

Ecogeographic survey and gap analysis of *Lathyrus* L. species

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Abstract The genetic diversity of the genus *Lathyrus* is of significant importance, particularly for its role in sustaining the livelihoods of local communities living under very harsh conditions and its potential to adapt to climate change. Grasspea (*L. sativus*) is the most widely used species and to a lesser extent *L. cicera* and *L. ochrus*, each is used for animal feed in many parts of the world and food in poorer regions, but human over-consumption of the seeds can lead to lathyrism, a disease caused by neurotoxins. This study has added substantial information and accuracy to the existing global *Lathyrus* database by combining diverse datasets and by adding information of major herbaria from Europe. This global *Lathyrus* database, available at ICARDA, was used to conduct gap analysis to guide future collecting missions and *in situ* conservation efforts for highest priority species originating from the Mediterranean Basin, and Caucasus, Central and West Asia region. The results showed the highest concentration of *Lathyrus* priority species are found in the Fertile Crescent countries, France, Italy and Greece. The area either side of the Lebanese/Syrian border near Tel Kalakh, Syria was

identified as the hotspot and the overall priority location for establishing the first *in situ* genetic reserve. The gap analysis for *ex situ* conservation shows that only six species (representing 16.6 %) of the 36 priority species are adequately sampled. Only *L. cicera* has already been well sampled among the closely related species to cultivated species *L. sativus*, indicating further collecting of *L. amphicarpos*, *L. belinensis*, *L. chrysanthus*, *L. hirticarpus*, *L. hirsutus* and *L. marmoratus* is required. In addition, six secondary priority *Lathyrus* species have no *ex situ* collections (*L. lentiformis*, *L. lycicus*, *L. phaselitanus*, *L. trachycarpus*, *L. tremolsianus* and *L. undulatus*) and also require targeted collecting.

Keywords Central and West Asia · Ecogeographic analysis · *Ex situ* conservation · Gap analysis · Grasspea · *In situ* conservation · *Lathyrus* · Mediterranean Basin

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Introduction

The fact that the human population has recently passed 7 billion and is forecast to approach 9 billion by 2050 (UN 2011), considered together with the likely adverse impact of climate change on agricultural production (Schmidhuber and Tubiello 2007; Lobell et al. 2008; Palm et al. 2010), means it is not surprising

that there is raised increasing awareness of issues related to global food security (IPCC 2007; FAO 2008). Although there are many approaches to improving food security (FAO 2012), one option that currently remains under-developed but that could potentially make a significant contribution is the improved systematic and targeted use of crop wild relatives (CWR) in crop improvement programmes (Maxted et al. 1997a). CWR have the potential to contribute beneficial traits to crops, such as biotic and abiotic resistance, leading to improved yield and stability (Maxted et al. 2006, 2012a; Maxted and Kell 2009; Guarino and Lobell 2011). One likely impact of climate change is that many current crop varieties will need to be replaced if the crop is to be grown in the same places in the future (Jones et al. 2003; Duveiller et al. 2007; Deryng et al. 2011; Li et al. 2011; Luck et al. 2011). Failure to meet this challenge could have a devastating impact not only on food security but on the global economy and societal stability.

Given their global value—one estimate is that the introduction of new genes from CWR contributes \$115 billion toward increased crop yields per year worldwide (Pimentel et al. 1997)—it might be expected that CWR would be effectively conserved and easily available for use by plant breeders. But conservation of CWR diversity is in fact yet to be addressed systematically on a national, regional or global scale. It has been estimated that CWR account for only 9 % of European gene bank collections and of the total number of CWR species that exist in Europe only about 6 % have any accessions conserved in gene banks (Maxted et al. 2010). The current situation regarding *in situ* conservation of CWR is equally ineffective with only a handful of genetic reserves established and of these few are regularly monitored to ensure the genetic diversity is being maintained, and the option of *in situ* CWR outside of protected areas has yet to be explored. Yet the requirement for systematic CWR conservation is recognised in the FAO Global Plan of Action for the Conservation and Sustainable Utilization of Plant Genetic Resources for Food and Agriculture (FAO 1997) and in Article 5 of the International Treaty on Plant Genetic Resources for Food and Agriculture (FAO 2001). The Global Strategy for Plant Conservation 2011–2020 (CBD 2010a) also states in Target 9: “70 per cent of the genetic diversity of crops including their wild relatives and other socio-economically valuable plant species conserved”. Further, recently

the Conference of the Parties to the CBD underlined the importance of CWR in their Strategic Plan (CBD 2010b) agreed in Nagoya: “Target 13. By 2020, the status of crop and livestock genetic diversity in agricultural ecosystems and of wild relatives has been improved”. CWR have been placed firmly on the international conservation agenda; however, there remains a need to implement practical strategies to address their conservation and meet the agreed targets.

One such novel approach to help prioritise conservation action is genetic gap analysis (Maxted et al. 2008a, 2012b). Conservation gap analysis is based on comparing natural diversity with that element of the diversity that is actively conserved to identify the ‘gaps’ and so revise the conservation strategy. This methodology has been applied for cowpea *Vigna unguiculata* and its wild relatives from Africa (Maxted et al. 2004), *Aegilops* species (Maxted et al. 2008b), *Phaseolus* species (Ramírez-Villegas et al. 2010), six legume genera in the Mediterranean region (Maxted et al. 2012c) and the Global Crop Diversity Trust gap analysis project of 13 crop gene pools (gisweb.ciat.cgiar.org/gapanalysis/). The genus *Lathyrus* is an ideal candidate for the application of gap analysis as there has been no previous systematic *in situ* and *ex situ* conservation assessment and yet the most important crop, grasspea (*L. sativus* L.) has climate change mitigation potential because of its adaptation to harsh environments where it is used for food and animal feed among subsistence farmers.

Lathyrus is a large genus containing around 160 species (Lewis et al. 2005), located mainly in Europe and Asia with a secondary centre in the Americas, but with its centre of diversity primarily in the Mediterranean and Irano-Turanian regions (Kupicha 1983). Several *Lathyrus* species, primarily drawn from *Lathyrus* sect. *Lathyrus* are cultivated for human consumption, animal feed, and fodder [*L. sativus*, *L. cicera* L., *L. ochrus* (L.) DC. and to a lesser extent *L. clymenum* L.], as well as for ornamental purposes (*L. odoratus* L., *L. latifolius* L. and *L. sylvestris* L.), in addition to their having benefits as soil nitrifiers and as dune stabilizers (Sarker et al. 2001). The over-consumption of *L. sativus* seeds can lead to lathyrism, a disease caused by a neurotoxins, either beta-N-oxalyl-diamino-propionic acid (beta-ODAP) or beta-(N)-oxalylamino-L-alanine acid (BOAA), that result in irreversible paralysis, characterized by lack of strength in, or inability to move the lower limbs (Barrow et al.

1974; Rutter and Percy 1984; Kaul and Combes 1986). This is a particular problem in drought regions of Bangladesh, Ethiopia, India and Nepal where *L. sativus* is often grown in area prone to drought as it provides a yield to subsistence farmers even when other crops fail. The continuation and expansion of *Lathyrus* cultivation is tightly linked to the ability of breeders to access genetic resources to solve the problem of lathyrism, as is happening with the release of zero or very-low neurotoxin varieties (Malek et al. 1996; Tadesse et al. 1997; Sarker et al. 2001; Agrawal et al. 2011). The objective of this paper is to present a genetic gap analysis for *Lathyrus* species to guide future complementary *in situ* and *ex situ* conservation.

Materials and methods

Significant digitized ecogeographic datasets for *Lathyrus* species are held by the International Centre for Agricultural Research in the Dry Areas (ICARDA) and the global biodiversity information facilities (GBIF) and these were combined with authors own herbarium based datasets and used for this analysis. However, the dataset is not systematic in that the *Lathyrus* species included are primarily from the Mediterranean Basin and Caucasus, Central and West Asia regions. Focusing the study on this region necessarily includes the predominantly annual, cultivated and closely related species, particularly the species of *Lathyrus* sect. *Lathyrus* (which includes the bulk of the primary and secondary wild relatives of *L. sativus*, *L. cicera*, *L. odoratus*, *L. latifolius* and *L. sylvestris*) and sect. *Clymenum* (Mill.) DC. ex Ser. (which contains *L. clymenum*, *L. ochrus* and *L. gloeospermus* Warb. et Eig only), however, it excludes the American and Southern Asian taxa as well as the other predominantly perennial cool-temperate species. Although the latter are members of the tertiary gene pool of the cultivated species and may contain traits of breeding interest so do themselves warrant further study. One *Lathyrus* species, *L. sativus*, was excluded from the analysis as its natural distribution is obscured by cultivation.

The herbarium based datasets were obtained from seven major international herbaria (the Royal Botanic Gardens in Kew, UK, the Royal Botanic Gardens in Edinburgh, UK, the Natural History Museum, London, UK, the Natural History Museum, Paris, France,

the University of Montpellier, France, the Botanic Gardens in Geneva, Switzerland, and Florence University in Italy), as well as several ecogeographic surveys of food and forage legumes undertaken jointly by ICARDA and the University of Birmingham between 1998 and 2010. As suggested by Maxted et al. (2006), the analysis focus on both the full set of *Lathyrus* species with ecogeographic data, as well as the highest priority species, defined as those most closely related to the crops using gene pools (GP1B and GP2) and/or taxon groups (TG1b and TG2) concepts (Table 1). A total of 61,081 unique herbarium and germplasm accessions were included for 95 *Lathyrus* species, and 18,147 unique herbarium and germplasm accessions for the 36 priority species. Data were standardized to a single format; duplicate observations and errors that could not be rectified were identified and removed. In addition, occurrences identified as being outside of the natural range of the species were considered to be introductions and therefore were not considered in the final analysis. The dataset is available from the author on request.

DIVA-GIS version 7.1.7 (www.diva-gis.org) was used for the spatial analysis. Species richness was calculated using the number of different classes (richness) and identifying complementary hotspots of species diversity using the iterative procedure (Rebelo and Siegfried 1992; Rebelo 1994) in the 'reserve selection' manner locate the optimal locations to establish future *in situ* reserves using a $100 \times 100 \text{ km}^2$ grid cells (Hijmans et al. 2005a). It is assuming that when recommending a site for the establishment of a CWR genetic reserve that it is preferably to do so within an existing protected area to avoid the costs and social disruption of establishing a new protected area (Maxted et al. 1997b; Heywood and Dulloo 2005; Iriondo et al. 2008). For this reason the results of the complementarity analysis were compared with the UNEP WCMC World Database of Protected Areas (<http://www.protectedplanet.net/>) to identify existing protected areas within the complementarity analysis hotspots or failing that those relatively close.

DIVA-GIS was also used with the global climatic data with 2.5 min resolution (diva_worldclim_2-5 m.zip) using the Bioclim method (Hijmans et al. 2005b) to produce predictive distribution maps based on the climatic data for each *Lathyrus* taxon. This allowed a comparison between the distribution map

Table 1 *Lathyrus* species germplasm accessions and herbarium specimens included in study, those in bold are priority species

Species	Germplasm accession in			Total germplasm accessions	Herbarium specimens	Geo-referenced germplasm and herbaria specimens
	SINGER	EURISCO	USDA GRIN			
<i>L. alpestris</i>	0	0	0	0	2	2
<i>L. amphicarpos</i>	4	2	0	6	9	15
<i>L. angulatus</i>	0	0	0	0	539	539
<i>L. annuus</i>	33	30	7	70	595	665
<i>L. aphaca</i>	300	0	0	300	3,238	3,538
<i>L. armenus</i>	5	0	0	5	1	6
<i>L. aureus</i>	36	0	0	36	37	73
<i>L. basalticus</i>	6	0	1	7	21	28
<i>L. bauhini</i>	14	0	0	14	23	37
<i>L. belinensis</i>	1	0	0	1	4	5
<i>L. bijugas</i>	1	0	0	1	0	1
<i>L. blepharicarpus</i>	48	0	1	49	354	403
<i>L. boissieri</i>	13	0	0	13	3	16
<i>L. brachypterus</i>	12	0	0	12	0	12
<i>L. cassius</i>	8	4	2	14	47	61
<i>L. chloranthus</i>	4	19	2	25	9	34
<i>L. chrysanthus</i>	4	1	1	6	18	24
<i>L. cicera</i>	214	558	42	814	507	1,321
<i>L. cilicicus</i>	5	0	0	5	15	20
<i>L. ciliolatus</i>	7	1	3	11	17	28
<i>L. cirrhosus</i>	1	1	2	4	24	28
<i>L. clymenum</i>	14	84	25	123	824	947
<i>L. cyaneus</i>	2	0	0	2	81	83
<i>L. czechotianus</i>	0	0	0	0	18	18
<i>L. davidii</i>	0	0	0	0	8	8
<i>L. digitatus</i>	0	0	0	0	119	119
<i>L. elongatus</i>	0	0	0	0	10	10
<i>L. filiformis</i>	0	0	0	0	115	115
<i>L. gloeospermus</i>	2	1	0	3	6	9
<i>L. gmelinii</i>	0	0	0	0	22	22
<i>L. gorgoni</i>	61	8	1	70	236	306
<i>L. grandiflorus</i>	0	0	1	1	36	37
<i>L. heterophyllus</i>	0	2	0	2	113	115
<i>L. hierosolymitanus</i>	129	7	4	140	304	444
<i>L. hirsutus</i>	29	129	21	179	1,353	1,532
<i>L. hirticarpus</i>	2	0	0	2	2	4
<i>L. humilis</i>	0	0	0	0	8	8
<i>L. hygrophilus</i>	0	0	0	0	7	7
<i>L. inconspicuus</i>	190	0	0	190	321	511
<i>L. incurvus</i>	0	0	0	0	36	36
<i>L. japonicus</i>	0	0	0	0	474	474
<i>L. karsianus</i>	0	0	0	0	4	4

Table 1 continued

Species	Germplasm accession in			Total germplasm accessions	Herbarium specimens	Geo-referenced germplasm and herbaria specimens
	SINGER	EURISCO	USDA GRIN			
<i>L. komarovii</i>	0	0	0	0	3	3
<i>L. krylovii</i>	0	0	0	0	1	1
<i>L. latifolius</i>	4	36	12	52	3,124	3,176
<i>L. laxiflorus</i>	0	0	0	0	276	276
<i>L. layardii</i>	0	0	0	0	3	3
<i>L. lentiformis</i>	0	0	0	0	1	1
<i>L. libani</i>	0	0	0	0	4	4
<i>L. linifolius</i>	0	0	0	0	10,183	10,183
<i>L. lycicus</i>	0	0	0	0	4	4
<i>L. marmoratus</i>	36	4	1	41	223	264
<i>L. mulkak</i>	1	0	0	1	26	27
<i>L. neurolobus</i>	0	0	0	0	8	8
<i>L. niger</i>	0	0	0	0	2,357	2,357
<i>L. nissolia</i>	12	0	0	12	1,654	1,666
<i>L. nivalis</i>	0	0	0	0	9	9
<i>L. occidentalis</i>	0	0	0	0	117	117
<i>L. ochrus</i>	160	185	25	370	116	486
<i>L. odoratus</i>	4	33	52	89	77	12
<i>L. pallescens</i>	1	0	0	1	44	45
<i>L. palustris</i>	0	0	0	0	1,206	1,206
<i>L. pannonicus</i>	0	0	0	0	208	208
<i>L. phaselitanus</i>	0	0	0	0	2	2
<i>L. pisiformis</i>	0	0	0	0	22	22
<i>L. pratensis</i>	0	0	0	0	16,567	16,567
<i>L. pseudocicera</i>	74	2	1	77	101	178
<i>L. pyrenaicus</i>	0	0	0	0	6	6
<i>L. quadrimarginatus</i>	0	0	0	0	1	1
<i>L. quinquenervius</i>	0	0	0	0	1	1
<i>L. roseus</i>	0	0	0	0	107	107
<i>L. rotundifolius</i>	5	29	11	45	129	174
<i>L. satdaghensis</i>	0	0	0	0	2	2
<i>L. saxatilis</i>	0	0	0	0	107	107
<i>L. setifolius</i>	8	0	0	8	207	215
<i>L. spathulatus</i>	0	0	0	0	44	44
<i>L. sphaericus</i>	27	0	0	27	651	678
<i>L. stenolobus</i>	2	0	0	2	5	7
<i>L. stenophyllus</i>	2	0	2	4	23	27
<i>L. sylvestris</i>	4	1	32	37	3,956	3,993
<i>L. tauricola</i>	0	0	0	0	2	2
<i>L. tingitanus</i>	18	81	4	103	8	111
<i>L. trachycarpus</i>	0	0	0	0	2	2
<i>L. tremolsianus</i>	0	0	0	0	118	118

Table 1 continued

Species	Germplasm accession in			Total germplasm accessions	Herbarium specimens	Geo-referenced germplasm and herbaria specimens
	SINGER	EURISCO	USDA GRIN			
<i>L. tuberosus</i>	7	38	20	65	3,498	3,563
<i>L. tukhtensis</i>	0	0	0	0	8	8
<i>L. undulatus</i>	0	0	0	0	4	4
<i>L. variabilis</i>	0	0	0	0	14	14
<i>L. venetus</i>	0	0	0	0	57	57
<i>L. vernus</i>	0	0	0	0	3,313	3,313
<i>L. vinealis</i>	4	0	0	4	26	30
<i>L. vivanii</i>	0	0	0	0	7	7
Totals	1,514	1,256	273	3,043	58,036	61,081

based on *ex situ* germplasm accession data and that based on the herbarium information and the predicted distribution maps generated from their climatic envelope data. *Ex situ* conservation gaps were identified as regions where the species was predicted to occur but had not been previously collected, or areas predicted to be under sampled. Also the level of *ex situ* conservation priority for each of the *Lathyrus* species was ranked (high, medium and low) as follows: High priority: Species with, 200 germplasm accessions conserved *ex situ* and/or species for which *ex situ* collections inadequately represented their geographic range with several predicted under-sampled regions; Medium priority: Species well represented in *ex situ* collections across their geographic range, with only a few predicted under-sampled regions, but with <500 germplasm accessions conserved *ex situ*. Low priority: Species well represented throughout their geographic range with more than 500 accessions conserved *ex situ* and only a few, if any, under-sampled areas predicted.

Results

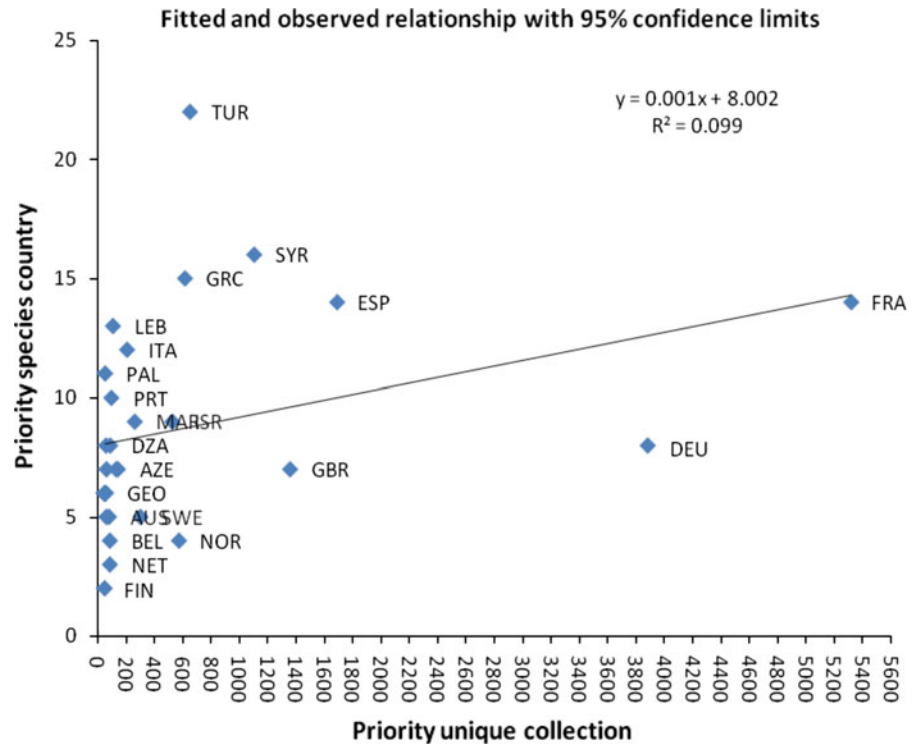
Spatial analysis

The entire dataset revealed that the most frequently recorded species were: *L. pratensis* L. (16,567), *L. linifolius* (Reichard) Bässler (10,183), *L. sylvestris* L. (3,992), *L. tuberosus* L. (3,563), *L. aphaca* L. (3,538), *L. vernus* (L.) Bernh. (3,313), *L. latifolius* L. (3,176), *L. niger* (L.) Bernh. (2,536), *L. nissolia* L. (1,666), *L. hirsutus* L. (1,532) and *L. cicera* L.

(1,321), which reflects their frequent and widespread distribution. Among these common species *L. sylvestris*, *L. tuberosus*, *L. latifolius*, *L. hirsutus* and *L. cicera* are among the CWR of grasspea. There are also 31 rare and restricted species with less than ten records; including: *L. gloeospermus* Warb. et Eig (9), *L. belinensis* Maxted et Goyder (5), *L. lycicus* Boiss. (4), *L. hirticarpus* J. Mattatia et Heyn (4), *L. undulatus* Boiss. (4), *L. trachycarpus* (Boiss.) Boiss. (2), *L. phaselitanus* Hub.-Mor et Davis (2), and *L. lentiformis* Plitm. (1).

It is well known that *Lathyrus* has primarily a Mediterranean-Western Asiatic centre of species diversity and the analysis showed that 89.5 % (54,677 accessions) were collected from Europe, 10.3 % (6,318 unique accessions) in Central and West Asia and North Africa region (CWANA) and less than one per cent (86 accessions) from southern and East Asia, and Africa. However, this is likely to reflect intensity of collecting rather than true species concentration. If numbers of species present in each region is considered, there are 77 *Lathyrus* species and 31 priority species present in CWANA, 61 *Lathyrus* species and 25 priority species present in Europe, and 8 species and 1 priority species present in southern and East Asia. So although there are significantly more collections available with geo-referenced data for Europe than CWANA, the highest concentration of all species and priority species is clearly in CWANA and fewer collections and species are found in southern and East Asia, and Africa. The seven countries with the highest number of *Lathyrus* species were Turkey (57), Spain (43), France (39), Syria (30), Greece (30), Russian Federation (29) and Lebanon (23), while for

Fig. 1 Regression of *Lathyrus* priority species against the number of accessions collected from each country (countries are indicated with standard three letter ISO codes)



priority species they were Turkey (22), Syria (16), Greece (15), Spain (14), France (14) and Lebanon (13). However, even absolute numbers of species masks concentration; for example, although Syria has a relatively high number of species (including priority species), they are restricted to a relatively small part of the country, mainly in semi-arid and humid regions, compared to Turkey where the species distributions are more evenly spread throughout the whole country.

Under-estimation of species richness in the under-sampled areas can come from unequal sampling across a species' native range (Maxted et al. 2004) and as already noted above *Lathyrus* is very well sampled from Europe but less well sampled from CWANA. The regression analysis for the number of priority *Lathyrus* species recorded against the number of accessions collected has a regression line ($y = 8.0027 + 0.0012 \log_{10}X$) with 95 % confidence intervals (Fig. 1). The result indicates several countries rich in *Lathyrus* species are each worthy of additional collection, particularly Turkey, Syria, Spain, Greece and Lebanon.

Both species richness and complementarity analysis maps were produced for all 95 *Lathyrus* species and the 36 priority species. Figure 2 shows that the

Lathyrus species are distributed from North Western Europe/North Africa to Central Asia, Afghanistan and India, however, the highest species concentration is found in both the Iberian Peninsula and the Fertile Crescent regions. Complementarity analysis for all *Lathyrus* showed that the major diversity hotspots are found in North East Spain, with 17–21 species, and around Tel Kalakh in Homs Province in Syria, with 14–17 priority *Lathyrus* species, followed by the locations in eastern Central Turkey and in Palestine (Fig. 3). Figure 4 and 5 show the same analysis for the 36 priority species alone. The highest species richness for priority *Lathyrus* species is in Western Europe through to Central Asia and Afghanistan, with the highest concentration found in the western Fertile Crescent region (Fig. 4), while the complementarity analysis of priority species identifies the area around Tel Kalakh, Homs Province, Syria as the first hotspot, followed by northeast Spain/southwest France, then several equal priority locations in Georgia, central eastern Turkey, Jordan, France and Spain (Fig. 5). It is interesting to compare Fig. 3 and 5 and note that the relative importance of northeast Spain and Tel Kalakh, Syria are reversed depending on whether all 95 *Lathyrus*

Fig. 2 Species richness for 95 *Lathyrus* species accessions in 100 × 100 km grid cells

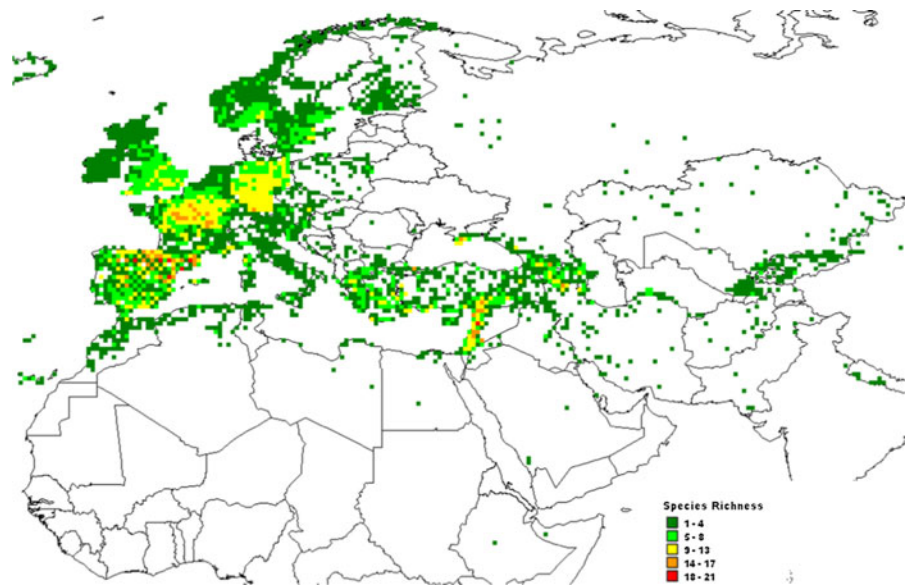


Fig. 3 Hotspots for 95 *Lathyrus* species identified using complementarity analysis



species or the 36 priority species are used as a basis for the analysis.

In situ conservation

The *Lathyrus* priority species spatial analysis clearly identifies two hotspots of complementary *Lathyrus* species diversity in Tel Kalakh, Syria, and northeast Spain and southwest France. As there are currently no protected areas where *Lathyrus* species or genetic diversity is actively conserved, the hotspots identified are those where genetic reserves should be established. While it is relatively easy to suggest protected areas in

Spain/France where genetic reserves might be established and which should be field surveyed to find local priority *Lathyrus* populations (i.e. Pyrénées catalanes, Forêt de la Massane National Nature Reserve or La Narbonnaise Regional Nature Park in France and Garrotxa Volcanic National Park, Isla de Fuvia Nature Reserve or Santa Quirze de Colera Nature Reserve in Spain), the situation is more difficult in the Tel Kalakh region of Syria and neighbouring Bekaa valley region in Lebanon as designated protected areas are absent. There are five existing IUCN-recognized protected areas within a 100 km radius of the hotspots (Table 2), but only one of these has official IUCN designation, Qattina Lake

Fig. 4 Species richness for 36 priority *Lathyrus* species in 100 × 100 km grid cells

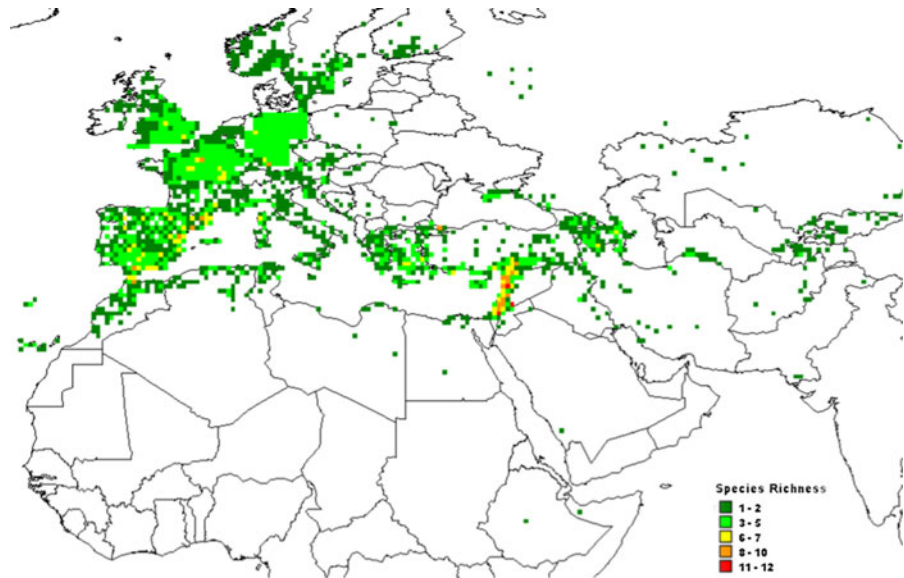


Fig. 5 Hotspots for 36 priority *Lathyrus* species identified using complementarity analysis

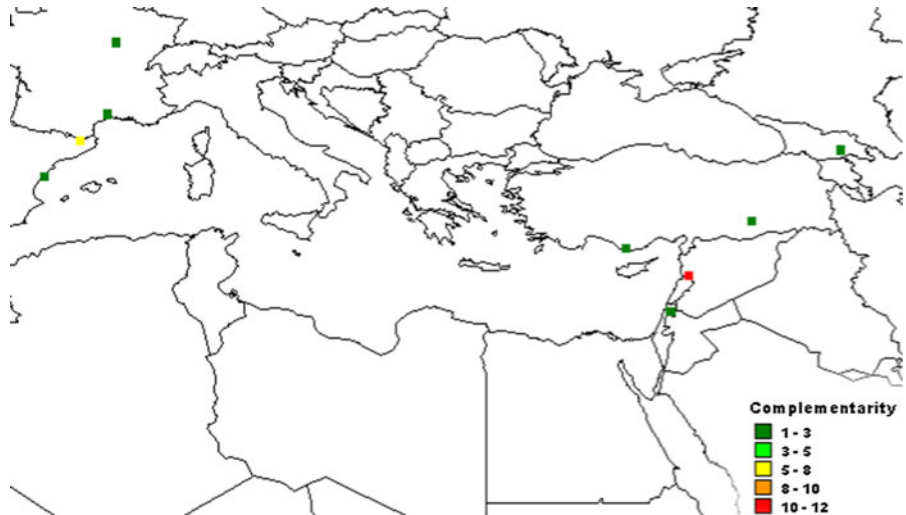


Table 2 IUCN recognized protected areas within 100 km radius of *Lathyrus* priority species hotspot

Country	Protected area name	Type of protected area	Location	Area (ha)
Syria	Al Sha'ara National PA	Protected Area	36.00 N 35.00 E	1,000
	Abu Kubeiss National PA	Protected Area	36.80 N 35.00 E	11,000
	Qattina lake National PA	Protected Area	36.58 N 34.67 E	6,000
Lebanon	Horsh Ehden National Reserve	National Reserve	36.00 N 34.32 E	–
	Arz Bcharreh National Protected Zone	Protected Zone	36.08 N 34.25 E	–

National Park, however this is a lake and so unsuitable for *Lathyrus* growth. Therefore, it likely that significant additional field surveying within the region to find a

location where a new protected area could be designated for the *in situ* conservation of *Lathyrus* priority species within the region of highest species concentration.

Ex situ conservation

A summary of the gene bank holdings for the three most comprehensive online databases for *Lathyrus* species is provided in Table 1 together with total numbers of georeferenced herbaria and gene bank accessions. The largest number of germplasm accessions (1,256) is held in EURISCO, which provides information on European *ex situ* collections, while 1,514 (882 priority) accessions of *Lathyrus* are held by the Consultative Group on International Agricultural Research (CGIAR) centres, indicated by the System wide Information Network of Genetic Resources (SINGER) holdings, the bulk of which are held at the gene bank of ICARDA. A further 273 accessions held by United States Department of Agriculture (USDA).

It is generally accepted that without knowledge of a taxon's pattern of genetic diversity distribution, a random sample of 50 sites per species per region would provide an adequate minimum sample of genetic diversity (Brown and Marshall 1995); so assuming the conservationist would wish some additional safety collections in excess of the minimum, and allowing for a certain percentage of duplication of conserved germplasm samples between SINGER, EURISCO and USDA collections, a figure of 100 germplasm collections would be an adequate sample of natural diversity of a priority species (Hawkes et al. 2000). Table 1 shows that only six priority species (16 %) out of the 36 priority species are adequately

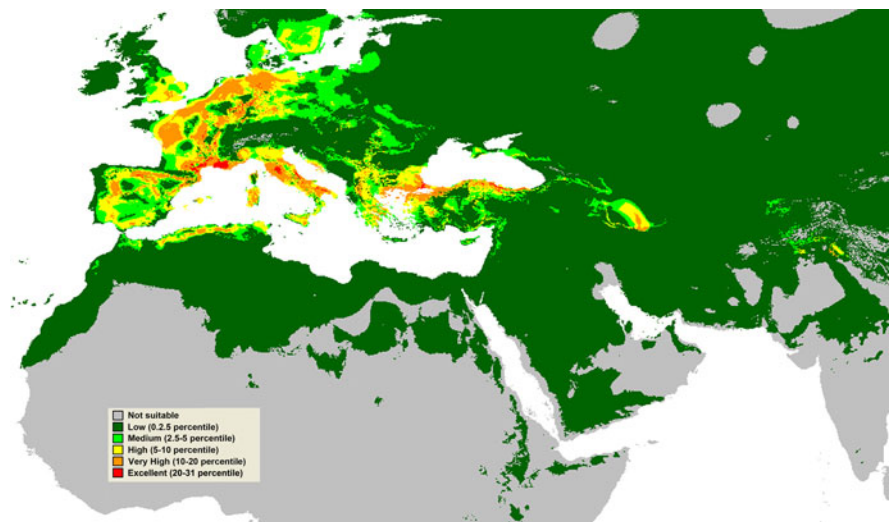
sampled and 18 priority species have less than 10 samples conserved *ex situ* including some close wild relatives of crops such as *Lathyrus basalticus*, *L. ciliolatus*, *L. amphicarpos*, *L. cirrhosus*, *L. stenopyhyllus*, *L. gloeospermus*, *L. heterophyllus*, *L. hirticarpus*, *L. belinensis*, *L. grandiflorus* and *L. mulkak*. Six priority species are not completely conserved *ex situ*, but have specimens in the herbaria.

DIVA-GIS analysis based on the methodology described above allowed producing modules for predictive maps based on the climatic data for each *Lathyrus* taxon. This helped the comparison between the distribution map based on *ex situ* germplasm accession data and that based on the herbarium information and the predicted distribution maps generated from their climatic envelope data. Figure 6 shows the predicted areas for additional *ex situ* conservation of the 36 priority species of genus *Lathyrus* from sections *Lathyrus* and *Clymenum*.

Discussion

This study has added substantial information and accuracy to the existing Global *Lathyrus* database held by ICARDA by combining diverse germplasm accession and herbarium specimen datasets. For most priority *Lathyrus* species, there are significantly larger numbers of herbaria specimens than seed accessions conserved *ex situ* in gene banks and there remains no protected area where *Lathyrus* species or genetic

Fig. 6 Predicted areas for additional *ex situ* conservation for the priority *Lathyrus* species



diversity conservation is given priority. *Lathyrus* species distribution in the old world ranges from the Canary Islands to Japan and extends north to Iceland, the Scandinavian countries and Siberia, and south to Ethiopia, Somalia and the Indian subcontinent covering different climatic zones from arid-hot to cold.

The highest concentration of *Lathyrus* priority species is found in the countries of the Fertile Crescent, France, Italy and Greece, but while existing protected areas in Europe could be modified to act as genetic reserves this is not the case in the Fertile Crescent where there is a dearth of protected areas. The need for a novel protected area in the Tel Kalakh region of Syria and northern Bekaa valley region of Lebanon was also noted by Maxted (1995), Whitehouse (2011) and Maxted et al. (2012c) who each called for the establishment of a genetic reserve in this area because of the wealth of legume and cereal priority species diversity. Field surveys in this region over many years by staff from ICARDA and the University of Birmingham have identified the highest concentration of target priority legume and cereal taxa in the valley below the castle of Qal'at Al Hosn, which not only containing numerous *Lathyrus* species, notably *L. annuus* L., *L. basalticus* Rech. fil., *L. cicera*, *L. clymenum*, *L. gorgoni* Parl., *L. hierosolymitanus* Boiss., *L. marmoratus* Boiss. et Bl. and *L. ochrus*; as well as: *Pisum sativum* L. and *P. fulvum* Sibth. et Sm.; *Vicia narbonensis* L., *V. johannis* Tamamsch., *V. hyaeniscyamus* Mout., *V. kalakhensis* Khatlab, Maxted et Bisby, *V. eristalioides* Maxted, *V. sativa* L.; *Triticum baeoticum* Boiss., *T. urartu* Tumanian ex Gandilyan, *T. turgidum* L. subsp. *dicoccoides* (Körn. ex Asch. et Graebn.) Thell. and several *Aegilops* species; *Hordeum vulgare* subsp. *spontaneum* (C. Koch.) Thell.; *H. bulbosum* L., *H. murinum* L. subsp. *leporinum* (Link) Arcang. and *H. marinum* Huds. subsp. *gussoneanum* (Parl.) Asch. et Graebn.; and *Avena barbata* Pott. ex Link., *A. clauda* Durieu, *A. damascena* Rajhathy et B. R. Baum, *A. sativa* L. and *A. sterilis* L.; as well as wild vegetables oil plants (e.g. flax *Linum usitatissimum* L.) and fruit trees (e.g. *Pistacia* spp., *Malus* spp., *Pyrus* spp.). Vincent et al. (2013) as part of a global assessment of priority CWR have suggested that this valley has not just national and regional, but global importance as the premier hotspot of temperate food and agricultural CWR diversity. However, a recent study by (Keiša et al. 2007) showed this area is being

developed rapidly for tourism and is highly threatened with genetic erosion as a result of habitat destruction; however, much of the development is concentrated in a restricted ribbon around the most fertile soil of the valley bottom and suitable sites could still be found above this development in the traditionally farmed or abandoned terraces. More systematic surveying in the Crack de Chevalier (Qal'at Al Hosn) valley is required and the designation and establishment of the genetic reserves is an urgent global priority which requires national and international support. This management could include technological options using water-harvesting, combined with community managed grazing, to investigation of alternative sources of income to support the livelihood of local communities to continue their efforts to conserve the remaining agro biodiversity. Promoting eco-tourism, targeting awareness increase and effective contribution to conservation activities could be developed as an alternative source of income for the custodians of local biodiversity. In addition, enabling policies to empower local communities and general public awareness actions should be developed.

Having stressed the need for further surveying and the designation of novel protected areas in which to establish genetic reserves, it should be stressed that CWR are often located in pre-climax communities (Jain 1975; Maxted et al. 1997b; Stolton et al. 2006); therefore, the likely site management to maintain pre-climax conditions in the genetic reserve may need to be intensive. Although protected areas do not have to be established in climax vegetation and they can contain agricultural lands, the option of conserving *in situ* CWR diversity outside of traditional protected area should also be considered, especially where CWR population maintenance can be associated with traditional farming practices (Maxted et al. 2008c). The *in situ* conservation of CWR diversity outside of protected areas, although discussed, has yet to be enacted; therefore, it should clearly not be seen as an alternative to protected area conservation but as a means of complementary conservation.

The gap analysis for *ex situ* conservation shows that only eight *Lathyrus* species have over 100 germplasm collections, (*L. aphaca* with 300 accessions, *L. cicera* with 814, *L. clymenum* with 123, *L. hierosolymitanus* with 140, *L. hirsutus* with 179, *L. inconspicuus* with 190, *L. ochrus* with 370, and *L. tingitanus* with 103) and of these only *L. cicera* could be considered well sampled. Further even for these species, as their

inherent pattern of genetic diversity is unknown, we cannot confirm the maximum range of genetic diversity within the species is conserved and for the majority of species further collection is justified. Of the closely related species to the cultivated *L. sativus*, *L. amphicarpos*, *L. belinensis*, *L. chrysanthus*, *L. hirticarpus*, *L. hirsutus* and *L. marmoratus* are all under-represented in gene bank collections and *L. lentiformis*, *L. lycicus*, *L. phaselitanus*, *L. trachycarpus*, *L. tremolsianus* and *L. undulatus* have no *ex situ* collections, so extensive targeted further *ex situ* collecting is required. The efficient conservation of these species is essential in order to assist plant breeders in fulfilling the high production demands thought to be required in the future if food security is to be maintained and adaptation to the adverse effects of climate change is to be achieved. Future collecting missions and *in situ* conservation efforts could also be guided, in addition to herbaria, by the traits sought by various users including breeders. Accessions with adaptation to heat, drought, salinity and other abiotic and biotic stresses can be targeted special efforts by mapping the distribution of *Lathyrus* species to environmental gradients with typical stresses.

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