute	site 2 Nature of storage	site 2% of collection		
ECU023	No safety duplicates in another genebank			N/A				
ESP004	No safety duplicates in another genebank			N/A				
ESP009	CRF, INIA-CSIC Plant Genetic Resources Center	Fully integrated	100	N/A				
ESP109	CRF, INIA-CSIC Plant Genetic Resources Center	Fully integrated	12.6	N/A				
EST019	Nordgen	Black box	82.1	SGSV	Black box	35.9		
FRA043	No safety duplicates in another genebank	-	-	-				
GBR017	Warwick Crop Centre HRI Wellesbourne	Black box	86.2	Members saved seed				
GBR165	SASA	Black box	N/A	N/A				
GBR247	Svalbard Vault	Black box	100	SGSV				
IND001	No safety duplicates in another genebank	-	-	-				
ITA394	CNR-IBBR, Bari	Unknown	28.6	N/A				
JPN183	No safety duplicates in another genebank	-	-	-				
LBN002	CIMMYT	Black box	19.4	ICARDA-Morocco		30.1	Svallbard	24.5
LVA009	NordGen	Black box	21.3					
NLD037	Warwick Crop Centre - GR Unit, Wellesbourne, England	Black box	100	SGSV	Black box	91.2		
POL003	No safety duplicates in another genebank	-		-				
PRT001	Estação Nacional de Melhoramento de Plantas	Breeders collection	23.9	N/A				
PRT102	No safety duplicates in another genebank	-		-				
RUS001	Genetic Bank of Seeds (Kuban region) VIR's branch	Fully integrated	60.2	SGSV	Black box	2.4		
SRB002	Directorate for national reference laboratories, Ministry of Agriculture,							
SWE054	NordGen, placed at Aarhus University, Denmark	Nordgen facility	92	SGSV	Black box	80		
TUR001	Field Crops Central Research Institute	Black box	16	N/A				
TWN001	NPGRC-Taiwan	Black box	31.9	SGSV	Black box	14.4		
UKR001	No safety duplicates in another genebank	-		-				
USA022	Agricultural Genetic Resources Preservation Research	Fully integrated	68.1	SGSV	Black box	34.7		
USA974	United States Department of Agriculture	Black box	34.8	SGSV	Black box	15.7		

scores. Seven institutions (20.6%) scored current access as not sufficient (CHN001, FRA043, ECU023, ESP109, LVA009, SRB001 and TUR001). The future expectations were higher, with only two institutes (ECU023 & LVA009) having a poor outlook for access to germplasm information.

The current active support and feedback from users was rated as high by 15.6% of respondents and adequate by 50%. However, there was a marked upswing in future expectations of active support and feedback by users, with a doubling of the high rating (31%).

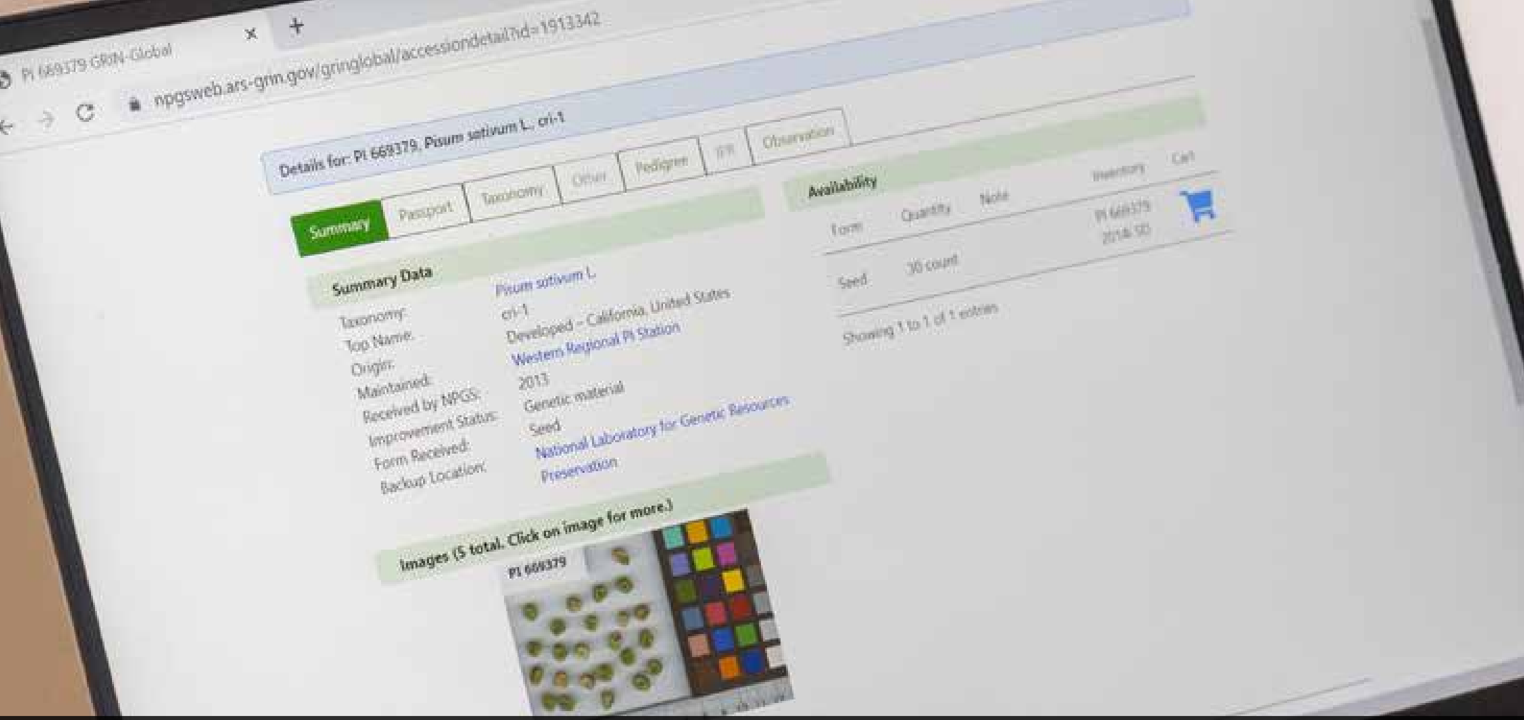
When asked about the level of use by breeders, the scores were very evenly spread (26.5% high, 35.3% adequate and 35.3% not sufficient) with very little difference between the current view and future expectations.

Table 8.5 Current opinions on PGR issues raised in the *Pisum* Survey.

	1 = high/good		**2 = adequate/moderate**		**3 = not sufficient/bad**		**NA = not applicable**	
Funding for routine operations and maintenance	26.5%	9	50.0%	17	23.5%	8	0.0%	0
Retention of trained staff	35.3%	12	32.4%	11	32.4%	11	0.0%	0
Interest for Plant Genetic Resource Conservation by donors	15.6%	5	53.1%	17	15.6%	5	15.6%	5
Genetic variability in the collection as needed by users/breeders	52.9%	18	35.3%	12	2.9%	1	8.8%	3
Access to germplasm information (passport, characterization, evaluation)	44.1%	15	32.4%	11	20.6%	7	2.9%	1
Active support/feedback by users	15.6%	5	50.0%	16	28.1%	9	6.3%	2
Level of use by breeders	26.5%	9	35.3%	12	35.3%	12	2.9%	1

Table 8.6 Expectations about PGR issues in three years' time. Directional arrows indicate changes from current.

	1 = high/good		**2 = adequate/moderate**		**3 = not sufficient/bad**		**NA = not applicable**	
Funding for routine operations and maintenance	↑42.4%	14	↓42.4%	14	↓15.2%	5	0.0%	0
Retention of trained staff	↑39.4%	13	↑39.4%	13	↓21.2%	7	0.0%	0
Interest for Plant Genetic Resource Conservation by donors	↑33.3%	10	↓40.0%	12	↓13.3%	4	↓13.3%	4
Genetic variability in the collection as needed by users/breeders	↑53.1%	17	↑37.5%	12	↓0.0%	0	↑9.4%	3
Access to germplasm information (passport, characterization, evaluation)	↑53.1%	17	↑37.5%	12	↓6.3%	2	↑3.1%	1
Active support/feedback by users	↑31.0%	9	↑51.7%	15	↓13.8%	4	↓3.5%	1
Level of use by breeders	↑29.0%	9	↑38.7%	12	↓29.0%	9	↑3.2%	1



Details for: PI 669379, Pisum sativum L., cri-1

Summary Data

Taxonomy: Pisum sativum L.
Top Name: cri-1
Origin: Developed – California, United States
Maintained: Western Regional PI Station
Received by NPGS: 2013
Improvement Status: Genetic material
Form Received: Seed
Backup Location: National Laboratory for Genetic Resources Preservation

Availability

Form	Quantity	Note	Inventory	Cart
Seed	30 count		PI 669379 2014 SD	

Showing 1 to 1 of 1 entries

Images (5 total. Click on image for more.)

PI 669379

Record for a pea accession on GRIN-Global. Photo: Michael Major

9 INFORMATION AND DOCUMENTATION SYSTEMS

The majority of collections (83.8%) reported that they have electronic information systems in place for use in stock control and management. A further 10.8% stated that their records were partially electronic. A wide range of software packages are used (Table 9.1). The most frequently cited are local versions of GRIN-Global used by 12 institutions. Two collections (AUS165 & SWE054) migrated their data into GRIN-Global during the course of the review. Excel is used by nine collections and MS Access by four. Four institutions use various versions of SQL for their systems.

The proportion of data computerized within collections varied greatly (Figure 9.1). The most highly computerized category was passport data, with 26 collections (86.6%) reporting complete coverage (Table 9.2). This was followed by characterization data, with seven collections (23.3%) reporting complete coverage and a further 12 collections (40%) reporting coverage levels of between 40–95%. Evaluation data was the category with the least computerized data, with six collections reporting complete coverage and seven others reporting coverage levels of between 2–35%.

The proportions of data in three categories stored in paper format or computerized in each collection are shown in Table 9.2. Six collections (CHL150, EST019, GBR247, LBN002, NLD027 and USA022) reported 100% computerization of passport, characterization and evaluation data.

Recommendation: *Increase the percentage of passport, characterization and evaluation data that is available in electronic format to facilitate access to information and use of the materials.*

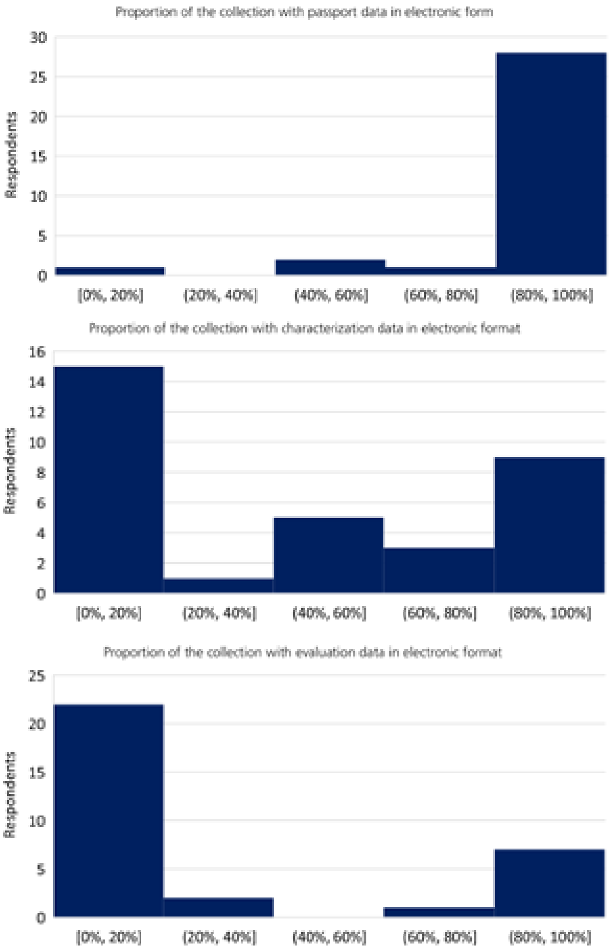


Figure 9.1 a, b, c. Histograms showing the distribution of the answers regarding the percentage of the collection data computerized by category. Responses in the survey were binned in five categories.

Table 9.1 Half diallel of responses about software used for documentation systems. Some institutions use more than one type of software, e.g., of the 12 institutes using GRIN-Global, one is also using MS Access and one is also using SQL DB. * SQL includes Microsoft and My SQL systems.

	Excel	GRIN-Global	Oracle	MS Access	Alelo	Paradox	SQL DB	FoxPro	FileMaker
Excel	9								
GRIN Global	1	12							
Oracle			2						
MS Access	2	1		4					
Alelo					1				
Paradox	1					1			
SQL DB	1	1					4		
FoxPro	1							1	
FileMaker									1

Table 9.2 Percentage of passport, characterization and evaluation data computerized in each collection. Figures in parentheses show % that exist in paper form where the number is greater than that which is computerized.

	Passport data (%)	Characterization data (%)	Evaluation data (%)
AUS165	100	50	0 (50)
BGR001	90	0 (10)	0 (5)
BRA003	100	0	0
CAN004	100	50	20
CHE063	100	0	0
CHL150	100	99	100
CHN001	100	80	35
CZE122	100	95	0
DEU146	100	10 (90)	0 (10)
ECU023	95	0 (69)	0
ESP004	100	50 (70)	0
ESP009	0 (100)	0 (100)	0 (100)
ESP109	55 (100)	0 (20)	0 (20)
EST019	100	100	100
FRA043	100	40	15
GBR017	100	62	62
GBR165	100	90	90
GBR247	100	100	100
ITA394	52	15	15 (40)
LBN002	100	100	100
LVA009	100	0	0
NLD037	100	100	100
POL003	100	50	0
PRT001	100	0	0
PRT102	100	5	5
RUS001	100	70	35
RUS255	100	0	0
SRB002	50	50	20
SWE054	100	10 (15)	10 (15)
TUR001	100	2	2
TWN001	100	100	0
UKR001	78	0	0
USA022	100	100	100

Pisum sativum at Nordgen, Sweden.
Photo: Peter Giovannini for Crop Trust

10 ACCESS AND AVAILABILITY

One of the primary functions of the PGRFA conservation community is to supply information and resources to the user community. This encompasses access to information on holdings, provenance and availability. The availability of characterization and evaluation data allows users to make more informed choices about the selection of germplasm for particular uses. In addition, it is important to have sufficient clean seeds and provide them under clear terms and conditions so that the client understands their obligations in using the materials and their freedom to operate. Initiatives such as the GreenPass protocol developed by the CGIAR Genebank Platform aim to ensure that best phytosanitary practices are used at all stages of handling seed transfers. Such protocols mean that countries can be confident in accepting germplasm entering their borders.

10.1 Germplasm Availability

Issues of policy, ownership, regeneration and quarantine frequently mean that not all accessions in a particular collection are available to users at any one time. The number of accessions unavailable varied significantly across collections as shown in Table 10.1.

The class of germplasm with the highest availability was landraces (62.9%) and that with the lowest was wild species (50.2%).

10.2 Information and Data Availability

Headline: National, regional and international data portals are helping to add value to individual collections and are now an integral component in PGRFA awareness and provision.

External users of collections depend on websites to access information about collection holdings. Of the survey respondents, 70.6% reported that they maintain their own external websites (Table 10.2).

Individual collection websites enable collections to develop their own external profile and to provide specialist information in the form of metadata files or applications for users. One example is the ‘Core Selection’ functionality developed by CGN (Centre for Genetic Resources, the Netherlands) which uses the available crop-specific data to generate core sets of a size defined by the users (van Hintum 1999). Another example is the community resource for exploring and utilizing genetic diversity in the USDA Pea Single Plant Plus Collection (PSPPC). This is a subset of the USDA Pea Collection (USA022), which is available for trait association and genomics-assisted breeding and includes single nucleotide polymorphism (SNP) and FastA data (Holdsworth et al. 2017). The expansion of datasets for different subsets of germplasm is one way of adding value in terms of utility to users. In the three years since this resource has been made available, there have been 40 requests and a total 10,091 seed samples shipped. Table 10.3 lists some other examples.

The majority of survey respondents (85%) reported regularly uploading passport data into third-party centralized PGRFA portals. These operate and function at a range of levels. National inventories are now a common feature of many countries' web presence as a means of facilitating access to PGRFA information, as well as resources linked to obligations of contracting parties to the CBD and the ITPGRFA. There are three regional portals hosting records on *Pisum* germplasm, namely GBIS (Baltic States), AVGRIS (WorldVeg) and EURISCO (Weise et al. 2017) (Table 10.5). The current global PGRFA portal is Genesys, which includes regular uploads from the databases of AVGRIS and EURISCO.

Regional and global data portals offer distinct advantages to institutions because they provide straightforward third-party support. In addition, they are a cost-effective means of promoting germplasm holdings to the user community while saving on staff and overheads that would be required to maintain such services in-house. Seven collections operate in this manner:

- ESP009 uploading to Centro Nacional de Recursos Fitogenéticos (CRF, INIA-CSIC) (ESP004) uploading to EURISCO;
- EST019 uploading to NordGen;
- AUS165, LBN002 and UKR001 uploading directly to Genesys;

Table 10.1 Genebank responses for the total number of accessions with the % currently available shown in parentheses. Respondents who did not answer the questions about availability are omitted from the table.

Institute Code	Wild related species	Landraces	Obsolete improved varieties	Advanced improved varieties	Breeding/research materials	Specialist Genetic Stocks	Unknown	Other
AUS165	71 (61%)	2451 (78%)		942 (94%)	1082 (90%)	63 (89%)	1782 (86%)	
CAN004	1 (100%)	377 (100%)	706 (100%)		383 (100%)	1 (100%)	10 (100%)	
CHE063	2 (100%)	55 (100%)						
CHL150					914 (99%)			
CHN001	103 (1%)	5945 (86%)	88 (1%)	48 (1%)	246 (4%)	500 (7%)		
CZE122	84 (99%)	12 (92%)	1264 (68%)		70 (69%)		4 (100%)	
DEU146	60 (98%)	1545 (95%)	3051 (97%)	26 (0%)	348 (94%)	24 (96%)	343 (90%)	
ESP004	12 (50%)	577 (96%)	73 (100%)		10 (100%)		36 (100%)	
ESP009								
EST019		4 (50%)		67 (100%)	152 (20%)			
FRA043	158 (100%)	237 (100%)	514 (?)	1383 (?)	1200 (?)	151 (?)	1660 (?)	7800 (?)
GBR017		30 (0%)						108 (0%)
IND001	2 (100%)	167 (0%)	10 (100%)	93 (100%)	667 (0%)	5 (100%)	67 (0%)	1879 (0%)
ITA394		675 (25%)		75 (0%)	1260 (0%)			
JPN183	5 (0%)	115 (32%)	20 (70%)				211 (70%)	
LBN002	242 (61%)	1008 (69%)	708 (75)	5 (80)	183 (74)	34 (59)	3944 (66)	
LVA009		9 (100%)	9 (100%)	5 (100%)	28 (0%)		10 (0%)	
NLD037	13 (99%)	350 (99%)	145 (99%)	365 (99%)	86 (99%)		51 (99%)	
POL003	120 (100%)	170 (100%)	810 (100%)	370 (100%)	640(100%)	680(100%)	161 (100%)	
RUS001	56 (0%)	2645 (80%)	477 (100%)	2699 (82%)	740 (100%)		1642 (0%)	
RUS255	21 (57%)							
SRB002	6 (5%)	30 (10%)	42 (25%)	7 (100%)	267 (0%)		48 (100%)	
SWE054		143 (98%)	166 (87%)	22 (0%)	106 (98%)	1970 (99%)	28 (100%)	
TWN001		188 (91%)						
UKR001	1 (100%)	351 (99%)		1675 (95%)	776 (75%)			
USA022	262 (69%)	3000 (71%)	2000 (71%)	426 (92%)	505 (79%)	712 (78%)		

Table 10.2 Collection website addresses and PGR portals.

Institute Code	Primary web address and PGR portals	Secondary web address and PGR portals
AUS165	GENESYS	
BGR001	EURISCO	GENESYS
BRA003	http://alelobag.cenargen.embrapa.br/AleloConsultas/Passaporte/bancoAcesso.do?idb=138	GENESYS
CAN004	http://pgrc.agr.gc.ca/	
CHN001	http://www.cgris.net/	
CHE063	prospecierara.ch	pgrel.admin.ch, GENESYS
CHL150	www.inia.cl/recursosgeneticos	
CZE122	https://grinczech.vurv.cz/gringlobal/Login.aspx	EURISCO, GENESYS
DEU146	https://gbis.ipk-gatersleben.de/gbis2i/	EURISCO, GENESYS
ESP004	https://bancocrf.inia.es/en/ ; http://webx.inia.es/web_inventario_nacional/Introduccioneng.asp ; http://webx.inia.es/web_coleccionescrf/CaracterizacionCRF.asp	EURISCO; GENESYS
ESP009	https://bancocrf.inia.es/en/	EURISCO, GENESYS
ESP109	http://germoplasma.itacyl.es/colecciones-conservadas	EURISCO, GENESYS
EST019	https://nordic-baltic-genebanks.org (GENBIS)	EURISCO, GENESYS
FRA043	EURISCO, http://urgv.evry.inra.fr/UTILLdb	SIREGAL and Gnp-IS
GBR016	EURISCO	GENESYS
GBR017	EURISCO	GENESYS
GBR165	EURISCO	GENESYS,
GBR247	https://www.seedstor.ac.uk/	http://data.jic.ac.uk/pgene, EURISCO, GENESYS
IND001	PGR Portal	
ITA394	http://planta-res.politicheagricole.it/pages/species.php	EURISCO, GENESYS
JPN183	https://www.gene.affrc.go.jp/databases-plant_search_en.php	
LBN002	GENESYS	
LVA009	https://nordic-baltic-genebanks.org (GENBIS)	EURISCO, GENESYS
NLD037	www.wur.nl/cgn	EURISCO, GENESYS
POL003	EURISCO	GENESYS
PRT001	http://bpgv.iniav.pt/gringlobal/search.aspx	EURISCO, GENESYS
PRT102	http://isoplexis.uma.pt/gringlobal/search.aspx	EURISCO, GENESYS
RUS001	http://db.vir.nw.ru/virdb/maindb	GENESYS
RUS255	GRIN USDA	
SWE054	www.nordic-baltic-genebanks.org (GENBIS)	EURISCO, GENESYS
TWN001	AVGRIS, http://seed.worldveg.org/	GENESYS
UKR001	EURISCO	GENESYS
USA022	https://npgsweb.ars-grin.gov/gringlobal/search.aspx	PULSEDB.ORG, GENESYS
USA974	www.exchange.seedsavers.org	GENESYS

Table 10.3 Specialist material and data resources.

	Application	Web Links & References
FRA043	Forward & reverse genetics tool	http://urgv.evry.inra.fr/UTILLdb
GBR247	Germinate Pea 2.1: Germplasm, RBIP marker data and structure groups	http://bioinf.hutton.ac.uk/germinate_pea/app/ (Lee et al. 2005; Jing et al. 2005)
GBR247	PGene: Germplasm accession and gene list database for *Pisum*	http://data.jic.ac.uk/pgene/
NLD037	Core Selection	https://www.wur.nl/en/Research-Results/Statutory-research-tasks/Centre-for-Genetic-Resources-the-Netherlands-1/Core-selections.htm. (van Hintum 1999)
USA022	Characterization	Plant morphology, disease assessment and root descriptors
USA022	Trait mapping and genomics-assisted breeding: GBS SNP and Fasta	https://data.nal.usda.gov/dataset/data-community-resource-exploring-and-utilizing-genetic-diversity-usda-pea-single-plant-plus- collection

- LVA009 uploading directly to EURISCO; and
- USA974 uploading to the Seed Savers Exchange, who in turn upload to Genesys.

By these routes, the passport data for 67% of collections responding to the survey are ultimately available in Genesys. Table 10.4 shows collections additional to those included in the survey that have uploaded data for 8,796 *Pisum* accessions to Genesys (Table 10.4).

Five collections (15%) who participated in the survey reported that they do not make their data available to external users.

A further advantage of data portals is that they are, in general, well supported and are continually being developed with improved user functionality. These portals have now expanded well beyond just holding passport data to include images, and, in a number of cases, characterization data and relevant documents, reports and publications (Table 10.5).

The user-orientated interface and functionalities being developed by these portals in response to user feedback highlights their increasingly important role in the centralization of information for both collection users and managers. They have also served as invaluable points of reference and cross-validation in the development of this conservation strategy.

A further global entry point for information and knowledge for PGRFA conservation, management and utilization is the Global Information System (GLIS) of the ITPGRFA (Global Information System). GLIS serves to integrate and augment existing systems by working with key partner institutions including Genesys, SADC Plant Genetic Resources Center, DataCite (the provider of persistent identifiers (DOIs) for research data and other research outputs), EURISCO, GRIN-Global, WIEWS, ICRISAT SBDM Statistics, and Bioinformatics and Data Management and FAO Information Technology Services Division (CSI).

Table 10.4 Additional collections to those who responded to the survey who have uploaded *Pisum* records into Genesys. Source: Genesys (accessed on 10 June 2020).

INSTCODE	Number of *Pisum* accessions uploaded into Genesys
GBR016	2116
ITA436	1716
HUN003	1221
BRA012	958
USA962	712
SVK001	548
EST019	223
MDA010	169
UKR009	147
ROM081	130
ROM007	127
ETH013	126
GBR004	101
AUT001	86
AUT046	74
CHE001	44
ALB026	31
GRC005	29
ISR002	29
LTU001	26
ESP172	19
ARM005	16
ITA363	15
AZE005	14
HRV044	11
HRV053	9
LBN020	7
CYP004	6
ESP027	6
BIH039	6
KEN212	5
HRV021	5
JOR015	4
AUT005	4
ROM055	4
ETH085	4
DEU627	4
BEL002	4
DEU005	3
GEO013	3
DEU628	3
USA995	3
MKD001	3
SVN019	3
AUT047	3
ESP026	2
USA971	2
GBR006	2
ARM010	2
ROM021	2
ROM019	2
AUT025	2
HRV050	1
AZE014	1
ITA368	1
AZE003	1
GEO001	1
Total	8796

Recommendation: *Collections are encouraged to participate and upload data into regional PGRFA portals and Genesys in particular. Both are highly desirable for the conservation and user communities to enable more efficient monitoring of* Pisum *germplasm holdings and would ease the burden on collection managers continually having to respond to data requests.*

10.3 Evaluation and Characterization Data (Pea Descriptors and Descriptor States)

The widespread adoption of standardized Multi-Crop Passport Descriptors has greatly assisted the development of national inventories, and regional and global data portals. These standards have undergone periodic review, and in 2015 were expanded to include developments relating to the broader use of GPS tools and references to the ITPGRFA and the Multilateral System (MLS) for access and benefit sharing (Alercia et al. 2015).

The development of well-defined and thoroughly tested descriptor lists for characterizing germplasm has been actively promoted by Bioversity International (formerly IBPGR) since the 1970s. Many crop communities have adopted a widely accepted set of descriptors that can be used at different locations and can be easily understood by germplasm curators and users. The situation for characterization and evaluation data within the *ex situ Pisum* community remains complex and heterogeneous, because there is little standardization of descriptor lists and states among collections. The majority of these descriptors and descriptor states form the basis of the current descriptors used by CZE122 and parts have been adopted by CAN004 in their list, but not extensively by other collections.

The situation for the regional collection of AVGRIS (TWN001) is somewhat special in that their holdings predominantly consist of snow pea (*P. sativum* var. *macrocarpum*). In this respect, this regional collection operates more along the lines of a single institution and has undertaken characterization work centrally.

As of August 2022, EURISCO holds 113,762 data points of pea characterization and evaluation data obtained from 87 experiments, each with agreed metadata. The experimental materials comprise 3,394 pea accessions from the Czech Republic, Estonia, The Netherlands and NordGen. In principle, EURISCO already makes it possible to search for a trait across all accessions. The limiting factor is that there is still no generally accepted controlled vocabulary for traits and methods. Also, the IPGRI descriptors are often used in modified forms by different partners (S. Weise, personal communication, August 2022). There has been some movement towards the development of standardized minimum descriptors within a number of ECPGR working groups, who have developed minimum descriptor sets for a wide range of crops, including some grain legumes. To date, however, no minimum descriptor set has been developed for pea. Genesys allows uploading of, and filtering on, descriptor lists.

Discussions with curators as part of this review indicated that insufficient time and a lack of experienced staff were key factors limiting the collection of characterization data at present. With limited resources, some collections have decided to focus on small subsets of highly heritable traits that can assist in quality assurance of genebank management operations. Other collections that are more closely aligned to breeding programs were more likely to support broader characterization and evaluation programs.

The wealth of documented and characterized genetic mutations in *Pisum* and CWR as opposed to cultivated materials has led to extensive elaboration of many more descriptor states for a wide range of existing traits, as well as new descriptors. These capture novel or rare states to the level of specific alleles and individual genetic loci, as can be found in the phenotype descriptors used at GBR247. These additional descriptors and descriptor states are unlikely to be observed in many collections, so will not be taken up more widely. Nevertheless, this information, along with corresponding information for reference lines, is an important part of the data for *Pisum* that are available to the research community.

While phenotypic characterization data has been successfully used in phylogenetic studies on *Pisum*

Table 10.5 Regional PGRFA data portals holding records on *Pisum* germplasm. * Genesys holds descriptor lists for some contributing collections but does not hold characterization data for *Pisum*. Sources accessed on 27 June 2022.

	No. *Pisum* Records	Passport Data	Images	Characterization Data
AVGRIS	187	Yes	Yes	Yes
Seed Saver Exchange	340	No	No	Cultivars
EURISCO	38,914	Yes	Being planned	Yes
GenBIS	2,163	Yes	Yes	Genetic Stocks
GENESYS	59,496	Yes	Yes	No*

(Toker and Sari 2020), the most common points of reference for morphological characterization are the test guidelines and associated documents for cultivated peas produced by UPOV (UPOV Guide for PISUM_SAT, TG/7/10, 2009 and associated CPVO-TP/007/2 Rev.3 (CPVO 2020). These guidelines underpin the testing requirements of Distinctness, Uniformity and Stability (DUS) based on certain sets of characters. These can be used to produce consistent variety descriptions for the assessment and assignment of plant breeders' rights (PBR). The character sets cover plant habit and aspects of morphology including foliage, flowers, pods and seeds. These characters are sufficient to differentiate among various market types, and there are additional descriptors relating to disease assessment and protein content. As a result, these traits are familiar to breeders and many genebanks have used all or some of them in their descriptor sets. Collections focused on advanced cultivars are more likely to develop descriptor lists closely aligned to the UPOV test guidelines, such as those of the LVA009 (UPOV 2009). Specialist collections such as WorldVeg (TWN001) focus on a different subset of traits more aligned to *P. sativum* var. *macrocarpum* pod descriptors. Table 10.6 provides links to the descriptor lists used at individual genebanks.

A cross-sectional analysis was undertaken for 12 descriptor lists from genebanks around the world. These descriptor lists are in the public domain and are focused primarily on morphological, phenological and performance traits covered by the UPOV Guide for *Pisum sativum* (UPOV 2009). A further set used by AUS165 was made available on request for this exercise. The descriptor list published by Pavelková et al. (1986) was not included, as this exercise was focused on current lists, and that of CZE122, which is largely based on the 1986 list. This exercise highlighted the wide diversity of approaches taken with the different descriptor lists, which result in highly collection-specific profiles.

A total of 178 descriptors across the three categories were collated. It is evident that the descriptors are highly divergent among genebanks, that there are diverse approaches used to describe each character, that there is a wide range of terminology used for descriptor states, and that there are many descriptor states for any given trait. The complexity of the current position is highlighted by the large numbers of descriptor states for particular traits: e.g., 15 for growth habit; 27 for flower color; 15 for pod color; and 25 for seed shape. In some cases, quantitative traits such as lengths of tissues are actual measurements while in other cases the measurements are binned in specific ranges, which often differ among collections. In most cases, the descriptions of the particular stage of development and where on the plant the measurements were taken are not sufficiently explicit for comparative purposes. The wide range of approaches is partly because different collections have different holdings and focuses, and partly because the way measurements are taken has changed over time.

Given these findings, there is clearly significant scope for curators of *Pisum* germplasm to work collectively to review this topic in detail, with a view to developing a consensus approach. This will result in the standardization of approaches, terminology and descriptions of methods to record how and under what conditions a descriptor is measured or scored. This will bring about much-needed clarity and will make it easier to cross-reference across characteri-

Table 10.6 Links to pea descriptor lists used at individual genebanks.

Genebank	Source Reference / Website
CAN004	https://pgrc3.agr.gc.ca/cgi-bin/npgs/html/desclist.pl?177
CHL150	http://163.247.128.32/gringlobal/descriptors.aspx
DEU146	https://gbis.ipk-gatersleben.de/gbis2i/faces/index.jsf
CZE122	https://grinczech.vurv.cz/gringlobal/descriptors.aspx, Pavelková A, Moravec J, Hájek D, Bareš I, Sehnalová J, 1986. Descriptor list of the genus *Pisum* L. RICP Prague — Ruzyně, Genové zdroje 32: 46.
GBR247	https://www.seedstor.ac.uk/search-phenotypes.php
ESP004	http://webx.inia.es/web_coleccionescrf/CaracterizacionCRFeng.asp
LBN002	https://www.Genesys-pgr.org/descriptorlists/737e1c1d-4516-4ce6-9dab-4d5db736f4fb
LVA009	http://www.genres.lv/wp-content/uploads/2010/11/6.Peas_.doc
NLD037	Harm Dijkstra and Louis J.M. van Soest, 1986, Descriptor list pulses. CNG Internal Publication.
SWE054	https://sesto.nordgen.org/sesto/index.php?scp=ngb&thm=char_eval&mod=brws_project&pid=53
TWN001	http://seed.worldveg.org/public/download/descriptors/*Pisum*_2015.pdf
USA022	USDA GRIN Pea Descriptor List; https://npgsweb.ars-grin.gov/gringlobal/cropdetail.aspx?type=descriptor&id=177

zation efforts by different institutions. Thus, it will add significant value to the pea germplasm for users wishing to search for specific traits in databases.
The development of crop descriptor lists (Bioversity International 2007) and an analysis of survey and web statistics of their use by major stakeholders (Gotor et al. 2008) have provided useful contextual background to the initiation of such an initiative. The first three of the following bullet points outline non-mutually exclusive elements that might be considered, while the fourth indicates the importance of working across the widest possible range of organizations and linked initiatives to achieve the maximum impact and relevance.

- Minimum Descriptor List (1970s): A limited number of descriptors and descriptor states agreed upon by specific crop communities. Developed to be manageable and achievable.
- Comprehensive Descriptor List (1990s): This approach extends to cover all descriptors for characterization and evaluation for a particular crop. Requires significantly greater cooperation and time to develop.
- Highly Discriminating Descriptors (1994): This category was developed to flag those descriptors that have potential to discriminate between accessions and that are most useful in providing basic indicators of diversity within a collection.
- Key Descriptor Lists (2011): A comprehensive review and revision by Bioversity International, with the financial support of the Global Crop Diversity Trust, resulted in strategic sets of 'key access and utilization descriptors for crops' covering characterization and evaluation descriptors for 22 crops included in Annex I of the ITPGRFA (Alercia 2011). Notably, each crop group held an ontology workshop as part of their review process. The lists were published.

Where possible, it would also be useful to include diagrams and images to clarify descriptor states, and to include a reference standard when a descriptor state is open to interpretation or difficult to explain. Reference standards are used in the UPOV Guide for PISUM_SAT, TG/7/10, 2009 and associated CPVO-TP/007/2 Rev.3 (CPVO 2020).

Curators were very supportive of the need to establish, and recognize the potential benefits from, an *ad hoc* working group on pea descriptors. This project has already been initiated. Membership of the working group has been extended to include researchers and will expand further to include representatives from other disciplines to ensure the discussions and resulting actions have the broadest possible relevance to user communities. The working group has already agreed to explore the potential to scope the integration of such data into other initiatives through the use of plant and crop ontological approaches. AUS122 offered to share their experiences in using phenomics data for pea to help standardize issues involving pigment patterns and color (Nguyen and Norton 2020). One output of such an exercise should be the identification of a minimum descriptor list for pea that can be uploaded to Genesys. The need for a longer list capturing the widest range of descriptors and descriptor states has also been recognized. Pea is an Annex 1 crop of the ITPGRFA, and the ITPGRFA Secretariat has welcomed and supported discussions about descriptors for pea.

Recommendations: *An* ad hoc *working group should be established to review the output of the cross-sectional analysis of descriptor states, with a view to formulating options for revising and standardizing morphological descriptors with reference to the development and adoption of plant and crop ontologies.*

The community should work towards the delivery of a consensus minimum descriptor list for Pisum *that could be agreed upon and adopted by pea collections globally and uploaded into Genesys.*

The working group should liaise with the Secretariat of the ITPGRFA to ensure compliance with current international standards, as far as possible.

Pisum sativum. ICARDA Terbol station.
Photo: Michael Major for Crop Trust

11 DISTRIBUTION AND USE OF GENETIC RESOURCES

The proportions of collections accessible for distribution nationally, regionally and internationally reported in the survey are presented in Table 11.1 and Figure 11.1. Eight collections reported that 100% of their collections were available for distribution at all three levels (CAN004, CHL150, ESP009, FRA043, GBR247, NLD037, POL003 and USA974), with a further seven indicating availability of >90% of their collections for distribution (CHE063, CZE122, ESP004, LVA009, RUS001, SWE054 and TWN001). Four collections cited levels of availability for distribution at <50% (EST019, ITA394, PRT102 and TUR001). In the case of ITA394 and PRT102, this is because their main roles are in breeding and crop improvement at a more local level.

Overall, the majority of respondents who answered this question reported that between 80-100% of the collection was available for national and international distribution (Figure 1.1), although a significant number of respondents also reported that only 0–20% of the collection was available for international distribution.

The collections were asked to identify the main factors limiting the use of their materials. The most frequent answer was the availability of seeds (nine mentions), followed by the lack of characterization and evaluation data (five mentions), and a lack of communication channels with users (three mentions). Some respondents also mentioned legal aspects and low demand.

Headline: The standard material transfer agreement (SMTA) of the International Treaty is widely used in the majority of germplasm transactions and provides a clear and transparent audit trail for user compliance.

Table 11.1 Percentages of accessions accessible nationally, regionally and internationally, as reported in the survey responses.

Institute Code	Nationally	Regionally	Internationally
AUS165	85	85	85
CAN004	100	100	100
CHE063	98	98	98
CHL150	100	100	100
CHN001	100	0	0
CZE122	98	98	98
DEU146	85	85	85
ECU023	0	0	0
ESP004	96	96	96
ESP009	100	100	100
EST019	100	32	32
FRA043	100	100	100
GBR017	100	100	0
GBR247	100	100	100
IND001	68		68
ITA394	9	9	9
JPN183			80
LBN002	70	70	70
LVA009	90	90	90
NLD037	100	100	100
POL003	100	100	100
PRT102	5	10	5
RUS001	90	90	90
RUS255	57	57	57
SRB002	50	10	10
SWE054	97	97	97
TUR001	20	0	0
TWN001	94	94	94
UKR001	81	81	81
USA022	77	77	77
USA974	100	100	100

Users of germplasm are required to undertake due diligence by keeping auditable records relating to the use of PGRFA to demonstrate they have the necessary freedom to operate. This is now a prerequisite for the research and breeding community. *Pisum* is listed under Annex 1 of the ITPGRFA. The institutions located in countries that are party to the Treaty are able to issue SMTAs for *Pisum* material. The SMTA covers uses listed in the terms of the Treaty, namely training, research and breeding for food and agriculture. For all other uses, the default is the terms of the ABS Nagoya Protocol linked to the United Nations Convention of Biological Diversity. Access to germplasm is transacted through the use of material transfer agreements (MTAs or the SMTA) in 91% of institutes that replied to the *Pisum* Survey. Two institutions reported not using MTAs. In the case of VIR (RUS001), this is because there is no domestic legislation with respect to genetic resources, so no clear regulations are specified by the government for VIR to use as guidance. Consequently, VIR is unable to send out duplicates of accessions or distribute materials to requestors. ECU023 reported that the main difficulties in distributing germplasm are a lack of seeds and an external inventory.

During the consultation process, it became evident that the awareness of the complexity of due diligence was quite variable across the genebank community, both in terms of adding new materials into collections and sourcing new wild germplasm. Similarly, there was a range of awareness about compliance and auditing among users of the *Pisum* germplasm.

Recommendation: *It will be of great value to further raise awareness and increase training for genebanks so that they understand the compliance and due diligence requirements of the International Treaty and the Nagoya Protocol.*

All institutions holding *Pisum* germplasm reported that they distribute seeds to users with three exceptions: BRA001, which is a base collection (BRA012 is the active collection that distributes materials); ESP019, which holds a working collection (stock distribution is managed by ESP004); and ECU023, which has insufficient seeds and no electronic inventory accessible to external users. Insufficient quantities of seed to distribute to users was flagged by CHE066 and CHL003. Seed health was cited by only one institution (CHN001) as a problem relating to seed distribution to users.

While the majority of collections (55.5%) reported that they are able to distribute seeds to anyone, 44.5% reported that there were some restrictions as to which groups of users seeds could be distributed to. These were mostly associated with advanced cultivars that were registered and conserved but still covered by PBR. This was the case for AUS165 and USA022, and ITA314 reported that it restricts breeding materials to joint studies or exploitation. Materials from the Heritage Seed Library (GBR017) are restricted to members by subscription, a mechanism developed to ensure their operations comply with EU Seed Legislation.

Facilitated access to germplasm under agreed terms does not necessarily mean free of charge. Operational funding issues were highlighted in a significant number (54%) of survey responses (Chapter 8). Charging for certain elements of germplasm delivery to help offset costs associated with conservation efforts, in particular regeneration, shipping and phytosanitary certificates, has been a discussion point for several years. Charges can negatively affect the utilization and uptake of germplasm, especially for large-scale prospective screening and for individual growers or small companies, but this is mainly managed through the discretionary judgement of

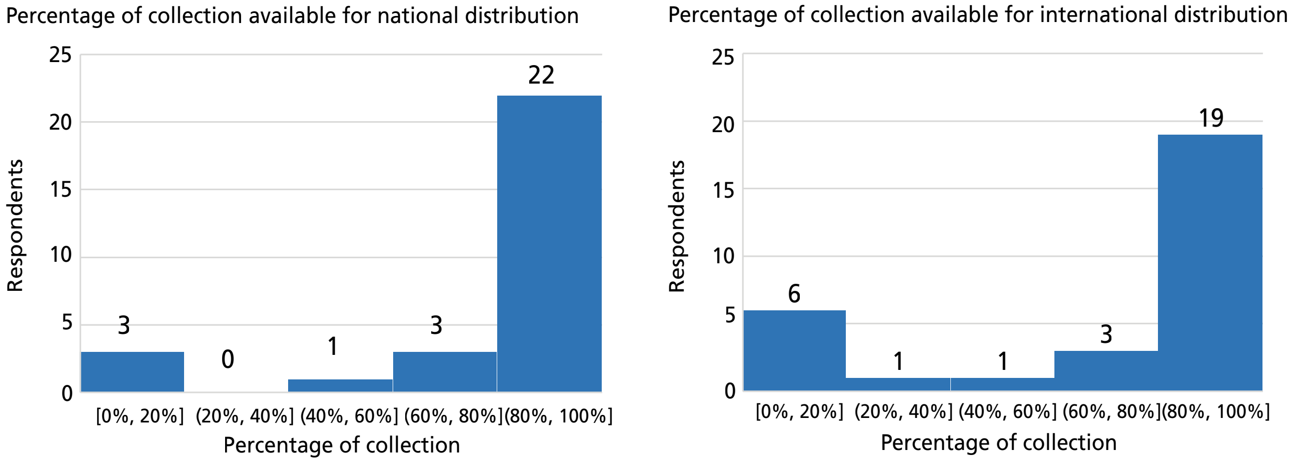


Figure 11.1 Histogram of percentage of collection available for distribution nationally (left) and internationally (right). Responses were binned in five categories.

curators. It has also been argued that the administrative overheads associated with billing and receipt of funds reduces resourcing for other staff and activities.

The survey responses (Table 11.1) revealed that, while 20 collections do not charge for germplasm provision, eight institutions charge for shipping, one charges for the cost of accessions, and three charge for the cost of both accessions and shipping.

Additional information about fees (Table 11.2) revealed that, when fees are charged, there is a high degree of flexibility and discretion as to which groups of users were charged and how the charges are calculated. A number of institutions reported that they do not charge academic/public sector researchers (CHE063, JPN183, PRT102 and SWE054), and SWE054 also extends this to breeders. Other institutions reported that they charge farmers and hobby gardeners (PRT102 and SWE054). GBR017 is an NGO and charges an annual subscription for membership of their Heritage Seed Library entitling members to request stocks. Special cases were also cited as to the final amount billed. Some institutions reported that they do not charge individual users or academia, while others reported scaled charges according to the number of accessions requested (Table 11.2).

Headline: Academic researchers and students are the largest category of users supported by collections.

The survey requested information as to which categories of users institutes supplied germplasm to, over the past three years. The responses are summarized in Table 11.3.

The categories of users supplied with materials varied considerably among the collections. Notably, BRA003 operates as a base collection and does not distribute to users other than restocking other working collections when requested; and statutory collections associated with Plant Variety Rights such as GBE165 do not distribute materials except in certain specific situations. Looking at provision of the germplasm across the collections to each category of users provides some useful summary insights (Figure 11.2). The user group receiving the highest proportion of materials distributed by genebanks was academic researchers and students (33% averaged across all the responding genebanks), and this was also the largest category of users of nine individual institutions. In some cases, this is because the main role of the collection is to underpin research (AUS165, CAN004, CH001, DEU146, FRA043, ITA394 and POL003). The second largest category of users was public plant breeders (receiving 21% of distributed materials, as averaged across the collections), and the next largest was farmers and farmers' organizations (average, 14%), followed by private plant breeders (average, 12%) and other genebank curators (average, 12%). Interestingly, the two classes of plant breeders were nearly always exclusive of each other with only two collections (NLD037 and SRB002) supplying materials to both public and private plant breeders.

The particular focus of the germplasm holdings of certain institutions (specialist or general) as well as their profile and main activities can explain why they supply certain groups of users. One example is ESP109, which is a technology institute working in the agricultural sector translating basic and applied research to industry. Their *Pisum* germplasm consists of landraces of local origin that are distributed equally between private plant breeders and farmers and farmers' organizations. Another example is PRT102, which is located at a university and holds local landraces in its collection. They reported that they distribute 85% of materials to farmers and farmers' organizations,

Table 11.2 Individual institute responses to policy and fee levels.

Inst. Code	Fee Policy and Levels
CHE063	No charge for volunteers, academia, genebanks.
DEU146	Handling fee 10 Euro, 2 Euro per sample. If phytosanitary certificate required 10 Euro.
ESP109	It depends on the destination and the shipping service company.
GBR017	Annual membership fee £54.
GBR247	Ordering up to three accessions is free of charge. £12 (UK sterling) flat fee for 3-10 accessions and £2 per accession thereafter is charged as handling fee.
JPN183	Free distribution to public research institutes.
PRT102	For material transfer agreements, no fees are charged. For local farmers, a fee is charged.
SWE054	Only for hobby gardeners (web shop), 25 SEK/accession. Distribution for breeders and researchers are free.
TWN001	Payment for seed processing and shipping fees (with one (standard airmail free).
UKR001	For scientific purposes, a small amount of seeds (up to 50 seeds) is transmitted subject to payment of shipping costs. Accessions exchange possible.
USA974	Charge for each crop type based on size of seeds.

10% to academic researchers and students and the remaining 5% to other genebanks. Two other institutes with a main focus on germplasm distribution are TUR001, which distributes 100% of materials for domestic public sector breeding and ITA394, which distributes 100% of materials to academic researchers and students.

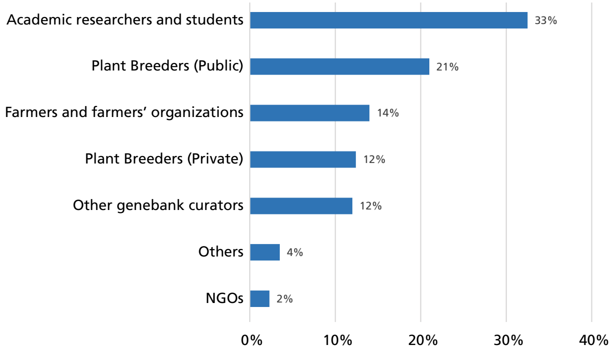


Figure 11.2 Categories of users supplied by respondents of the survey who provided data (n=36).

Table 11.3 Proportion of germplasm (as a % of total distribution) sent to different categories of users in the past three years.

Institute Code	Farmers and farmers' organizations	Other genebank curators	Academic researchers and students	Domestic users	Foreign users	Plant breeders - public sector	Plant breeders - private sector	NGOs
AUS165	0	0	81	97	3	11		0
BGR001		1	1			1		
BRA003	N/A		N/A	N/A	N/A	N/A	N/A	N/A
CAN004			80	70	30	20		
CHE063		5		93				
CHL150								
CHN001	10	10	60	10	0	10	0	0
CZE122	5	30	30	2	20	2	10	1
DEU146		4	55				25	5
ECU023	0	0	0	0	0	0	0	0
ESP004	19	3	17	6	0		13	6
ESP009	30	10	10	10				
ESP109		50					50	
EST019		50		20		30		
FRA043			80	5			15	
GBR017			1	99				
GBR165	N/A	N/A	N/A	N/A	N/A	N/A	N/A	N/A
GBR247	5	5	75			5	5	
IND001			10	6	1	80	1	1
ITA394	0	0	100	0	0	0	0	0
JPN183								
LBN002	20						80	
LVA009		50	50					
NLD037				20		10	40	30
POL003			60	15	5	20		
PRT001								
PRT102	85	5	10					
RUS001	0	0	13	31	0	56	0	0
RUS255		50				50		
SRB002	2	20	10	80	20	80	20	0
SWE054	76	0	5	80	20	3	1	3

Pea harvest in Brazil. Photo: Wenderson Araujo/Trilux

12 GENEBANK COLLABORATIONS AND NETWORKING

Many institutes maintaining PGRFA have been in existence for many years. RUS001 was founded in 1847, IPK in 1943, and CZE122 in 1951, with the others being formed between 1960 and 2017. The most recent to be formed is RUS255 in 2017. There is a long history of collaboration among collections and with organizations in the academic and breeding sectors. When asked about the nature of any ongoing collaborations on aspects of germplasm management apart from safety duplication, 58.3% of collections reported that they have active collaborations in place (Table 12.1).

The majority of collaborations were at the national level but EST019 reported regional collaborations and RUS255 and SRB002 reported international collaborations. The primary areas of collaboration were regeneration, characterization and preliminary evaluation (Figure 12.1). In general, these collaborations provide 'in-kind' benefits to the collections. A significant number of collaborations were in more than one area of genebank management, and in two instances collaborations were underway in three areas (PRT001 and RUS001). Other collaborations included seed storage (POL003 and RUS255) and databases and distribution (POL003). The majority of collaborations involved public academic institutions. NLD037 was an exception, with a collaboration for regeneration with the private sector breeding company Holland-Select B.V.

Some of these collaborations have been ongoing for many years. ESP009 has been collaborating with CRF, INIA-CSIC on regeneration and characterization since 1987, and POL003 has been collaborating with IHAR Radzików on seed storage, databases and distribution since 1978.

Collaborations in the areas of regeneration, characterization and evaluation are essential for the operational management of some institutions. Issues highlighted as part of this review involving limited operational funding, staff shortages and insufficient growing facilities suggest that such collaborations have become an operational necessity. There is also a significant but undocumented benefit in potential users of the germplasm becoming involved in the characterization and evaluation process. Their involvement can facilitate greater use of materials and increased communication and information exchange between the parties. While these collaborations may be mutually beneficial, they lack the assurance that *ex situ* collections require to be able to plan and manage their financial sustainability. Thus, there are potential risks if the benefits to the collections of these 'in-kind'

Table 12.1 Collaborations of genebanks with other genebanks and breeders on aspects of germplasm management apart from safety duplication.

Institute code	Collabora-tion	Name of institution/location	Area of collaboration	Type of collaboration	Starting date and frequency of collaboration
AUS165	Yes	Public	Prelim evaluation, characterization data	National	Annually
BGR001	No				
CAN004	Yes	University if Saskatchwan, Sasakatoon, Canada	Secondary evaluation	National	Annually
CHE063	Yes	National Swiss Genebank	Preliminary evaluation	National	Annually
CHL150	No				
CHN001	Yes				
CZE122	No				
DEU146	Yes				
ECU023	Yes				
ESP004	Yes	ITACYL- Valladolid	Regeneration, characterization	National	Seldom
ESP009	Yes	Plant Genetic Resources Center (CRF,INIA-CSIC)	Regeneration, characterization	National	
ESP109	Yes	Plant Genetic Resources Center (CRF, INIA-CSIC)	Regeneration	National	1987, once every few years
EST019	Yes	Nordgen	Regeneration, evaluation	Regional	
FRA043	No				1995, annually
GBR016					
GBR017	No				
GBR165					
GBR247	No				
IND001	Yes				
ITA394	Yes	University of Bari	Characterization and evaluation	National	2017, annually
JPN183	Yes				
LBN002	No				
LVA009	No				
NLD037	Yes	Holland-Select B.V, NLD (private)	Regeneration	National	
POL003	Yes	IHAR Radzików	Long term storage, database, distribution	National	1978, annually
PRT001	Yes	Estaçao Nacional de Melhoramento de Plantas	Regeneration, characterization, preliminary evaluation	National	Annually
PRT102	Yes	Banco Português de Germoplasma Vegetal	Characterization	National	Seldom
RUS001	Yes	Oryol city, Federal Scientific Center of Legumes and Groat Crops	Regeneration, characterization, preliminary evaluation	National	Annually
RUS255	Yes	USDA, Pullman, Washington	Storage	International	2018, only started, perhaps once every few years
SRB002	Yes	IBERS (public university)	Regeneration, characterization, preliminary evaluation	International	2018, annually
SWE054	Yes	KU Copenhagen	Regeneration, characterization	Regional	2015, once every few years
TUR001	No				
TWN001	No				
UKR001	No				
USA022	Yes	Washington State University/ Pullman, Public	Characterization, evaluation	National	1998, annually
USA974	Yes				

benefits were to be suddenly withdrawn unilaterally.

Collaborations bring many benefits, not only to the institutions directly, but also to the user community in terms of agreed common practices and methodologies. None more so than in the area of documentation, where agreed multi-crop passport descriptors have been in place since 1997.

Recommendation: *In-kind benefits of collaborations between* ex situ *collections and third parties can underpin key operational activities such as regeneration, evaluation and characterization, so they represent a potential risk if they were to be withdrawn suddenly. Collections are encouraged to quantify the nature of these in-kind benefits so they understand their exposure and potential financial shortfall if they are withdrawn.*

12.1 Crop Improvement Networks

In addition to formalized collaborations, genebanks are also involved in a number of public/private crop improvement networks comprising academia, breeders, producers and the retail sector (Table 12.2). The Pulse Genetic Improvement Network (PCGIN), which operates in the UK, is funded by the Department for Environment, Food & Rural Affairs (DEFRA) with the justification that it can capitalize on the output of academic public sector research and translate it to crop improvement, sustainability and healthier eating. A key point of these Genetic Improvement Networks (GINs) is that they explicitly involve the relevant genebank curators and staff to help ensure their knowledge and expertise forms an integral part of the program and discussions. This can provide important feedback on priority issues and future developments within the sector, and highlights the value of engaging with genebanks to the benefit of all parties.

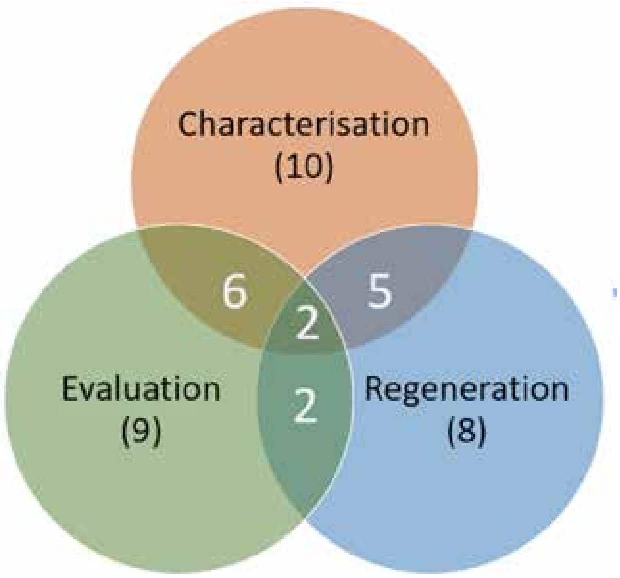


Figure 12.1. Venn diagram showing areas of collaborations with other institutions.

Table 12.2 Crop improvement networks involving peas with genebank participation.

Participating Institutions	Network	Website
GBR165, GBR247	PCGIN: Pulse Crop Improvement Network	www.jic.ac.uk/pulse-crop-genetic-improvement-network-pcgin/
USA022	NAPIA: North American Pulse Improvement Association	www.bic-napia.org/

Tecnicians at ICARDA Terbol station.
Photo: Michael Major for Crop Trust

13 GLOBAL STRATEGY FOR THE CONSERVATION OF *PISUM* GENETIC RESOURCES

Pisum diversity and genetic resource collections

Overall, there are over 130 institutions holding *Pisum* germplasm, conserving about 100,000 accessions. However, more than 80% of these are concentrated in 13 collections and it is difficult to estimate how many of the accessions held *ex situ* are unique. Pavan et al. (2022) found that the proportion of the accessions with at least one duplicate within the same collection was 17% at the Pea Single Plant Plus collection (USDA) and 3% at the collection held by the Italian Council for Agricultural Research and Economics. Most of the *Pisum* Survey's respondents indicated that they consider their collections to be mostly or partially unique. However, we also know that between 1920 and 1980, accessions were widely shared among countries, and that in many cases this information was not recorded in the passport data (Judith Burstin, personal communication).

Improved and additional passport, phenotypic and genetic data will be helpful for assessing the uniqueness of accessions and for further rationalizing of collections and global systems for the conservation of pea genetic resources.

In terms of the number of accessions, the diversity of the collections (i.e., the number of countries of origin represented), and the number of accessions of landraces and CWRs, the following collections are particularly significant: FRA043, RUS001, CHN001, AUS165, USA022, LBN002, DEU146, GBR247, GBR165, POL003, UKR001, SWE054, ITA394, ETH085, ESP109, ITA436, PAK001, CZE122, BGR001, HUN003, NLD037, PRT001 and GBR004. Most of these institutions also maintain their pea collections under long-term conditions, with the exceptions being RUS001, UKR001 and PRT001.

Furthermore, the Kew Millenium Seed Bank maintains a significant collection of wild *Pisum*. The collections at IND001, ESP004, ETH085, CAN04, JPN183, ZMB030, ROM007, ETH123, ECU023 and BOL317 are significant because of their high representation of the diversity of pea materials in the country where they are located. Notably, the low response rate from African genebanks to the *Pisum* Survey means that some important collections in Africa may have not been identified.

Priority action 1: Establish a global pea working group with representatives from key collection holders, breeders and research institutions

We recommend establishing a global pea working group with representatives from key collection holders, breeders, research institutions, and existing relevant networks such as the ECPGR grain legumes working group, PCGIN and NAPIA. An additional *ad hoc* working group (see priority 4) could be established to work on specific technical issues related to the conservation of pea genetic resources. The global pea working group could then take leadership in implementing this strategy, and specifically the priority actions described in this chapter. The global pea working group could also take responsibility for future updates of the global conservation strategy for pea genetic resources.

Priority action 2: Rationalize the global *Pisum* collection

We recommend to rationalize collections by increasing data accessible on international PGRFA portals, improving passport data completeness, using digital object identifiers (DOIs), and genotyping all *Pisum* accessions conserved *ex situ* in key collections. These activities will create a global core collection and identify unintended duplicates. We also recommend to establish written procedures and protocols to cover all routine operations in key *Pisum* collections.

Documentation and information sharing for Pisum *genetic resources*

The majority of collections have electronic information systems in place for use in stock control management, but the proportion of data computerized within collections and within types of data (passport, characterization and evaluation data) varies greatly among collections. To facilitate access to information and the use of materials, and to rationalize *Pisum* collections, it is recommended to further increase the percentage of passport, characterization and evaluation data that is available in electronic format in databases, increase the use of DOIs, and increase the percentage of genotyped accessions in the collections. These data can be used to identify duplicates within and among collections, which will be useful for rationalization.

There is a need to have a common database for information regarding *Pisum* genetic resources to better assess and rationalize the composition of collections at the global level. We found that national, regional and international data portals are helping to add value to individual collections and are now an integral component in PGRFA awareness and supply. Therefore, it is recommended that coverage of *Pisum* collections accessible on international PGRFA portals is increased to include *Pisum* collections that are not yet sharing their data.

As of June 2022, 34% of accessions recorded in Genesys and WIEWS lack information on biological type (the SAMPSTAT field in Multi Crop Passport Descriptors). In some cases, the information on country of origin is obsolete and does not reflect current national jurisdictions. This hinders a more precise assessment of the gaps in *ex situ* collections. Verifying the biological type, and updating passport records to reflect current national jurisdictions while preserving the original data when the accessions were collected will help to improve the quality of estimates of coverage and gaps in future studies.

Recent studies on CWR have identified significant numbers of accessions for which the records are not yet uploaded into regional or central PGRFA portals. Action should be taken to ensure that such data are uploaded to central portals to enable better estimates of germplasm coverage and the identification of gaps where further collections may be required. More collections are encouraged to participate and upload data into regional PGRFA portals, and Genesys in particular. Both are highly desirable for the conservation and user communities to enable more efficient monitoring of *Pisum* germplasm holdings, and would ease the burden on collections managers continually having to respond to data requests.

Genotyping of all accessions in key Pisum *collections*

In rationalizing the global collection of *Pisum* genetic resources, a priority should be to genotype *Pisum* accessions from as many genebanks as possible and include detailed information about the geographical and environmental distribution of *Pisum* genetic resources. Such initiatives would identify unintended duplicates and would also support the use of *Pisum* genetic resources. This effort should give priority to the largest collections identified in this document, as these collections likely cover most of the *Pisum* diversity conserved in genebanks.

Management systems and conditions at Pisum *collections*

Another finding of the survey is that some genebank operations are less covered by management systems or written procedures and protocols than others. This creates a risk in terms of the quality of the operations and transfer of knowledge within these organizations, and may undermine the trust of users who want to access PGRFA.

Written procedures and protocols that cover routine operations in all the key *Pisum* collections should be prepared and shared among collection holders. This will enable the genebanks to identify gaps in procedures, harmonize quality control points, and facilitate the onboarding of new staff. Ultimately, standardized and transparent procedures will increase user confidence when requesting and utilizing germplasm. Harmonization efforts will also allow genebanks to optimize the efficiency of their operations and reduce costs. As mentioned above, efforts should be made to rationalize collections through the elimination of unintended duplicate accessions (at a global level). To this end, capacity-building events could be organized for the *Pisum* community, with a focus on selected topics such as protocol-writing, genotyping, passport data management, traceability and barcoding. These events would develop and strengthen skills while maximizing knowledge exchange and opening dialogue about priorities.

Priority action 3: Acquisition priorities

In terms of the composition of the collections, the analyses revealed that landraces from some countries are underrepresented in *ex situ* collections. Similarly, pea CWR from some countries within their area of distribution are underrepresented *ex situ*.

Further collections of cultivated pea should prioritize landraces from Azerbaijan and Turkmenistan in the Caucasus; Southeast Asia; Iran in western Asia; South Africa, Kenya, and Malawi in Africa; Iraq, Israel, Jordan, Lebanon and Palestine in the Middle East; and Estonia, Lithuania, Finland, Norway and Belarus in Europe. Further collections of *P. elatius* should prioritize North Africa, Iran and Jordan, and of *P. fulvum* should prioritize Turkey.

Priority action 4: Establish an *ad hoc* working group to formulate options for revising and standardizing morphological descriptors with reference to the development and adoption of plant and crop ontologies

A cross-sectional analysis of descriptor lists from genebanks from around the world has highlighted the wide diversity of approaches taken in the past. This has resulted in highly collection-specific descriptors. Thus, there is a need to standardize approaches, terminology and descriptors, and the description of methods.

A dedicated *ad hoc* working group should work towards the specific delivery of a consensus Minimum Descriptor List for *Pisum* that could be agreed upon, and adopted by, pea collections globally and uploaded into Genesys. The working group should liaise with the Secretariat of the ITPGRFA to ensure compliance as far as possible with current international standards.

Photo: Bill Ebbesen/Wikipedia

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ACRONYMS, ABBREVIATIONS AND WEBSITES

AEGIS	European Genebank Integrated System (www.ecpgr.cgiar.org/aegis)
AQUAS	Quality System for AEGIS (www.ecpgr.cgiar.org/aegis/aquas/overview)
AVGRIS	Database at WorldVeg (genebank.worldveg.org)
BMEL	Federal Ministry of Food and Agriculture, Germany
CBD	Convention on Biological Diversity
CGIAR	Consultative Group on International Agricultural Research
CIAT	International Center for Tropical Agriculture (www.ciat.cgiar.org/)
Core Selection	www.wur.nl/en/Research-Results/Statutory-research-tasks/Centre-for-Genetic-Resources-the-Netherlands-1/Core-selections.htm
CRF, INIA-CSIC	Centro Nacional de Recursos Fitogenéticos
CWR	Crop Wild Relatives
DivSeek	www.divseekintl.org
ECPGR	European Cooperative Programme for Plant Genetic Resources (www.ecpgr.cgiar.org)
EURISCO	The European Search Catalogue for Plant Genetic Resources
GBIS	Genebank Information System
GCP	Generation Challenge Programme
GINs	Genetic Improvement Networks
GENESYS	www.Genesys-pgr.org
GLIS	Global Information System
GRIN	Germplasm Resources Information Network
ICARDA	International Center for Agricultural Research in Dry Areas
IPGRI	International Plant Genetic Resources Institute
IPK	Leibniz Institute of Plant Genetics and Crop Plant Research
IHAR	Plant Breeding and Acclimatization Institute, Poland
INRAE	Institute for Agriculture, Food and Environment, France

ITPGRFA	International Treaty on Plant Genetic Resources for Food and Agriculture (www.fao.org/plant-treaty/)
IUCN	International Union for Conservation of Nature
JIC	John Innes Centre
NGO	Non-governmental Organization
MLS	Multilateral System
MSB	Millennium Seed Bank
MTA	Material Transfer Agreement
NAPIA	North American Pulse Improvement Association (www.bic-napia.org)
NBPGR	National Bureau of Plant Genetic Resources, India
NORAD	Norwegian Agency for Development Cooperation (www.norad.no)
NP	Nagoya Protocol on Access and Benefit-Sharing (www.cbd.int/abs)
PBR	Plant Breeders' Rights
PCGIN	Pulse Crop Improvement Network (www.jic.ac.uk/pulse-crop-genetic-improvement-network-pcgin/)
PGR	Plant Genetic Resources
PSPPC	USDA Pea Single Plant Plus Collection
QMS	Quality Management System
SD	Safety Duplicates
SGRP	System-wide Genetic Resources Programme
SGSV	Svalbard Global Seed Vault
SMTA	Standard Material Transfer Agreement
SOP	Standard Operating Procedure
USDA	United States Department of Agriculture
UPOV	International Union for the Protection of New Varieties of Plants (www.upov.int/portal/index.html.en)
WIEWS	World Information Early Warning System for Plant Genetic Resources for Food and Agriculture (www.fao.org/wiews/en/)

ANNEXES

Annex 1. *Pisum* Conservation Strategy Survey

Increasing Efficiency and Effectiveness of the Conservation of Genetic Resources of the Pisum genus

Background

The Global Crop Diversity Trust ("The Trust") is supporting efforts to develop strategies for the more efficient and effective conservation of crop diversity, particularly in *ex situ* collections. The Trust has commissioned an independent external consultant (Mike Ambrose) to coordinate the development of a conservation strategy for crops of the *Pisum* genus. This questionnaire has been developed in order to seek the advice and input of representatives of relevant stakeholders around the world in the development of the conservation strategy. In particular, the questionnaire seeks to assess the status of the conservation and management of crop genetic resources of the *Pisum* genus throughout the world.

If you curate a collection that includes accessions of the *Pisum* genus, we kindly ask you to complete all sections of the questionnaire. If there are no *ex situ* collections of the *Pisum* genus in your institute, please complete sections 10-11 only. Please return the questionnaire to our external consultant as soon as possible but **not later than May 15, 2020**.

The Crop Trust are keen to have your active participation in the development of the conservation strategy of crops of the *Pisum* genus and will be pleased to keep you informed on its progress and consult you during the development until completion. If you have any questions about this questionnaire or about the proposed strategy in general, please contact; mike.ambrosepgr@outlook.com

1. ORGANIZATION INFORMATION:

Name and address of organization holding/maintaining the *Pisum* collection
Address:
City:
Postal Code:
Country:
Web site:
Curator in charge of the *Pisum* collection:
Name:
Address:
City:
Telephone:
Fax:
Email:
Name of respondent to this questionnaire if not as above
Contact details:
Date of response:

1.2 Additional key contact persons for the above germplasm collections:

Name	Title/Function	Email Address

1.3 Please describe the organization:

1 Governmental organization
1 University
1 Private organization
1 NGO or charity
1 Other: please describe: ____

1.4 Is the institution in charge of the *Pisum* collection the legal owner of the collection?

…. yes …. no

2. OVERVIEW OF THE PISUM COLLECTION:

2.1 Main objective of the collection (long-term conservation, working collection, breeding collection, reference collection)

____

Other. Please specify

2.2 Please indicate the % proportion of accessions by type of germplasm:

Type of germplasm (where known)	Number of species	Number of accessions	% available for distribution
Wild related species			
Landraces			
Obsolete improved varieties			
Advanced improved varieties			
Breeding/research materials			
Specialist Genetic Stocks			
Unknown			
Other, specify:			

2.3 To assist in developing an overview of specific subsets of *Pisum* germplasm could your report on the number of accessions today as per the following taxa;

Pisum fulvum
Pisum abyssinicum
Pisum sativum ssp. *elatius* var. *elatius*
Pisum sativum ssp. *elatius* var. *pumilio*
Pisum sativum ssp. *elatius* var. *brevipedunculatum*

2.4 Origin of the collection: please indicate the proportion (%) of accessions on the total amount that were:

	Percentage %
- collected originally in your own country (national origin)	
- collected originally in your own region (regional origin)	
- introduced from a collection abroad	
- from other origin (please define):	

2.5 Has your *Pisum* collection at least partially been screened for biotic stresses?

……yes …..no

If yes, for which major diseases or insect pests?

2.6 Has your *Pisum* collection at least partially been screened for abiotic stresses?

….yes …..no

If yes, for which abiotic stresses?

2.7 Has there been any genotyping or marker studies conducted on your *Pisum* collection?

….yes ….in the planning stage …. No

2.8 Please describe the main potential/importance of your collection for use and breeding:

3. CONSERVATION STATUS (GERMPLASM MANAGEMENT):

3.1. Conservation facilities:

Please indicate the proportion of the accessions maintained under: (Note: if accessions are maintained under more than one storage condition the total percentage may exceed 100%)	Percentage %
Short-term storage conditions	
Medium-term storage conditions	
Long-term storage conditions	
Other, please specify:	

3.2 Please describe the storage facilities (if more than one, please use the different columns):

	Facility 1	Facility 2	Facility 3 etc.
Type of facilities:			
Temperature:			
Relative Humidity (%):			
Packing material:			
Other, please specify:			

3.3 Have you established a genebank management system or written procedures and protocols for:

….. Acquisition (*including collecting, introduction and exchange*)
….. Regeneration
….. Characterization
….. Storage and maintenance
….. Documentation
….. Health of germplasm
….. Distribution
….. Safety-duplication
….. Other please specify: ____

3.3.1 In case you have procedures and protocols, are you able to provide the Global Crop Diversity Trust with this information (i.e. provide a copy)?

…. yes …. no

3.4 Describe your quality control activities (in terms of frequency, protocols/methods and actions upon results):

Germination tests	
Viability testing	
Health testing	
Other, please specify:	

3.5 Is the collection affected by diseases that can restrict the distribution of the germplasm?

…. yes …. slightly, only few accessions …. no

3.6.1 If yes or slightly, are knowledge and facilities available at your institution for eradication of these diseases?

…. yes …. limited …. no

3.6 Please indicate the proportion (%) of the collection that requires urgent regeneration (apart from the normal routine regeneration):

Type of germplasm	% of accessions with urgent regeneration need
Wild species	
Landraces	
Obsolete improved varieties	
Advanced improved varieties	
Breeding/research materials	
Unknown	
Other, specify:	

3.7 Please indicate the current and expected situations of the collection with respect to the following factors, where:

1 = high/good, 2 = adequate/moderate, 3 = not sufficient/bad, NA = not applicable:

Factors	Current situation	Expected situation in 2010
Funding for routine operations and maintenance		
Retention of trained staff		
Interest for Plant Genetic Resource Conservation by donors		
Genetic variability in the collection as needed by users/breeders		
Access to germplasm information (passport, characterization, evaluation)		
Active support/feedback by users		
Level of use by breeders		
Level of use by researchers		
Other factors (please specify):		

4. SAFETY DUPLICATION

(defined as the storage of a duplicate/copy of an accession in another location for safety back-up in case of loss of the original accession):

4.1 Are accessions safety-duplicated in another genebank?

..... yes ..... no

4.1.1 If yes, please specify:

Name of institute maintaining your safety duplicates:	Number of accessions	Storage conditions (short, medium, long term)	Nature of the storage (e.g. black box, fully integrated in host collection, etc.)
Add lines as necessary			

4.2 Is there any germplasm of other Pisum collections safety-duplicated at your facilities?

.... yes .... no

4.2.1 If yes, please specify:

Name of holder of the original collection:	Number of accessions	Storage conditions (short, medium, long term)	Nature of the storage (e.g. black box, fully integrated in host collection, etc.)
Add lines as necessary			

4.3 To what extent do you consider the *Pisum* accessions in your collection to be unique and not duplicated extensively elsewhere (i.e. EXCLUDING safety-duplication)?

Are there any specific aspects relating to these unique accessions that are associated with this attribution e.g., National heritage, genetic stocks or host differentials.

..... Fully unique
..... Mostly unique
..... Partially unique
..... Fully duplicated elsewhere

4.4 Are there any constraints to duplicating the collection elsewhere outside your country?

.... yes ..... no

4.4.1 If yes, please specify. ____

5. INFORMATION MANAGEMENT:

5.1 Do you use an electronic information system for managing the collection (data related to storage, germination, distribution, etc.)?

..... yes ..... partly ..... no

5.1.1 If yes, what software is used? ____

5.2 Please indicate the proportion (%) of the following types of data is: (1) physically documented (in paper form) and (2) the proportion that is available in electronic format:

1. Type of germplasm	Passport data	Characterization data	Evaluation data			
	Doc.	Electr.	Doc.	Electr.	Doc.	Electr.
Wild species	%	%	%	%	%	%
Landraces	%	%	%	%	%	%
Obsolete improved varieties	%	%	%	%	%	%
Advanced improved varieties	%	%	%	%	%	%
Breeding/research materials	%	%	%	%	%	%
Unknown	%	%	%	%	%	%
Other, specify:	%	%	%	%	%	%

5.3 In case the collection is not computerized, are there plans to do so in the future?

..... No plans
..... Computerization planned within 3 years
..... Other

5.4 Is information of the collection accessible through the Internet?

..... yes ..... partly ..... no

5.5 Are data of the collection included in other databases?

- National ..... yes ..... partly ..... no
- Regional ..... yes ..... partly ..... no
- International ..... yes ..... partly ..... no

5.5.1 If yes or partly, specify the databases: ____

6. DISTRIBUTION AND USE OF MATERIAL:

6.1 What proportion (%) of the total collection is AVAILABLE for the following distributions?

Nationally: __________ Regionally: ___________% Internationally: __________%

6.1.1 Please fill in the number of accessions DISTRIBUTED annually, and indicate any expected change over the next 3-5 years, where: + = increasing 0 = no change - = decrease

	Number of accessions distributed annually (average of last 3 years)	Expected change for the next 3-5 years
Nationally		
Regionally		
Internationally		

6.2 Regarding the amounts of seed, do you set specific conditions for distribution? Please specify:

6.3 Is the germplasm sufficiently available in terms of QUANTITY for distribution?

Seeds: .... yes .... partly .... no
Other, please specify: .... yes .... partly .... no

6.4 Is the germplasm sufficiently available in terms of HEALTH for distribution?

.... yes .... partly .... no

6.5 Do you have adequate procedures in place for:

Phytosanitary certification?	…. yes	…. no
Packaging?	…. yes	…. no
Shipping?	…. yes	…. no
Other, please specify:	…. yes	…. no

6.6 Do you keep records of the distribution?

…. yes …. No

6.7 Which type of the following users received germplasm from you in the past 3 years?

Type of users:	Proportion of total distribution %
Farmers and farmers' organizations	
Other genebank curators	
Academic researchers and students	
Domestic users	
Foreign users	
Plant breeders - public sector	
Plant breeders - private sector	
NGOs	
Others, please specify:	

6.8 How do you inform potential users about the availability of accessions and their respective data in your collection?

6.9 What are the most important factors limiting the use of the material maintained in your collection?

6.10 Please describe your policy regarding accessibility and distribution of Pisum germplasm:

Cost of accessions:	…. free	…. cost: ____________
Cost of shipment:	…. free	…. cost: ____________
Cost of phytosanitary/growing season inspections:	…. free	…. cost: ____________

6.10.1 Do you have any restrictions on who can receive materials?

…. yes …. no

If yes, please specify:

7. MAJOR CONSTRAINTS:

Please list the five major limitations you are facing in the management of the collection:

1. ________________________________
2. ________________________________
3. ________________________________
4. ________________________________
5. ________________________________

8. Collaboration with other genebanks and/or breeders of the public or private sector in terms of germplasm management?

8.1 Does your genebank collaborate with other genebanks and/or breeders of the public and/or private sector on aspects of germplasm management (regeneration, characterization, preliminary evaluation), apart from safety duplication?

1 Yes 1 No

8.1.1 If yes, please provide the following information on your collaboration: (A) Name, location and type of institution or organization, (B) Type of collaboration (national, regional, international), (C) Area of collaboration, (D) Frequency of collaboration.

A – Name of institution: Location: Type (public or private):	B – Type of collaboration (national, regional, international):	C – Area of collaboration (regeneration, characterization, preliminary evaluation):	D – Starting date and frequency of collaboration (annually, once every few years, seldom):

9. NETWORKS OF *PISUM* GENETIC RESOURCES:

9.1 Do you collaborate in (a) network(s) as a *Pisum* collection holder?

…. yes …. no

9.1.1 If yes, please provide the following information for each of the networks: (A) name, (B) type (national, regional or worldwide), (C) main objectives and (D) a brief description of the main reasons to participate in the network.

A- Name of network	B - National/ Regional/ World-wide	C - Objectives	D - Reasons for participation

10. QUESTION CONCERNING INSTITUTES NOT MAINTAINING *EX SITU* COLLECTIONS OF *PISUM*:

If your institute does not maintain an *ex situ* collection of *Pisum*, please help us by indicating to the best of your knowledge, the following:

Current conservation activities:

Institute focal person to contact for further details:

Plans for any ex situ conservation:

Any other information:

11. PLEASE ADD ANY FURTHER COMMENTS YOU MAY HAVE:

Please return the questionnaire to the (mike.ambrosepgr@outlook.com) as soon as possible but not later than May 15, 2020.

Annex 2. Details of 37 institutions who completed the *Pisum* Survey.

Institute Code	Name of Organization	Address	Name	Type of Organization
AUS165	Agriculture Victoria - Australian Grains Genebank	110 Natimuk Road, Horsham, Victoria, Australia	Sally Norton	Governmental
BGR001	Institute of Plant Genetic Resources	2 Druzhba street, Sadovo, Plovdiv, Bulgaria	Sofia Petrova	Governmental
BRA003	Embrapa Recursos Genéticos e Biotecnologia	Parque Estação Biológica, PqEB, Av. W5 Norte (final), Brasilia, Brazil	Juliano Gomes Padua	Governmental
CAN004	Agriculture and Agri-Food Canada, Plant Gene Resources of Canada	107 Science Place, Saskatoon, SK, S7H2H8, Canada	Axel Diederichsen	Governmental
CHE063	ProSpecieRara	Unter Brüglingen 6, Basel, CH-4052, Switzerland	Mira Langegger	NGO
CHL150	INIA	Vicente Méndez 515, Chillán, Vilcún, Región de Ñuble, Chile	Rodrigo Diaz	Governmental
CHN001	Institute of Crop Sciences, Chinese Academy of Agricultural Sciences	No.12 Zhong Guan Cun South Avenue, Haidian District, Beijing, China	Zong Xuxiao	Governmental
CZE122	Crop Research Institute	Drnovska 507/73, Olomouc, Czech Republic	Miroslav Hybl	Governmental
DEU146	Leibniz Institute of Plant Genetics and Crop Plant Research (IPK)	Corrensstrasse 3, Gatersleben, Saxony Anhalt Germany	Ulrike Lohwasser	Governmental
ECU023	Instituto Nacional de Investigaciones Agropecuarias INIAP	Av. Eloy Alfaro N30 350 y Av. Amazonas. Edif. MAGAP 4th floor. Quito, Pichincha, Ecuador	Alvaro Monteros	Governmental
ESP004	CRF, INIA-CSIC (Spanish Plant Genetic Resources Center, The National Institute for Agricultural and Food Research and Technology)	FINCA LA CANALEJA, Autovía de Aragón km 36, Alcalá de Henares. Madrid, Spain	Lucía De la Rosa Fernández	Governmental
ESP009	MBG-CSIC	El Palacio-Salcedo. Carballeira 8, Pontevedra. Spain	Antonio De Ron	Governmental
ESP109	Instituto Tecnológico Agrario de Castilla y León	Ctra. Burgos Km. 119, Valladolid, Spain	Abel Barrios Casado	Governmental
EST019	Estonian Crop Research Institute	J. Aamisepa 1, Jõgeva, Estonia	Külli Annamaa	Governmental
FRA043	INRAE - UMR Agroecology	17 rue Sully, Dijon, France	Nadim Tayeh	Governmental
GBR016	Genetic Resources Unit, Institute of Biological, Environmental & Rural Sciences, Aberystwyth University	Plas Gogerddan, Aberystwyth, Ceredigion, Wales, SY23 3EB, United Kingdom	Lin Huang	Governmental
GBR017	Garden Organic (Heritage Seed Library)	Wolston Lane, Coventry, United Kingdom	Catrina Fenton	NGO
GBR165	SASA	Roddinglaw Road, Edinburgh, Midlothian, EH12 9FJ, United Kingdom	Lesley McCarthy	Governmental
GBR247	The John Innes Centre	Norwich Research Park, Norwich, United Kingdom	Noam Chayut	Independent Research Organisation
IND001	ICAR-National Bureau of Plant Genetic Resources, New Delhi, India	ICAR-NBPGR, Pusa Campus New Delhi 110012, New Delhi, India	Neeta Singh	Governmental
ITA394	Council for Agricultural Research and Economics (CREA), Research Centre for Animal Production and Aquaculture	viale Piacenza 29, Lodi, Italy	Paolo Annicchiarico	Governmental
JPN183	Genetic Resources Center (NARO Genebank)	Kannondai 2-1-2, Tsukuba-shi, Ibaraki-ken, Japan	Norihiko Tomooka	Governmental
LBN002	ICARDA	Dalia Building, Verdun, Terbol, Beirut, Lebanon	Ali Shehadeh	Governmental
LVA009	Latvian Gene Bank, Latvian State Forest Research Institute "Silava"	Rigas 111, Salaspils, Latvia	Dainis Rungis	Governmental
NLD037	Centre for Genetic Resources the Netherlands	Droevendaalsesteeg 1, Wageningen, The Netherlands	Noor Bas	Governmental
POL003	Poznań Plant Breeders Ltd, Wiatrowo Branch	Wiatrowo, Poznań, Poland	Wojciech Święcicki	Governmental

Institute Code	Name of Organization	Address	Name	Type of Organization
PRT001	Banco Português de Germoplasma Vegetal/INIAV	Quinta de São José, São Pedro de Merelim, Braga, Portugal	Filomena Rocha	Governmental
PRT102	ISOPlexis Universidade da Madeira	Campus Universitário da Penteada, Funchal, Madeira, Portugal	Humberto Nóbrega	University
RUS001	The NI Vavilov All-Russian Institute of Plant Genetic Resources 4	42, 44, Bolshaya Morskaya Str., St. Petersburg, Russian Federation	Margarita Vishnyakova	Governmental
RUS255	Institute of Cytology & Genetics of the Siberian Branch of the Russian Academy of Science	Academician Lavrentyev Avenue 10, Novosibirsk, Russian Federation	Oleg Kosterin	Governmental
SRB002	Institute of Field and Vegetable Crops	Maksima Gorkog 30, Novi Sad, Vojvodina, Serbia	Djura Karagic	Governmental
SWE054	NordGen, Nordic Genetic Research Centre	Box 41, Alnarp, Scania, Sweden	Ulrika Carlson-Nilsson	Governmental
TUR001	Aegean Agricultural Research Institute	35661 Menemen, Izmir, Turkey	Eylem Tuğay Karagül	Governmental
TWN001	World Vegetable Center	P. O. Box 42, Shanhua, Tainan, Taiwan, Province of China	Jessica Chang	NGO
UKR001	Plant Production Institute named after V.Ya. Yuriev of NAAS	Moskovskyi Ave. 142, Kharkiv, Ukraine	Nadiia Vus	Governmental
USA022	USDA Western Regional Plant Introduction Station	59 Johnson Hall, Pullman, Pullman, WA 99164-6402, USA	Clarice Coyne	Governmental
USA974	Seed Savers Exchange	3094 North Winn RD, Decorah, Iowa, USA	Philip Kauth	NGO

Annex 3. List of all taxon labels found recorded in Gensys and WIEWS for *Pisum* and standardized taxa.

Taxon as found in database	Standardized taxa
Pisum abyssinicum	*Pisum abyssinicum* A. Braun
Pisum abyssinicum var. *vavilovianum*	*Pisum abyssinicum* A. Braun
Pisum arvense	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum arvense L.	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum arvense subsp. *abyssinicum*	*Pisum abyssinicum* A. Braun
Pisum arvense subsp. *elatius*	*Pisum sativum* subsp. *elatius* (M. Bieb.) Asch. & Graebn.
Pisum arvense subsp. *humile*	*Pisum sativum* var. *pumilio* Meikle
Pisum arvense subvar. *ecaducum*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum arvense var. *abyssinicum*	*Pisum abyssinicum* A. Braun
Pisum arvense var. *ecirrosum*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum arvense var. *glaucospermum*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum arvense var. *roseum*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum arvense var. *ruminatum*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum arvense var. *seminanum*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum arvense var. *spesiosum*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum arvense var. *viridipunctata*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum arvense var. *vitellinum*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum arvense var. *vulgatum*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum arvense var. *abissinicum*	*Pisum abyssinicum* A. Braun
Pisum arvense var. *contecstum*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum arvense var. *majakense*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum arvense var. *medullare*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum arvense var. *spesiosum*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum arvense var. *stabilisum*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum ekadukum L. var. *ekadukum*	*Pisum sativum* L.
Pisum elatius	*Pisum sativum* subsp. *elatius* (M. Bieb.) Asch. & Graebn.
Pisum fulvum	*Pisum fulvum* Sm.
Pisum fulvum L.	*Pisum fulvum* Sm.
Pisum fulvum Pisum	*Pisum fulvum* Sm.
Pisum humile	*Pisum sativum* var. *pumilio* Meikle
Pisum jomadri	*Pisum sativum* subsp. *jomardii* (Shrank) Kosterin
Pisum jomardi	*Pisum sativum* subsp. *jomardii* (Shrank) Kosterin
Pisum jomardii	*Pisum sativum* subsp. *jomardii* (Shrank) Kosterin
Pisum L.	*Pisum* sp.
Pisum macrocarpum Ser. ex Schur	*Pisum sativum* var. *macrocarpum* Ser.
Pisum Pisum sativum	*Pisum sativum* L.
Pisum Pisum sativum convar. *vulgare* Alef subvar. *gratioso-glaucum* var. *gratiosum*	*Pisum sativum* L.
Pisum Pisum sativum ssp. *sativum* c. *sativum*	*Pisum sativum* L.
Pisum Pisum sativum ssp. *sativum* c. *speciosum*	*Pisum sativum* L.
Pisum Pisum sativum ssp. *sativum* conv.	*Pisum sativum* L.
Pisum Pisum sativum ssp. *sativum* convar. *sativum*	*Pisum sativum* L.
Pisum Pisum sativum subsp. *sativum* convar. *medulare* var. *pliculum*	*Pisum sativum* L.
Pisum Pisum sativum var. *ponderosum* Alef, subvar. *ponderosum*	*Pisum sativum* L.
Pisum pumilio (Meikle)	*Pisum sativum* var. *pumilio* Meikle
Pisum sativum	*Pisum sativum* L.
Pisum sativum 'Merveille de Kelvedon'	*Pisum sativum* L.
Pisum sativum arvense	*Pisum sativum* var. *arvense* (L.) Poir.

Taxon as found in database	Standardized taxa
Pisum sativum asiaticum	*Pisum sativum* subsp. *asiaticum* Govorov
Pisum sativum c. *sativum* var. *ponderosum* subvar. *ponderosum*	*Pisum sativum* L.
Pisum sativum cinerium	*Pisum sativum* L.
Pisum sativum conv. *medullare*	*Pisum sativum* L.
Pisum sativum conv. *sativum*	*Pisum sativum* L.
Pisum sativum convar. *axiphium*	*Pisum sativum* var. *macrocarpum* Ser.
Pisum sativum convar. *Fganicum*	*Pisum sativum* L.
Pisum sativum convar. *medullare*	*Pisum sativum* L.
Pisum sativum convar. *medullo sacharatum*	*Pisum sativum* L.
Pisum sativum convar. *sativum*	*Pisum sativum* L.
Pisum sativum convar. *sativum* var. *glaucosperm*	*Pisum sativum* L.
Pisum sativum convar. *sativum* var. *mesomelane*	*Pisum sativum* L.
Pisum sativum convar. *sativum* var. *superfluens*	*Pisum sativum* L.
Pisum sativum convar. *speciosum*	*Pisum sativum* L.
Pisum sativum convar. *vulgare* subvar. *gratioso-glaucum* var. *gratiosum*	*Pisum sativum* L.
Pisum sativum elatius	*Pisum sativum* var. *elatius* (M. Bieb.) Alef.
Pisum sativum L.	*Pisum sativum* L.
Pisum sativum L. convar. *sativum*	*Pisum sativum* L.
Pisum sativum L. Partim	*Pisum sativum* L.
Pisum sativum L. subsp. *arvense*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum sativum L. subsp. *sativum*	*Pisum sativum* L.
Pisum sativum L. var. cirroso-*sativum*	*Pisum sativum* L.
Pisum sativum L. var. *sativum*	*Pisum sativum* L.
Pisum sativum sativum	*Pisum sativum* L.
Pisum sativum siberiacum	*Pisum sativum* L.
Pisum sativum ssp. *abyssinicum*	*Pisum abyssinicum* A. Braun
Pisum sativum ssp. *asiaticum*	*Pisum sativum* subsp. *asiaticum* Goverov
Pisum sativum ssp. *sativum*	*Pisum sativum* subsp. *sativum* L.
Pisum sativum ssp. *sativum* var. *arvense*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum sativum ssp. *transcaucasicum*	*Pisum sativum* subsp. *transcaucasicum* Govorov
Pisum sativum subsp. *abyssinicum*	*Pisum abyssinicum* A. Braun
Pisum sativum subsp. *abyssinicum* var. *vavilovianum*	*Pisum abyssinicum* A. Braun
Pisum sativum subsp. *abyssinicum* var. *viridulogriseum*	*Pisum abyssinicum* A. Braun
Pisum sativum subsp. *arvense*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum sativum subsp. *arvense sativum*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum sativum subsp. *arvense* var. *arvense*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum sativum subsp. *asiaticum*	*Pisum sativum* subsp. *asiaticum* Govorov
Pisum sativum subsp. *biflorum*	*Pisum sativum* subsp. *elatius* (M. Bieb.) Asch. & Graebn.
Pisum sativum subsp. *biflorum* (Raf.) Soldano	*Pisum sativum* subsp. *elatius* (M. Bieb.) Asch. & Graebn.
Pisum sativum subsp. *brevipedunculatum* (Davis & Meikle)	*Pisum sativum* subsp. *elatius* var. *brevipedunculatum* (Davis & Meikle)
Pisum sativum subsp. *cinereum*	*Pisum sativum* L.
Pisum sativum subsp. *elatius*	*Pisum sativum* subsp. *elatius* (M. Bieb.) Asch. & Graebn.
Pisum sativum subsp. *elatius*	*Pisum sativum* subsp. *elatius* (M. Bieb.) Asch. & Graebn.
Pisum sativum subsp. *elatius* var. *elatius*	*Pisum sativum* subsp. *elatius* (M. Bieb.) Asch. & Graebn.
Pisum sativum subsp. *elatius* var. *pumilio*	*Pisum sativum* subsp. *elatius* (M. Bieb.) Asch. & Graebn.
Pisum sativum subsp. *hibernicum*	*Pisum sativum* var. *sativum* L.
Pisum sativum subsp. *hortense*	*Pisum sativum* var. *sativum* L.
Pisum sativum subsp. *humile*	*Pisum sativum* var. *pumilio* Meikle
Pisum sativum subsp. *ircutianum*	*Pisum sativum* L.

Taxon as found in database	Standardized taxa
Pisum sativum subsp. *pumilio*	*Pisum sativum* subsp. *elatius* var. *pumilio*
Pisum sativum subsp. *sativum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* c. *sativum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* c. *speciosum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* conv.	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *asiaticum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *axiphium*	*Pisum sativum* var. *macrocarpum* Ser.
Pisum sativum subsp. *sativum* convar. *axiphium* var. *bretonicum*	*Pisum sativum* var. *macrocarpum* Ser.
Pisum sativum subsp. *sativum* convar. *axiphium* var. *cerocarpum*	*Pisum sativum* var. *macrocarpum* Ser.
Pisum sativum subsp. *sativum* convar. *axiphium* var. *compocarpum*	*Pisum sativum* var. *macrocarpum* Ser.
Pisum sativum subsp. *sativum* convar. *axiphium* var. *dinocarpum*	*Pisum sativum* var. *macrocarpum* Ser.
Pisum sativum subsp. *sativum* convar. *axiphium* var. *durius*	*Pisum sativum* var. *macrocarpum* Ser.
Pisum sativum subsp. *sativum* convar. *axiphium* var. *furcans*	*Pisum sativum* var. *macrocarpum* Ser.
Pisum sativum subsp. *sativum* convar. *axiphium* var. *giganteum*	*Pisum sativum* var. *macrocarpum* Ser.
Pisum sativum subsp. *sativum* convar. *axiphium* var. *kappertii*	*Pisum sativum* var. *macrocarpum* Ser.
Pisum sativum subsp. *sativum* convar. *axiphium* var. *melileucum*	*Pisum sativum* var. *macrocarpum* Ser.
Pisum sativum subsp. *sativum* convar. *axiphium* var. *notatum*	*Pisum sativum* var. *macrocarpum* Ser.
Pisum sativum subsp. *sativum* convar. *axiphium* var. *patris*	*Pisum sativum* var. *macrocarpum* Ser.
Pisum sativum subsp. *sativum* convar. *axiphium* var. *pedale*	*Pisum sativum* var. *macrocarpum* Ser.
Pisum sativum subsp. *sativum* convar. *axiphium* var. *procerum*	*Pisum sativum* var. *macrocarpum* Ser.
Pisum sativum subsp. *sativum* convar. *axiphium* var. *pseudopatris*	*Pisum sativum* var. *macrocarpum* Ser.
Pisum sativum subsp. *sativum* convar. *axiphium* var. *punctato-marmoratum*	*Pisum sativum* var. *macrocarpum* Ser.
Pisum sativum subsp. *sativum* convar. *axiphium* var. *subreginae*	*Pisum sativum* var. *macrocarpum* Ser.
Pisum sativum subsp. *sativum* convar. *axiphium* var. *viridum*	*Pisum sativum* var. *macrocarpum* Ser.
Pisum sativum subsp. *sativum* convar. *medulare* var. *pliculum*	*Pisum sativum* var. *macrocarpum* Ser.
Pisum sativum subsp. *sativum* convar. *medullare*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *medullare*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *medullare* var. *balticum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *medullare* var. *ecirrhosum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *medullare* var. *gribowoense*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *medullare* var. *pervicax*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *medullare* var. *pliculum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *medullare* var. *reginae*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *medullare* var. *schneebergeri*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *medullare* var. *unionis*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *medullare* var. *vilmorini*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *medullosa*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *medullosaccharatum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *medullosaccharatum* var. *körnickei*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *medullosaccharatum* var. *majakense*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *medullosaccharatum* var. *prasinum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *sativum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *sativum* v	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *sativum* var. *arcuatum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *sativum* var. *atrovirens*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *sativum* var. *chloromelan*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *sativum* var. *cimitari*	*Pisum sativum* L.

Taxon as found in database	Standardized taxa
Pisum sativum subsp. *sativum* convar. *sativum* var. *coronatum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *sativum* var. *episcopi*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *sativum* var. *fabiforme*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *sativum* var. *fasciato-vitellinum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *sativum* var. *fonticulorum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *sativum* var. *glaucospermum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *sativum* var. *gratiosum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *sativum* var. *jessenii*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *sativum* var. *laetum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *sativum* var. *mesomelan*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *sativum* var. *nanoanglicum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *sativum* var. *nanoviride*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *sativum* var. *ponderosum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *sativum* var. *pretiosum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *sativum* var. *pseudomesomelan*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *sativum* var. *superfluens*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *sativum* var. *vitellinum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *sativum* var. *waterlooensis*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum Population*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *alveolare*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *alveolatum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *angulare*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *angulatum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *ankoberense*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *apunctatum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *arvense*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *asmaricum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *biannulatum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *bimaculatum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *capucinorum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *centrali-sibiricum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *commato-semineum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *concolor*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *fusco-umbilicatum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *grandigriseum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *griseo-coloratum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *harraricum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *hibernicum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *hiemale*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *ircutianum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *melanocarpum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *minuto-semineum*	*Pisum sativum* L.

Taxon as found in database	Standardized taxa
Pisum sativum subsp. *sativum* convar. *speciosum* var. *nanoquadratum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *navale*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *nigro-umbilicatum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *nigro-violaceum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *praecox*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *pseudoroseum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *punctatum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *roseum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *sanguivitta*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *sanguivittopsis*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *subgriseo-viridulum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *subharraricum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *subrufum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *subunicolor*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *thebaicum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *urgaeum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *violaceo-punctatum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *viridipunctulum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *speciosum* var. *zeylanicum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* convar. *transcauc*	*Pisum sativum* subsp. *transcaucasicum* Govorov
Pisum sativum subsp. *sativum* var. *afghanisten*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* var. *arcuatum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* var. *arvense*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum sativum subsp. *sativum* var. *asiaticum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* var. *balticum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* var. *coronatum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* var. *ecirrhosum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* var. *korni*.	*Pisum sativum* L.
Pisum sativum subsp. *sativum* var. *sativum*	*Pisum sativum* L.
Pisum sativum subsp. *syriacum*	*Pisum sativum* var. *pumilio* Meikle
Pisum sativum subsp. *thebaicum*	*Pisum sativum* L.
Pisum sativum subsp. *tibetanicum*	*Pisum sativum* L.
Pisum sativum subsp. *transcaucasicum*	*Pisum sativum* subsp. *transcaucasicum* Govorov
Pisum sativum subsp. *urgaeum f. speciosum*	*Pisum sativum* L.
Pisum sativum subsp. *arvense* var. *marmotatum*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum sativum subsp. *arvense* var. *viridi punctul*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum sativum subsp. *sativum* var. *glaucospermum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* var. *vulgatum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* var. *convar spectos*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* var. *glaucospermum*	*Pisum sativum* L.
Pisum sativum subsp. *sativum* var. *vulgatum*	*Pisum sativum* L.
Pisum sativum subunicolor	*Pisum sativum* L.
Pisum sativum Subunicolor	*Pisum sativum* L.
Pisum sativum subvar. *contextum*	*Pisum sativum* L.
Pisum sativum subvar. *correctum*	*Pisum sativum* L.

Taxon as found in database	Standardized taxa
Pisum sativum subvar. *ecaducum*	*Pisum sativum* L.
Pisum sativum subvar. *stabilisum*	*Pisum sativum* L.
Pisum sativum transcaucasicum	*Pisum sativum* subsp. *transcaucasicum* Govorov
Pisum sativum var. *durius*	*Pisum sativum* L.
Pisum sativum var. *aethiopicum*	*Pisum sativum* L.
Pisum sativum var. *alveolatum*	*Pisum sativum* L.
Pisum sativum var. *angulare*	*Pisum sativum* L.
Pisum sativum var. *ankoberense*	*Pisum sativum* L.
Pisum sativum var. *apunctatum*	*Pisum sativum* L.
Pisum sativum var. *arcuatum*	*Pisum sativum* L.
Pisum sativum var. *arvense*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum sativum var. *asmaricum*	*Pisum sativum* L.
Pisum sativum var. *atrovirens*	*Pisum sativum* L.
Pisum sativum var. *axiphium*	*Pisum sativum* var. *macrocarpum* Ser.
Pisum sativum var. *balticum*	*Pisum sativum* L.
Pisum sativum var. *biannulatum*	*Pisum sativum* L.
Pisum sativum var. *biannulatum¬†*	*Pisum sativum* L.
Pisum sativum var. *biannulatum√Ç*	*Pisum sativum* L.
Pisum sativum var. *biannulatum√Ç¬†*	*Pisum sativum* L.
Pisum sativum var. *bimaculatum*	*Pisum sativum* L.
Pisum sativum var. *capucinorum*	*Pisum sativum* L.
Pisum sativum var. *centrali-sibiricum*	*Pisum sativum* L.
Pisum sativum var. *chloromelan*	*Pisum sativum* L.
Pisum sativum var. *cimitari*	*Pisum sativum* L.
Pisum sativum var. *cinereum*	*Pisum sativum* L.
Pisum sativum var. *cirrosum*	*Pisum sativum* L.
Pisum sativum var. *commato-semineum*	*Pisum sativum* L.
Pisum sativum var. *compocarpum*	*Pisum sativum* L.
Pisum sativum var. *concolor*	*Pisum sativum* L.
Pisum sativum var. *Contecstum*	*Pisum sativum* L.
Pisum sativum var. *contecsum*	*Pisum sativum* L.
Pisum sativum var. *Contextum*	*Pisum sativum* L.
Pisum sativum var. *coronatum*	*Pisum sativum* L.
Pisum sativum var. *determinante habit*	*Pisum sativum* L.
Pisum sativum var. *dinocarpum*	*Pisum sativum* L.
Pisum sativum var. *divulgatum*	*Pisum sativum* L.
Pisum sativum var. *durius*	*Pisum sativum* L.
Pisum sativum var. *ecaducum*	*Pisum sativum* L.
Pisum sativum var. *ecirrosum*	*Pisum sativum* L.
Pisum sativum var. *elatius*	*Pisum sativum* subsp. *elatius* (M. Bieb.) Asch. & Graebn.
Pisum sativum var. *episcopi*	*Pisum sativum* L.
Pisum sativum var. *exguisitum*	*Pisum sativum* L.
Pisum sativum var. *fonticulorum*	*Pisum sativum* L.
Pisum sativum var. *fusco-umbilicatum*	*Pisum sativum* L.
Pisum sativum var. *glaucospermum*	*Pisum sativum* L.
Pisum sativum var. *grandigriseum*	*Pisum sativum* L.
Pisum sativum var. *grandisemineum*	*Pisum sativum* L.
Pisum sativum var. *gratiosum*	*Pisum sativum* L.
Pisum sativum var. *griseo-coloratum*	*Pisum sativum* L.
Pisum sativum var. *hibernicum*	*Pisum sativum* var. *sativum* L.

Taxon as found in database	Standardized taxa
Pisum sativum var. *hiemale*	*Pisum sativum* L.
Pisum sativum var. *hortense*	*Pisum sativum* var. *sativum* L.
Pisum sativum var. *jessenii*	*Pisum sativum* L.
Pisum sativum var. *levanticum*	*Pisum sativum* L.
Pisum sativum var. *macrocarpum*	*Pisum sativum* var. *macrocarpum* Ser.
Pisum sativum var. *majakense*	*Pisum sativum* L.
Pisum sativum var. *medullare*	*Pisum sativum* L.
Pisum sativum var. *medullosaccharatum*	*Pisum sativum* L.
Pisum sativum var. *melileucum*	*Pisum sativum* L.
Pisum sativum var. *mesomelan*	*Pisum sativum* L.
Pisum sativum var. *minuto-semineum*	*Pisum sativum* L.
Pisum sativum var. *nanoanglicum*	*Pisum sativum* L.
Pisum sativum var. *nanoquadratum*	*Pisum sativum* L.
Pisum sativum var. *nanoviride*	*Pisum sativum* L.
Pisum sativum var. *navale*	*Pisum sativum* L.
Pisum sativum var. *nigro-umbilicatum*	*Pisum sativum* L.
Pisum sativum var. *nigroviolaceum*	*Pisum sativum* L.
Pisum sativum var. *omphalodes*	*Pisum sativum* L.
Pisum sativum var. *pachylobum*	*Pisum sativum* L.
Pisum sativum var. *pedale*	*Pisum sativum* L.
Pisum sativum var. *persistens*	*Pisum sativum* L.
Pisum sativum var. *pervicax*	*Pisum sativum* L.
Pisum sativum var. *ponderosum*	*Pisum sativum* L.
Pisum sativum var. *praecox*	*Pisum sativum* L.
Pisum sativum var. *procerum*	*Pisum sativum* L.
Pisum sativum var. *pseudoroseum*	*Pisum sativum* L.
Pisum sativum var. *pumilio*	*Pisum sativum* var. *pumilio* Meikle
Pisum sativum var. *punctatum*	*Pisum sativum* L.
Pisum sativum var. *puncto-maculatum*	*Pisum sativum* L.
Pisum sativum var. *roseum*	*Pisum sativum* L.
Pisum sativum var. *ruminatum*	*Pisum sativum* L.
Pisum sativum var. *sacharatum*	*Pisum sativum* L.
Pisum sativum var. *sanguivitta*	*Pisum sativum* L.
Pisum sativum var. *sanguivittopsis*	*Pisum sativum* L.
Pisum sativum var. *sativum*	*Pisum sativum* var. *sativum* L.
Pisum sativum var. *schneebergeri*	*Pisum sativum* L.
Pisum sativum var. *seminanum*	*Pisum sativum* L.
Pisum sativum var. *simitarii*	*Pisum sativum* L.
Pisum sativum var. *speciosum*	*Pisum sativum* var. *sativum* L.
Pisum sativum var. *speciosum* Alef.	*Pisum sativum* var. *sativum* L.
Pisum sativum var. *spesiosum*	*Pisum sativum* var. *sativum* L.
Pisum sativum var. *subcinereum*	*Pisum sativum* L.
Pisum sativum var. *subgriseo-viridulum*	*Pisum sativum* L.
Pisum sativum var. *subrufum*	*Pisum sativum* L.
Pisum sativum var. *superfluens*	*Pisum sativum* L.
Pisum sativum var. *thebaicum*	*Pisum sativum* L.
Pisum sativum var. *Tonica*	*Pisum sativum* L.
Pisum sativum var. *unikolor*	*Pisum sativum* L.
Pisum sativum var. *unionis*	*Pisum sativum* L.

Taxon as found in database	Standardized taxa
Pisum sativum var. *urgaeum*	*Pisum sativum* L.
Pisum sativum var. *vavilovianum*	*Pisum sativum* L.
Pisum sativum var. *violaceo-punctatum*	*Pisum sativum* L.
Pisum sativum var. *violaceopunctatum*	*Pisum sativum* L.
Pisum sativum var. *viridulogriseum*	*Pisum sativum* L.
Pisum sativum var. *vitellinum*	*Pisum sativum* L.
Pisum sativum var. *vulgatum*	*Pisum sativum* L.
Pisum sativum var. *waterlooensis*	*Pisum sativum* L.
Pisum sativum var. *woodfortii*	*Pisum sativum* L.
Pisum sativum var. *zeylanicum*	*Pisum sativum* L.
Pisum sativum var.-gr. *medullare*	*Pisum sativum* L.
Pisum sativum var. *arvense*	*Pisum sativum* var. *arvense* (L.) Poir.
Pisum sativum var. *axiphium*	*Pisum sativum* var. *macrocarpum* Ser.
Pisum sativum var. *cerinocarpum*	*Pisum sativum* L.
Pisum sativum var. *ciminarii*	*Pisum sativum* L.
Pisum sativum var. *contecstum*	*Pisum sativum* L.
Pisum sativum var. *coronatum*	*Pisum sativum* L.
Pisum sativum var. *correctum*	*Pisum sativum* L.
Pisum sativum var. *crispum*	*Pisum sativum* L.
Pisum sativum var. *divulgatum*	*Pisum sativum* L.
Pisum sativum var. *ecaducum*	*Pisum sativum* L.
Pisum sativum var. *makasheviae*	*Pisum sativum* L.
Pisum sativum var. *medulare*	*Pisum sativum* L.
Pisum sativum var. *medullosaccharatum*	*Pisum sativum* L.
Pisum sativum var. *medullsaxaratum*	*Pisum sativum* L.
Pisum sativum var. *multifoliolatum*	*Pisum sativum* L.
Pisum sativum var. *ponderosum*	*Pisum sativum* L.
Pisum sativum var. *rosentalii*	*Pisum sativum* L.
Pisum sativum var. *ruminatum*	*Pisum sativum* L.
Pisum sativum var. *sativum*	*Pisum sativum* var. *sativum* L.
Pisum sativum var. *seminanum*	*Pisum sativum* L.
Pisum sativum var. *stabilisum*	*Pisum sativum* L.
Pisum sativum var. *tonika*	*Pisum sativum* L.
Pisum sativum var. *vulgare*	*Pisum sativum* L.
Pisum sp.	*Pisum* sp.
Pisum spp.	*Pisum* sp.
Pisum spp.	*Pisum* sp.
Pisum syriacum	*Pisum sativum* var. *pumilio* Meikle
Pisum transcaucasicum	*Pisum sativum* subsp. *transcaucasicum* Govorov

Annex 4. Metrics by country of the pea landrace gap analysis conducted by CIAT

Country	ISO2	Gap area average in km square	Coverage in %
France	FR	25576.5	30.7
China	CN	17104.5	64.4
Turkey	TR	15022	67
Norway	NO	12865.5	41
Finland	FI	12230	36.2
Italy	IT	11527	33
Iran	IR	10888.5	51.2
United Kingdom	GB	10381.5	36.6
Germany	DE	8183	68.9
Poland	PL	7379.5	68.7
Romania	RO	5889.5	62.2
Spain	ES	5654	81.6
Sweden	SE	5494.5	74.8
Russia	RU	5085.5	66.6
India	IN	5053.5	65.8
Ukraine	UA	3279	75.4
Afghanistan	AF	3215.5	76.7
Morocco	MA	3157.5	60.9
Mexico	MX	3133.5	68.5
Belarus	BY	2823	67.5
Ireland	IE	2596.5	45.6
Algeria	DZ	2509.5	60.6
Denmark	DK	2356	31.7
Austria	AT	2354	58.7
Ethiopia	ET	2284.5	81.2
Australia	AU	2272	53.5
Czechia	CZ	2264	59.3
Uzbekistan	UZ	2178	64.3
Portugal	PT	1876.5	64.4
Nepal	NP	1815	62.5
Chile	CL	1755.5	44.7
United States of America	US	1745	60.1
Bosnia and Herz.	BA	1675.5	38.5
South Africa	ZA	1674	38.6
Estonia	EE	1659.5	49.9
Serbia	RS	1654	62
Georgia	GE	1650.5	60.3
Greece	GR	1643.5	78.5
Kyrgyzstan	KG	1625	57.1
New Zealand	NZ	1581	41.8
Slovakia	SK	1542.5	54.8
Pakistan	PK	1481	71.4
Switzerland	CH	1450.5	42.6
Peru	PE	1394	54.1
Netherlands	NL	1387	37.7
Libya	LY	1359	56.7
Colombia	CO	1314	53.5
Croatia	HR	1195	60.9

Country	ISO2	Gap area average in km square	Coverage in %
Latvia	LV	1185	50.1
Bulgaria	BG	1164	67.1
Syria	SY	1106.5	79.5
Bolivia	BO	1014.5	58.2
Canada	CA	1002	55.8
Moldova	MD	988	49.9
Azerbaijan	AZ	919	71.8
Hungary	HU	918	85.4
Egypt	EG	886	63.3
Japan	JP	867.5	46.1
Tajikistan	TJ	841	82.1
Tunisia	TN	800	41
Slovenia	SI	763.5	41.2
Burundi	BI	738	28.6
Lithuania	LT	605.5	53
Albania	AL	561	67.1
Montenegro	ME	543	36
Belgium	BE	535.5	76.1
Iraq	IQ	439.5	75.7
Armenia	AM	433.5	68.5
Jordan	JO	384.5	69.2
Kosovo	XK	350.5	49.1
Tanzania	TZ	347.5	47.3
Madagascar	MG	347	49.1
Argentina	AR	344.5	43.4
Kazakhstan	KZ	338	49.1
Macedonia	MK	296	80.8
South Korea	KR	291.5	41.6
Iceland	IS	279.5	12.7
Brazil	BR	218	41.6
Indonesia	ID	215	38.4
Ecuador	EC	214	86
Bhutan	BT	200	46.7
Kenya	KE	189.5	50.4
Eritrea	ER	182.5	63.7
Yemen	YE	163.5	60.1
Dem. Rep. Congo	CD	158	23.7
Uruguay	UY	130.5	62.4
Guatemala	GT	119.5	77.8
Israel	IL	94.5	89.9
Zimbabwe	ZW	92	50
Rwanda	RW	76.5	72.1
Luxembourg	LU	75.5	59.8
North Korea	KP	72.5	48.9
Taiwan	TW	71.5	40.9
Oman	OM	70	38.1
Lebanon	LB	62	88.7
N. Cyprus	NC	54.5	71.6
Vietnam	VN	51	44
Turkmenistan	TM	46.5	44.6

Country	ISO2	Gap area average in km square	Coverage in %
Venezuela	VE	39.5	69.8
Lesotho	LS	34	46
Saudi Arabia	SA	31	48.3
Uganda	UG	30.5	71.8
Cyprus	CY	28.5	91
Andorra	AD	27	3.6
Zambia	ZM	26	49
Myanmar	MM	23	50
Philippines	PH	20.5	18
Ã…land	AX	20	71.4
Isle of Man	IM	19	50
Hong Kong	HK	19	24
Bahrain	BH	17	32
Qatar	QA	16.5	43.1
Palestine	PS	16.5	94.6
United Arab Emirates	AE	16	38.5
Malta	MT	14.5	3.3
Jersey	JE	8	0
Nigeria	NG	8	33.3
Bangladesh	BD	7	76.7
Dominican Rep.	DO	6.5	53.6
Angola	AO	6	14.3
Sri Lanka	LK	5	50
Liechtenstein	LI	5	44.4
Kuwait	KW	4.5	35.7
Honduras	HN	4.5	50
Thailand	TH	4	50
San Marino	SM	4	0
Guernsey	GG	3	0
Congo	CG	3	50
eSwatini	SZ	2.5	50
Senegal	SN	2.5	16.7
Faeroe Is.	FO	2	50
Siachen Glacier	-99	2	50
Mauritius	MU	1	0
Mali	ML	1	50
St. Pierre and Miquelon	PM	1	50
Greenland	GL	1	0
Cambodia	KH	1	50
Sierra Leone	SL	0.5	50
Mozambique	MZ	0.5	50
Mongolia	MN	0.5	50
El Salvador	SV	0.5	95
Cóte d'Ivoire	CI	0.5	50
Cameroon	CM	0.5	50

Annex 5. Details of 133 Institutions reported as maintaining *Pisum* germplasm

Estimates of *Pisum* accessions were made with data from FAO WIEWS and Genesys (June 2022)

INST-CODE	*Pisum* accessions	ACRONYM	FULL_NAME	TYPE
AUS165	7575	AGG	Australian Grains Genebank, Department of Economic Development Jobs Transport and Resources	Governmental
USA022	6319	W6	Western Regional Plant Introduction Station, USDA-ARS, Washington State University	Governmental
DEU146	5359	IPK	Genebank, Leibniz Institute of Plant Genetics and Crop Plant Research	Governmental
LBN002	4596	ICARDA	International Centre for Agricultural Research in Dry Areas	CGIAR
IND001	4415	NBPGR	National Bureau of Plant Genetic Resources	Governmental
GBR247	3562		Germplasm Resources Unit, John Innes Centre, Norwich Research Park	
GBR165	3298	SASA	Science and Advice for Scottish Agriculture, Scottish Government	Governmental
POL003	3156	IHAR	Plant Breeding and Acclimatization Institute	Governmental
CZE122	2437	CRI	Genebank	Governmental
SWE054	2414	NORDGEN	Nordic Genetic Resource Center	Regional
UKR001	2305	IR	Institute of Plant Production n.a. V.Y. Yurjev of UAAS	Governmental
GBR016	2116	IBERS-GRU	Genetic Resources Unit, Institute of Biological, Environmental & Rural Sciences, Aberystwyth University	Governmental
ETH085	1886	EBI	Ethiopian Biodiversity Institute	Governmental
BGR001	1749	IPGR	Institute for Plant Genetic Resources 'K.Malkov'	Governmental
ITA436	1716	IBBR	Istituto di Bioscienze e Biorisorse, Consiglio Nazionale delle Ricerche	Governmental
PAK001	1502	PGRP	Plant Genetic Resources Program	Governmental
ITA394	1225	CREA-ZA-LO	CREA-Centro di Ricerca Zootecnia e Acquacoltura, sede di Lodi	Governmental
HUN003	1221	RCA	Institute for Agrobotany	Governmental
USA974	1125	SSE	Seed Savers Exchange	Non-Governmental
BRA003	1080	CENARGEN	Embrapa Recursos Genéticos e Biotecnologia	Governmental
CHL150	1054	INIA Carillanca	Banco Activo INIA Carillanca	Governmental
NLD037	1014	CGN	Centre for Genetic Resources, the Netherlands	Governmental
ESP109	977	ITACYL	Junta de Castilla y León. Instituto Tecnológico Agrario de Castilla y León. Centro de Investigación de Zamadueñas	Governmental
BRA012	958	CNPH	Embrapa Hortaliças	Governmental
BLR011	786		Republican Unitary Enterprise 'Scientific Practical Centre of the National Academy of Sciences of Belarus for Arable Farming'	Governmental
USA962	712	GSPI	G.A. Marx Pea Genetic Stock Center, Western Regional Plant Introduction Station, USDA-ARS, Washington State University	Governmental
ESP004	708	CRF, INIA-CSIC	Centro Nacional de Recursos Fitogenéticos	Governmental
CAN004	616	PGRC	Plant Gene Resources of Canada, Saskatoon Research and Development Centre	Governmental
FRA043	611	INRA-DIJON	Agroecology, Plant Biology and Breeding, INRA Dijon	Governmental
SVK001	548	SVKPIEST	Plant Production Research Center Piestany	Governmental
PRT001	478	BPGV-DRAEDM	Portuguese Bank of Plant Germplasm	Governmental
COL017	460	ICA/REGION 1	Corporacion Colombiana de Investigación Agropecuaria Tibaitata, CORPOICA	Governmental
JPN183	347	NARO	NARO Genebank	Governmental
LSO015	307	LNPGRC	Lesotho National Plant Genetic Resources Centre	Governmental
MNG030	306	PSARTI	Plant Science Agricultural Research and Training Institute	Governmental
ECU023	253	DENAREF	Departamento Nacional de Recursos Fitogenéticos	Governmental
EST019	223	ETKI	Estonian Crop Research Institute	Governmental
TUR001	196	AARI	Plant Genetic Resources Department	Governmental

INST-CODE	*Pisum* accessions	ACRONYM	FULL_NAME	TYPE
TWN001	195	AVRDC	World Vegetable Center	Non-Governmental
MDA010	169	LPGR	Laboratory for Plant Genetic Resources	Governmental
ZMB030	169	SRGB	SADC Plant Genetic Resources Centre	Regional
BGD003	165	BARI	Bangladesh Agricultural Research Institute	Governmental
COL029	160	CORPOICA	Centro de Investigación La Selva, Corporación Colombiana de Investigación Agropecuaria	Governmental
ARG1350	153	BGLACONSULTA	Banco Activo de Germoplasma de La Consulta	Governmental
UKR009	147	LDS	Luganskaya Experimental Station	Governmental
GBR017	140	HDRA	Henry Doubleday Research Association	Non-Governmental
MAR088	131	INRA CRRAS	Centre Régional de la Recherche Agronomique de Settat	Governmental
ROM081	130			
ROM007	127	BRGV Suceava	Suceava Genebank	Governmental
ETH013	126	ILRI-Ethiopia	International Livestock Research Institute	CGIAR
GBR004	103	RBG	Millennium Seed Bank Project, Seed Conservation Department, Royal Botanic Gardens, Kew, Wakehurst Place	Governmental
TJK027	91	RNGRC	Republican National Genetic Resource Center	Governmental
AUT001	86	BVAL	AGES Linz - Austrian Agency for Health and Food Safety / Seed Collection	Governmental
PRT102	85	ISOPlexis	Banco de Germoplasma - Universidade da Madeira	Governmental
BLR016	76		Republican Unitary Enterprise 'Research and Practical Center of the National Academy of Sciences of Belarus for Potato, Fruit and Vegetable Growing'	Governmental
BOL317	76	EE-Toralapa INIAF	Estaci√≥n Experimental de Toralapa	Governmental
AUT046	74	ARCHE	Arche Noah Association	Non-Governmental
CUB014	72	INIFAT	Instituto de Investigaciones Fundamentales en Agricultura Tropical	Governmental
LVA009	61	LSFRI	Latvian State Forest Research Institute 'Silava'	Governmental
ARM059	57	SC AB	Scientific Center of Agrobiotechnology	Governmental
EGY087	52	NGB	National Gene Bank	Governmental
AZE015	50	GRI	Genetic Resources Institute	Governmental
CHE001	45	Agroscope Changins	Agroscope Changins	Governmental
ESP009	42	MBG-CSIC	Consejo Superior de Investigaciones Científicas. Misión Biológica de Galicia	Governmental
ERI003	42	NARI	National Agricultural Research Institute	Governmental
TZA016	33	NPGRC	National Plant Genetic Resources Centre	Governmental
UGA132	33	PGRC	Plant Genetic Resource Centre	Parastatal
ALB026	31	PGRC	Plant Genetic Resources Center	Governmental
GRC005	29	GGB-NAGREF	Greek Genebank, Agricultural Research Center of Macedonia and Thrace, National Agricultural Research Foundation	Governmental
ISR002	29	IGB	Israel Gene Bank for Agricultural Crops, Agricultural Research Organisation, Volcani Center	Governmental
LTU001	26	LIA	Lithuanian Institute of Agriculture	Governmental
TUR034	24	FCCRI	Field Crop Central Research Institute	Governmental
ROM008	24	SCDA Simnic	Agricultural Research and Development Station Simnic-Dolj	Governmental
LBY006	23	NBPGR	National Bank for Plant Genetic Resources	Governmental
CYP004	22	ARI	National (CYPARI) Genebank, Agricultural Research Institute, Ministry of Agriculture, Rural Development and Environment	Governmental
ESP172	19	CCBAT	Cabildo Insular de Tenerife. Centro de Conservación de la Biodiversidad Agrícola de Tenerife	Governmental
UZB006	19	UzRIPI	Uzbek Research Institute of Plant Industry	Governmental
LKA036	17	PGRC	Plant Genetic Resources Centre	Governmental
ESP027	16	CITA-HOR	Gobierno de Aragón. Centro de Investigación y Tecnología Agroalimentaria. Banco de Germoplasma de Hortícolas	Governmental

INST-CODE	*Pisum* accessions	ACRONYM	FULL_NAME	TYPE
ARM005	16		Institute of Botany	Governmental
ZMB048	15	NPGRC	National Plant Genetic Resources Centre	Governmental
ITA363	15	PERUG	Dipartimento di Biologia Applicata, Université degli Studi Perugia	Governmental
AZE005	14	VGRƒ∞	Vegetable Growing Research Institute	Governmental
ZAF062	14	DAFF	Genetic Resources Directorate, Department of Agriculture, Forestry and Fisheries	Governmental
MEX208	13	CNRG	INIFAP, Centro Nacional de Recursos Genéticos (CNRG)	
LBN020	13	LARI	Lebanese Agricultural Research Institute	Governmental
HRV044	11	VGUK	College of Agriculture at Križevci	Governmental
SDN002	11	ARC	Agricultural Plant Genetic Resources Conservation and Research Centre	Governmental
HRV053	9	ZSR	Institute for Seed and Seedlings	Governmental
KGZ040	7	KYRGGEN	Plant Genetic Bank of the Kyrgyz Republic	Governmental
BIH039	6	GRIBL	Genetic Resources Institute, University of Banja Luka	Governmental
TUN029	6	BNG	Banque national de gènes de Tunisie	Governmental
HRV021	5	AIOS	Agricultural Institute Osijek	Governmental
MWI041	5	MPGRC	Malawi Plant Genetic Resources Centre	Governmental
KEN212	5	GeRRI	Genetic Resources Research Institute	Parastatal
BEL002	4		Gembloux agro-biotech, Université de Liège, département des Sciences agronomiques, Phytotechnie tropicale et Horticulture	Governmental
DEU627	4		van Waveren Saaten GmbH	Private
BLR026	4		The Polessye Institute of Plant Growing	Parastatal
JOR105	4	NARC	National Agricultural Research Center	Governmental
JOR015	4		Agricultural Research Service	
AUT005	4	RINN	Genebank Tyrol / Tyrolean Government	Governmental
ROM055	4	SCDL Bacau	Research and Development Station for Vegetables - Bacau	Governmental
USA995	3	NCGRP	National Center for Genetic Resources Preservation	Governmental
DEU005	3	HOHENL	Norddeutsche Pflanzenzucht Hans-Georg Lembke KG	Private
AUT047	3	HBLFAG	Horticultural College and Research Institute Schoenbrunn	Governmental
DEU628	3		KWS LOCHOW GMBH	Private
GEO013	3		Niko Ketskhoveli Institute of Botany	Governmental
MKD001	3		Faculty of Agriculture, University Ss. Cyril and Methodius	Governmental
THA300	3		Genebank	Governmental
NPL069	3	NAGRC	National Agriculture Genetic Resources Centre-Genebank	Governmental
SVN019	3	AISLJ	Crops and Seed Production Department, Agricultural Institute of Slovenia	Governmental
ROM021	2	SCDCPN Dabuleni	Research and Development Station for Plant Culture on Sands Dabuleni	Governmental
ESP026	2	BGUPV	Generalidad Valenciana. Universidad Politécnica de Valencia. Escuela Técnica Superior de Ingenieros Agrónomos. Banco de Germoplasma	Governmental
ROM023	2	USAMVB Timisoara	University of Agricultural Sciences and Veterinary Medicine Timisoara	Governmental
USA971	2	DLEG	Desert Legume Program	Governmental
ARM010	2		Armenian Botanical Society	Non-Governmental
AUT025	2	WIES	Office of the Styrian Regional Government, Department for Plant Health and Special Crops	Governmental
GBR006	2	HRIGRU	Warwick Genetic Resources Unit	Governmental
ROM019	2	ICDLF Vidra	Research and Development Institute for Vegetables and Floriculture Vidra	Governmental
CUB284	2	CIAP	Centro de Investigaciones Agropecuarias	Governmental
HRV050	1	IPTPO	Institute of Agriculture and Tourism	Governmental

INST-CODE	*Pisum* accessions	ACRONYM	FULL_NAME	TYPE
BLR019	1		State research institution ‘The Central Botanical Gardens of the National Academy of Sciences of Belarus’	Governmental
MMR015	1	MSB	Myanmar SeedBank	Governmental
AZE014	1	ASAU	Azerbaijan State Agrarian University	Governmental
MEX263	1	DNRS	SNICS, Depositario Nacional de Referencia de Semillas (DNRS)	
BGD028	1	BINA	Bangladesh Institute of Nuclear Agriculture (BINA)	Governmental
ITA368	1	BAGAV	Banca del germoplasma autoctono vegetale regionale	Governmental
MEX194	1	ICAMEX	Instituto de Investigación y Capacitación Agropecuaria, Acuícola y Forestal	
MEX006	1	BANGEV	UACh, Banco Nacional de Germoplasma Vegetal (BANGEV)	Parastatal
NZL001	1	AGRESEARCH	Margot Forde Forage Germplasm Centre, AgResearch Ltd	Governmental
AZE003	1	RICH	Research Institute of Crop Husbandry	Governmental
ECU167	1	BG-UNPL	Banco de Germoplasma de la Universidad Técnica Particular de Loja	Private
GEO001	1		I.Lomouri Institute of Farming	Governmental

Annex 6. Table of primary and secondary seed storage facilities reported in the *Pisum* Survey.

Institute code	Primary storage facility	Temperature	Relative Humidity (%)	Packing material	Secondary storage facility	Temperature	Relative Humidity (%)	Packing material
AUS165	Long-term storage	-20°C		Triple laminated foil packets - heat sealed or vacuum sealed	Medium term	-20°C		Triple laminated foil packets - heat sealed or vacuum sealed
BGR001	Long-term storage	-18°C	5%+-2%	Three laminated aluminum foil packets	Medium-term storage	+6°C	40-50%	Paper bags
BRA003	Cold chambers	-18°C						
CAN004	Medium-term storage = working collection	+4°C	20%	Paper envelopes	Long-term storage = base collection	-20°C	50??	Sealed laminated aluminum envelopes
CHE063	Climate-controlled container	+15°C	15%	Paper	Freezer	-20°C	NA	Air tight material
CHL150	Bank of germplasm	+5°C	20%	Frasco	Bank of germplasm	-20°C	20%	Sealed envelope
CHN001	Long-term storage	-18°C	50	Metal				
CZE122	Long-term storage	-25°C	5	Glass jars	Working collection	-17°C	14	Aluminum packets
DEU146	Cold room, active collection	-18°C	10-15%	Sealed glass jar with silica gel	Cold room, base collection	-18°C	10-15%	Aluminum foil, vacuum
ECU023	Cold room	-18°C		Aluminum foil bags				
ESP004	Medium term storage room	-4°C		Glass jars	Long-term storage room	-18°C		Aluminum cans
ESP009	Cold chamber	+5°C	40-50%	Paper bags				
ESP109	Cold chamber	2°C	40%	Glass				
EST019	Deep freezer	-18°C	na	Alu-folium bags				
FRA043	Seed laboratory	Ambient	Ambient	Kraft bags	Cold storage room	7°C	15	Kraft bags
GBR017	Cold store	+8°C	15%	Mix of paper/foil sealed				
GBR165	Deep freeze seed store	-22°C	15%	High Density Poly Ethylene (HDPE) containers	Cool temperature seed store	0 to 4°C	15	High Density Poly Ethylene (HDPE) Containers
GBR247	Cold store	+4-6°C	8%	Plastic jars				
IND001	Long term	-18°C	Not controlled	Three layered vacuum sealed aluminum pouches	Medium-term	5°C	30%	Cloth bags
ITA394	Freezer (long-term storage)	-18°C		Sealed bags	Fridge (mid-term to short-term storage)	5°C		Sealed or paper bags
JPN183	Short-term	-1°C	30%	Bottle	Long-term	-18°C	30	Vacuumed can
LBN002	Medium-term storage	+ 0-4°C	Up to 18%	Plastic bottles	Long-term storage	-20°C	No control	Aluminum foil pouches
LVA009	Commercial freezers	-20°C	-	Foil bags				
NLD037	Storage rooms and freezers	-20°C	NA	Laminated aluminum foil bags				
POL003	Chambers	0	5-7%	Glass jars				

Institute code	Primary storage facility	Tempera-ture	Relative Humidity (%)	Packing material	Secondary storage facility	Tempera-ture	Relative Humidity (%)	Packing material
PRT001	Long-term conservation chamber	-18ºC	45	Aluminum bags	Medium-term conservation chamber	0-5ºC		Plastic boxes
PRT102	Walk-in cold storage chamber	+5ºC		Aluminum foil bags	Walk in cold storage chamber	-18ºC		Aluminum foil bags
RUS001	Short-term storage	Room temperature	8-9%	Paper packages, metal boxes	Medium-term	+4°C	6%	Aluminum foil packages
SRB002	Cold chamber	0-10°C	40-50%	Paper bags	Plain storage	0-20°C		Paper bags in plastic boxes
SWE054	Chest freezers	-18°C	N/A (15% RH inside bags)	Three-layer laminated aluminum foil				
TUR001	Cold rooms	0 C	-	Can, glass jar	Cold room	-18/20°C	-	Can, glass jar
TWN001	Long-term storage room	-20°C	Ice free	Aluminum foil bag	Medium-term storage room	5°C	45%	Aluminum foil bag
UKR001	Short-term storage	Non-regulated	Non-regulated	Hermetically sealed glass bottles	Medium-term storage	+4°C	Seeds are dried	Foil
USA022	Cooler	2°C	30%	Metal or plastic	Freezer	-20°C		Foil packets
USA974	Walk-in freezer	-18°C	20-30%	Foil packets	Walk-in storage room	8-10°C	20-30%	Foil packets
ZMB030 (SADC)	Freezers	-20°C	15%	Foil packets and bottles				

Annex 7. Survey responses on the primary objective of the collection

Institute Code	Long-term conservation	Working	Breeding	Reference	Heritage
AUS165	Y	Y	Y	Y	
BGR001	Y	Y			
BRA003	Y				
CAN004	Y	Y			
CHE063	Y				Y
CHL150	Y	Y	Y		
CHN001	Y	Y	Y	Y	
CZE122	Y	Y			
DEU146	Y				
ECU023	Y	Y			
ESP004	Y	Y			
ESP009		Y	Y		
ESP109		Y	Y		
EST019	Y	Y	Y		
FRA043	Y	Y	Y	Y	
GBR016			Y		
GBR017	Y	Y		Y	
GBR165				Y	
GBR247	Y	Y			
IND001	Y				
ITA394	Y	Y	Y	Y	
JPN183	Y		Y		
LBN002	Y	Y			
LVA009	Y				
NLD037	Y				
POL003	Y				
PRT001	Y				
PRT102	Y	Y			
RUS001	Y	Y	Y	Y	
RUS255	Y	Y		Y	
SRB002	Y	Y	Y	Y	
SWE054	Y				
TUR001	Y		Y		
TWN001	Y	Y			
UKR001	Y	Y	Y		
USA022	Y	Y	Y	Y	
USA974	Y	Y			

Annex 8. Selected indicator metrics on conservation and use of crop genetic resources collected by Khoury et al. (2021) for peas and common bean (as a comparison).

This annex is a summary of Khoury et al. (2021) written by Dr. Felix Frey, International Consultant, Global Crop Diversity Trust

Khoury et al. (2021) compiled a comprehensive dataset as part of a project funded by the International Treaty on Plant Genetic Resources for Food and Agriculture and the Crop Trust, led by the International Center for Tropical Agriculture (CIAT). The aim was to introduce five normalized, reproducible indicators that provide an evidence base to prioritize actions with respect to conservation and use of crop genetic resources for food and agriculture. The indicators include metrics associated with: the USE of a crop (global importance); the INTERDEPENDENCE between countries with respect to genetic resources; the DEMAND of researchers for genetic resources; the SUPPLY of germplasm by genebanks; and the SECURITY of germplasm conservation. To generate the five indicators, Khoury et al. (2021) collected a comprehensive dataset from multiple sources.

To put the numbers into context, we compare peas with common beans, and for each crop the dry and green crop figures are combined into a single total. The two crops are comparable with respect to type of propagation, cultivation and genetics of genepools. In contrast to beans, which have a wide cultivation range, pea has a narrower range of cultivation areas worldwide. Khoury et al. (2021) used *Pisum* and *Phaseolus* to represent the genera of peas and common bean, respectively. To represent the most important species of peas, they used *P. sativum*, and common bean was represented by the species *P. vulgaris*.

The metrics for “Global production”, “Food supply” and “Quantity exported globally” from the indicator domain USE are annual average values drawn from FAOSTAT data (FAOSTAT 2019) between 2010 and 2014. The percentage of countries producing and consuming (being supplied with) the crop is calculated as the number of countries, where the respective crop is within the top 95% of most important crops divided by the total number of countries that report respective numbers (production 216, food supply 175). The global production of peas is about 27 Million tons annually, which is about 5 % of the global bean production (47 M t). The quantity of food supply by peas, i.e. the average global consumption, is 2 g per capita per day, which is 32% of the value of beans (7 g). The lower food supply by peas compared with beans could be associated with the increased use of peas as animal feed. Peas are produced in 53% of countries and consumed in 83% of countries worldwide, while beans are produced in 74% of countries and consumed in 87 % of countries. This relatively higher international importance of peas than beans is reflected by relatively high export numbers. In total, 4.8 M t of peas is exported (17% of global production), but only 10% of the global production of beans is exported (4.6 M t).

The crop use metrics with respect to research were assessed by manual searches on Google Scholar, searching for the respective genus or species in the titles of publications, including patents and citations, between 2009 and 2019. Google Scholar search hits represent the scientific interest in a crop. The pea genus *Pisum* was found in half of the number of publication titles (4,490 – 3,810 for species *P. sativum*), compared to *Phaseolus*, the genus of common bean with 9,870 (8,220 for species *P. vulgaris*).

Khoury et al. (2021) defined INTERDEPENDENCE as a measure of the degree of dependence of the global cultivation and use of a certain crop on germplasm from the primary centers of diversity of the crop. Primary centers of diversity are not represented by countries, but by 23 geographical zones (Khoury et al. 2016), because crop diversity does not follow national borders but rather climatic and agro-ecological boundaries. Interdependence is high in crops that originate from a small area and are cultivated and used globally. For production, interdependence is calculated by dividing a crops’ production outside of the primary center of diversity by its global production. If all production is outside the primary center of diversity, then interdependence is 100%. For food supply, interdependence is calculated by dividing the food supply by the world average. Food supply can be higher outside than inside the primary regions of diversity and thus, it can be higher than the global mean. Therefore, interdependence with respect to food supply can be above 100%. Interdependence is high for both peas and common beans, which have values between 92–100% with respect to production and food supply. Thus, large shares of global production as well as food supply are highly dependent on germplasm originating from different regions of the world. This is especially interesting for pea, because it has a very widespread primary center of origin spanning the regions East Africa, West Asia, South and East Mediterranean, and South Eastern and South Western Europe. However, peas are mainly produced in different areas of the world, foremost in East and Southeast Asia and North America and Central Europe. Similarly, common beans, originating from Central America and Mexico as well as Andean South America, are mainly produced in Asia, Brazil and North America. Food supply with respect to both crops is widely distributed throughout the world and not especially predominant in the primary centers of origin.

The DEMAND for germplasm is defined by two metrics. First, by the number of distributions of accessions by genebanks, as an annual average between 2014 and 2017 drawn from the Plant Treaty Global Information System. Second, by the number of varieties released during the 5 years between 2014 and 2018, obtained from the International Union for the Protection of New Varieties of Plants (UPOV, www.upov.int). The number of pea accessions distributed by genebanks (4,129) is about one-third that of bean accessions (13,378). However, in the last five years, 15,025 new pea cultivars have been released, but only 11,440 new bean varieties.

Khoury et al. (2021) illustrated the SUPPLY of germplasm with the number of accessions available in *ex situ* collections around the world, with respect to the crop genus and the most important species of the respective crop. Furthermore, they assessed the number of accessions (again with respect to genus and species) that were available under the multilateral system (MLS) of the Plant Treaty. This was done first, directly, as notation (in MLS/not in MLS) in the public online databases Genesys, WIEWS and GBIF. Secondly, the availability of accessions was assessed *via* the status of the country where the institution holding the germplasm collection was located. If the country was a contracting party of the Plant Treaty, the respective accession was regarded as available in the MLS. Global *ex situ* collections count a total of 66,041 *Pisum* accessions (62,294 accessions of *P. sativum*). The global pea collection is about 40% of the size of the global bean collections (180,615 *Phaseolus* and 157,632 *P. vulgaris* accessions). Similar proportions of genebank accessions (30-40 %) of both crops are directly available through the multilateral system (MLS). If we consider the Treaty status of countries holding collections, almost all (about 95%) pea accessions are available under the MLS, but 86% of all bean accessions.

The SECURITY of germplasm conservation is represented here with two metrics, the safety duplication status at the Svalbard Global Seed Vault (SGSV) and the equality of global distribution with respect to several crop use metrics. The numbers of accessions safety duplicated with respect to genus and species were drawn from the website of the SGSV and divided by the total number of accessions stored in global *ex situ* collections (see above), resulting in the percentage of safety duplicated germplasm.

To represent the equality of distribution across different agro-ecological regions of the world (Khoury et al. 2016), Khoury et al. (2021) used the reciprocal 1-Gini index with respect to the different crop use metrics. The Gini index is the most commonly used inequality index (Gini index 2008), and is best known for its use in quantifying global income inequality. The 1-Gini index, presented here, ranges from 0 to 1, where 0 reflects very unequal distribution across world regions, and 1 represents a completely equal global distribution of the respective metric across the world's regions. It reflects the security of crop cultivation and use, where, for example, small indices of production and thus geographical restriction go hand in hand with a higher vulnerability of supply, e.g., in cases of natural disasters. The safety duplication status of global pea accessions is relatively low (13% of pea accessions are duplicated at SGSV, compared with 22% of global bean accessions). The equality of the distribution with respect to global production of peas (0.02) is lower than that of common beans (0.04), indicating that peas are more unequally distributed across the worlds' regions. This is obviously due to the more restricted area of production, as stated above. Pea supply is thus more vulnerable to regional shortfalls in production. The equality of the distribution of food supply across the different regions of the world of peas and beans, 0.14 and 0.13, respectively, are much higher than the equality of production.

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Table 1. Selected metrics collected by Khoury et al. 2021 for pea and beans, subdivided by indicator domain

Indicator domain | subdomain	Metric	Peas	Common bean	Peas/common bean	Source
Crop use | Production	Global production [tons]	27453607	46946853	58%	FAOSTAT, annual average (2010-2014), http://www.fao.org/faostat
Crop use | Food supply	Food supply (Amount consumed) [g/capita/day]	2	7	32%	FAOSTAT, annual average (2010-2014), http://www.fao.org/faostat
Crop use | Count countries (Production)	Percentage of countries producing crop *	53%	74%	71%	FAOSTAT, annual average (2010-2014), http://www.fao.org/faostat
Crop use | Count countries (Food supply)	Percentage of countries consuming (being supplied with) crop *	83%	87%	96%	FAOSTAT, annual average (2010-2014), http://www.fao.org/faostat
Crop use | Trade	Quantity exported globally [t]	4754237	4594794	103%	FAOSTAT, annual average (2010-2014), http://www.fao.org/faostat
Crop use | Research	Number of publications between 2009-2019, including patents and citations, searching title of publication (Google scholar search hits) for genus **	4490	9870	45%	Google scholar, manual search
Crop use | Research	Number of publications between 2009-2019, including patents and citations, searching title of publication (Google scholar search hits) for species ***	3810	8220	46%	Google scholar, manual search
Interdependence | Production	Interdependence of global production from germplasm from primary centers of diversity [0-1] ****	93%	97%	96%	
Interdependence | Food supply	Interdependence of global food supply from germplasm from primary centers of diversity [0-1] ****	100%	92%	108%	
Demand | Distribution	Accessions distributed from gene banks (Annual average 2014-2017)	4129	13378	31%	Plant Treaty Information System (2014-2017)
Demand | Variety release	Variety releases in five years (2014-2018)	15025	11440	131%	UPOV (International Union for the Protection of New Varieties of Plants) https://www.upov.int
Supply | Genebank collections	Number of accessions in ex situ collections of genus **	66041	180615	37%	Databases: Genesys, FAO WIEWS, and GBIF (living specimens only)
Supply | Genebank collections	Number of accessions in ex situ collections of species ***	62294	157632	40%	Databases: Genesys, FAO WIEWS, and GBIF (living specimens only)

Indicator domain | subdomain	Metric	Peas	Common bean	Peas/common bean	Source
Supply | Multilateral system	Accessions of the genus ** available through Multilateral System (MLS) directly noted in databases [%]	39%	34%	115%	Databases: Genesys, FAO WIEWS, and GBIF (living specimens only)
Supply | Multilateral system	Accessions of the species *** available through Multilateral System (MLS) directly noted in databases [%]	37%	33%	112%	Databases: Genesys, FAO WIEWS, and GBIF (living specimens only)
Supply | Multilateral system	Accessions of the genus ** available through Multilateral System (MLS) indirectly by matching institute countries with party status [%]	95%	86%	111%	Plant Treaty website 2019/3/12
Supply | Multilateral system	Accessions of the species *** available through Multilateral System (MLS) indirectly by matching institute countries with party status [%]	96%	86%	111%	Plant Treaty website 2019/3/12
Security | Safety duplication	Accessions of genus ** safety duplicated in Svalbard Global Seed Vault [%]	13%	21%	60%	https://seedvault.nordgen.org; Databases: Genesys, FAO WIEWS, and GBIF (living specimens only)
Security | Safety duplication	Accessions of species *** safety duplicated in Svalbard Global Seed Vault [%]	13%	23%	56%	https://seedvault.nordgen.org; Databases: Genesys, FAO WIEWS, and GBIF (living specimens only)
Security | Equality of distribution	1-GINI index for equality of production across the world [0-1] *****	0.02	0.04	60%	1- GINI index (equality between countries) using summed average to derive regional values; FAOSTAT, annual average (2010-2014), http://www.fao.org/faostat
Security | Equality of distribution	1-GINI index for equality of food supply across the world [0-1] *****	0.14	0.13	109%	1- GINI index (equality between countries) using weighted average to derive regional values; FAOSTAT, annual average (2010-2014), http://www.fao.org/faostat

* Counting countries which list the crop as within top 95% (FAOSTAT); Calculated as: Number of countries counting crop (top 95%) / Total number of countries (production 216, food supply 175)
** Peanuts: *Arachis*; Soybeans: Glycine
*** Peanuts: *Arachis hypogaea*; Soybeans: *Glycine max*
**** Global metric / Metric at primary center of diversity
***** Relative equality of crop use across world regions (same regions as used in interdependence domain), high equality give high indicator value

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