

Genetic gap analysis of wild *Hordeum* taxa

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Abstract

To facilitate the updating of *in situ* and *ex situ* conservation strategies for wild taxa of the genus *Hordeum* L., a combined ecogeographic survey and gap analysis was undertaken. The analysis was based on the Global Inventory of Barley Plant Genetic Resources held by ICARDA plus additional datasets, resulting in a database containing 17,131 wild *Hordeum* accessions. The analysis concluded that a genetic reserve should be established in the Mendoza Province of Argentina, as this is the most species-rich area globally for *Hordeum*. A network of reserves should also be set up across the Fertile Crescent in Israel, Palestine, Syria, Jordan, Lebanon and Turkey to provide effective conservation within the centres of diversity for gene pools 1B (*Hordeum vulgare* subsp. *spontaneum* (C. Koch) Thell.) and 2 (*Hordeum bulbosum* L.). The majority of the species were deemed under-collected, so further collecting missions are required worldwide where possible. Although *ex situ* and *in situ* conservation strategies have been developed, there needs to be further investigation into the ecological environments that *Hordeum* species occupy to ensure that any adaptive traits expressed are fully conserved. Additionally, studies are required to characterize existing collections and test the viability of rare species accessions held in genebanks to determine whether further *ex situ* collections are required alongside the proposed *in situ* conservation.

Keywords: crop wild relatives; ecogeographic survey; *ex situ*; gap analysis; *Hordeum*; *in situ*; introduction; plant conservation

Genetic diversity within and between populations is essential for adaptation and survival of any species. Plant breeders use this breadth of genetic diversity to generate new cultivars. The current need for genetic diversity is critical because of the predicted threats to agricultural production from climate change combined with the ever-increasing human population (FAO, 2008). The Intergovernmental Panel on Climate Change (IPCC) (2007) concluded that the poorest countries

would be hardest hit, with increased food insecurity impacting most tropical and subtropical regions due to decreased water availability and new or changed insect pest incidence. Although there are many approaches to improving food security (FAO, 2012a, b), one option that is currently underdeveloped but which could potentially make a significant contribution is a more systematic and targeted use of crop wild relatives (CWR) in crop improvement programmes. CWR have the potential to contribute beneficial traits to crops, such as biotic and abiotic stress resistance, leading to improved yield and stability (Prescott-Allen and Prescott-Allen, 1988; Feuillet *et al.*, 2008; Maxted *et al.*, 2006; Maxted *et al.*, 2008a;

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Guarino and Lobell, 2011). While climate change will directly impact CWR diversity itself, it will also undoubtedly alter the conditions under which our crops grow. It is likely that many current crop varieties will need to be replaced if the crop is to be grown in the same places in the future (see Jones *et al.*, 2003; Duveiller *et al.*, 2007; Deryng *et al.*, 2011; Li *et al.*, 2011; Luck *et al.*, 2011; Yadav *et al.*, 2011). Failure to meet this challenge could have a devastating impact not only on food security but also on the global economy and social stability.

Yet CWR, like other wild plant species, are highly threatened. It is estimated that 20% of all plants globally are threatened with extinction (Brummitt and Bachman, 2010) and specifically for European CWR species, 11.5% (66) of the species are considered as threatened using the IUCN (2001) Red List Criteria, with 3.3% (19) of them being Critically Endangered, 4.4% (22) Endangered and 3.8% (25) Vulnerable – a further 4.5% (26) of the species are classified as Near Threatened (19) (Kell *et al.*, 2011). Furthermore, Jarvis *et al.* (2008) found that 16–22% of CWR species of three target gene pools would go extinct by 2055 with 50% loss of distributional range for the majority of species. The potential threat and the possible exploitation benefit of sustainably using CWR have been placed firmly on the international conservation agenda with explicit mention of the need for conservation in the Global Plan of Action for the Conservation and Sustainable Utilization of Plant Genetic Resources for Food and Agriculture (FAO, 1996), the Global Strategy for Plant Conservation (CBD, 2010a) and the Conference of the Parties to the Convention on Biological Diversity (CBD) in their Strategic Plan agreed in Nagoya (CBD, 2010b).

To help ensure the effective conservation of crop gene pools, a methodology for genetic gap analysis (Maxted *et al.*, 2008b) has been proposed and has been applied for several crops (Maxted *et al.*, 2004, 2008c; Ramírez-Villegas *et al.*, 2010). The methodology utilizes the GIS to compare *in situ* CWR diversity with diversity that has been sampled and conserved either *in situ* or *ex situ*. The aim of this paper is to undertake gap analysis of wild taxa of the genus *Hordeum* as represented in genebank collections and to propose conservation strategies to conserve *Hordeum* genetic diversity.

The genus *Hordeum* L. belongs to the *Triticeae* tribe of the family *Poaceae* (*Gramineae*) and consists of 32 species and, in total, 45 taxa (Bothmer *et al.*, 1995). The primary gene pool of cultivated barley (*Hordeum vulgare* subsp. *vulgare*) consists of the wild relative *H. vulgare* subsp. *spontaneum* (C. Koch) Thell., the secondary gene pool consists of *Hordeum bulbosum* L. and the tertiary gene pool consists of all the remaining *Hordeum* species (Bothmer *et al.*, 1995). The species are annual or perennial grasses and are found in the

Mediterranean, western North America, southern South America and Central Asia, but the crop barley was domesticated in the Israeli–Jordan part of the Fertile Crescent about 10,000 years ago (Badr *et al.*, 2000). *Hordeum* species inhabit a wide range of habitats such as sandy beaches, grasslands, fresh and saltwater areas, steppes and alpine meadows (Bothmer *et al.*, 1995). Cultivated barley is used widely in brewing alcoholic beverages, or as human foods and livestock feeds.

Materials and methods

Data preparation

Data were gathered from seven sources selected among the largest collections of wild *Hordeum* accessions (Knüppfer, 2009). A total of 16,716 wild *Hordeum* accessions were taken from the Global Inventory of Barley Plant Genetic Resources, which was compiled at the International Centre for Agricultural Research in the Dry Areas (ICARDA, Aleppo, Syria); Leibniz Institute of Plant Genetics and Crop Plant Research (Gatersleben, Germany) provided data for 1280 accessions of *Hordeum* wild taxa, Nordic Genetic Resource Centre (Alnarp, Sweden) provided data for 1333 *Hordeum* accessions, EURISCO (Web-based catalogue of *ex situ* plant collections maintained in Europe – <http://eurisco.ecpgr.org/static/index.html>) provided data for 5646 *Hordeum* accessions, Plant Gene Resources of Canada (Saskatoon Research Centre, Saskatchewan, Canada) provided data for 56,309 *Hordeum* accessions, GRIN (Genetic Resources Information Network, United States Department of Agriculture – Agricultural Research Service, Beltsville, MA, USA) provided data for 30,617 *Hordeum* accessions, and R. von Bothmer compiled 2763 *Hordeum* accessions from various sources. Taxonomic data from each source were standardized using the Bothmer *et al.* (1995) nomenclature (hybrid accession data were retained in all datasets where there were adequate location identifiers). For each dataset, the countries listed were converted to the three-letter ISO ALPHA-3 standard using the website <http://unstats.un.org/unsd/methods/m49/m49alpha.htm> (accessed February 2012). The longitude and latitude coordinates in each dataset were converted to decimal degrees to enable the data to be processed by GIS (Geographic Information System) tools.

The seven separate data sources contained duplicate accessions, and these were identified and removed to ensure uniqueness and maximum accuracy. Accessions that had neither locality nor coordinate data in the database were deleted. All accessions without latitude and

longitude were georeferenced using an online global gazetteer (Falling Rain, 2012) with the locality data provided. Coordinates of localities which could not be found using the gazetteer were found using either 'Google Earth' (2012) or the National Geospatial-Intelligence Agency website (2012); however, the accessions for which no coordinates could be found were deleted from the datasets.

All accessions were mapped using DIVA-GIS (Hijmans *et al.*, 2005) and any accessions that obviously had wrong coordinates (for example, were in the sea) were clearly noticeable and were recorded. Each of these accessions was then examined and reassigned coordinates using Google Earth (2012) or the Falling Rain (2012) gazetteer. Google Earth (2012) was used to update accession details held in countries which are no longer recognized, such as the former USSR and former Yugoslavia (UN World Macro Regions and components, 2009). The database was searched for all accessions associated with countries which are no longer recognized, and these entries were updated with the current country name. The final version of the *Hordeum* database contained the data of 17,131 unique georeferenced germplasm accessions and represents all of the 45 wild taxa in the genus *Hordeum*. This database is available on request from the Genetic Resources Section, ICARDA, PO Box 5466, Aleppo, Syrian Arab Republic.

Spatial analysis

DIVA-GIS version 5.2 is a free GIS computer program that was downloaded from 'www.diva-gis.org' along with current WorldClim climatic data at the 10 min resolution and a world map with administrative boundaries. Data on current and proposed global protected areas were downloaded from the IUCN and UNEP-WCMC (2010) website as a polygon shapefile. This contained both IUCN reserves and other conservation bodies such as the World Heritage Convention.

Ex situ conservation gap analysis

Distribution maps of all the species and subspecies were created by importing the georeferenced data into DIVA-GIS and placing them on a world map. Predicted distribution maps were then created for each species and subspecies using the Bioclim method in DIVA-GIS. This algorithm uses climate data and the known localities of a species to suggest areas where that species is likely to exist. Each distribution map was then compared with its predicted distribution map to identify regions where further *ex situ* collecting

missions might be beneficial (depending on whether missions are permitted in that region or country). The priorities for *ex situ* conservation were ranked based upon perceived threat (inferred from narrow geographical distribution).

In situ conservation species richness and complementary analysis

DIVA-GIS version 5.2 was used to produce a global map of species richness for the *Hordeum* genus. A species-rich area in this case will be one where there are many different species of *Hordeum* present. The default cell size was used (1°) and the output variable was defined as 'Richness' and 'Number of different classes'. This method was also used to produce a map of observation richness (areas with the highest number of accessions) but the output variables were defined here as 'Richness' and 'Number of observations'. The reserve selection algorithm was also used in DIVA-GIS to identify which regions would be best for conserving all of the diversity of the genus *Hordeum* using a minimum number of 100 km × 100 km grid cells. All of these maps were then compared with the global protected areas dataset to discover where species exist in established reserves. This is an important procedure, as often it costs less to incorporate a species into an existing reserve management plan than to set up a whole new reserve.

Results

Database content

The data for the accessions listed in the *Hordeum* database were rarely complete, and many accessions contained just taxonomic data and collection location details. The taxonomic data in the *Hordeum* database were 100% complete and the majority of the geographic data were also complete; however, there were a few accessions that had missing location descriptions but had georeferenced coordinates. The amount of ecological and curatorial data was relatively poorly represented with only 19.7% of accessions having altitude data. This highlights the importance of recording complete and detailed data during germplasm collection expeditions.

H. vulgare subsp. *spontaneum* was the most frequently collected taxon within the database with 13,258 accessions (77.4% of total accessions). In the database, there were 21 species that have fewer than 100 accessions; these accounted for only 4.4% of the total accessions (Table 1). *Hordeum guatemalense* Bothmer, Jacobsen & Jørgensen and *Hordeum erectifolium*

Table 1. Number of database seed accessions and priority ranking for *ex situ* collection for *Hordeum* species

<i>Ex situ</i> conservation priority ranking	<i>Hordeum</i> taxa	Number of <i>ex situ</i> seed accessions in the database
High priority	<i>H. guatemalense</i>	1
	<i>H. erectifolium</i>	1
	<i>H. capense</i>	8
	<i>H. cordobense</i>	9
	<i>H. intercedens</i>	11
	<i>H. procerum</i>	14
	<i>H. arizonicum</i>	14
	<i>H. euclaston</i>	20
	<i>H. halophilum</i>	21
	<i>H. roshevitzii</i>	23
	<i>H. depressum</i>	23
	<i>H. flexuosum</i>	24
	<i>H. tetraploidum</i>	31
	<i>H. pusillum</i>	35
Medium priority	<i>H. muticum</i>	50
	<i>H. fuegianum</i>	53
	<i>H. secalinum</i>	62
	<i>H. comosum</i>	76
	<i>H. stenostachys</i>	79
	<i>H. parodii</i>	82
	<i>H. bogdanii</i>	92
Low priority	<i>H. patagonicum</i>	111
	<i>H. jubatum</i>	118
	<i>H. brevisubulatum</i>	138
	<i>H. brachyantherum</i>	160
	<i>H. lechleri</i>	164
	<i>H. chilense</i>	165
	<i>H. pubiflorum</i>	212
	<i>H. marinum</i>	317
	<i>H. bulbosum</i>	792
	<i>H. murinum</i>	967
	<i>H. vulgare</i> subsp. <i>spontaneum</i>	13,258

Bothmer, Jacobsen & Jørgensen are highlighted as being the most poorly represented species quantitatively in the database with one accession each. It is also likely that duplicates exist in the database as when accessions could not be verified as a complete match they were left in. One source of error is the rather frequent wrong determinations of the wild taxa. This could skew the results of the analysis, particularly for those taxa with few accessions, causing a false impression of the current state of conservation for the taxon.

Geographical distribution

The genus *Hordeum* is widely distributed from subtropical areas in South America to arctic areas in Central Asia and North America and is found from sea level up to more than 4500 m altitude. *Hordeum* species can be found in temperate regions in both the northern and southern hemispheres.

The primary gene pool (*H. vulgare* subsp. *spontaneum*) is centred in the Middle East, spreading from around Libya and Egypt in the west, Greece across the Fertile Crescent as far east as Kyrgyzstan and as far south-east as Pakistan. The secondary gene pool (*H. bulbosum*) is centred in the Mediterranean (mainly Greece and Turkey) spreading west to southern Spain and eastwards through Iran to Kyrgyzstan and Uzbekistan. Western Asia has most accessions (13,226) constituting 77% of the total accessions, although it is not a particularly species-rich area. The region with the highest number of species (21) is South America; other species-rich regions include North America (11) and Eastern Europe (10). The majority of the accessions in the database were collected in Israel (62%) where only four of the 32 species of *Hordeum* occur; however, many of these collected accessions are from the same populations and so could be considered duplicates. The countries in which the least number of accessions were collected include Austria (1), Brazil (1), Albania (2) and

Guatemala (2). The analysis of the database shows that the countries with the highest species richness include Afghanistan (7), Argentina (20), Chile (10), Russia (7) and the USA (11). Conversely, there are 26 countries in which two or less *Hordeum* species have been collected. This suggests that these countries are species-poor for *Hordeum*; however, this may not be an accurate

assessment of the situation, as Maxted *et al.* (2004) state that unequal sampling techniques can often lead to underestimation of species richness in under-sampled areas. However, the distribution of *Hordeum* species is already well known due to previous thorough surveying of herbarium material, so we can assume that these countries are species-poor for *Hordeum* rather than under-sampled.

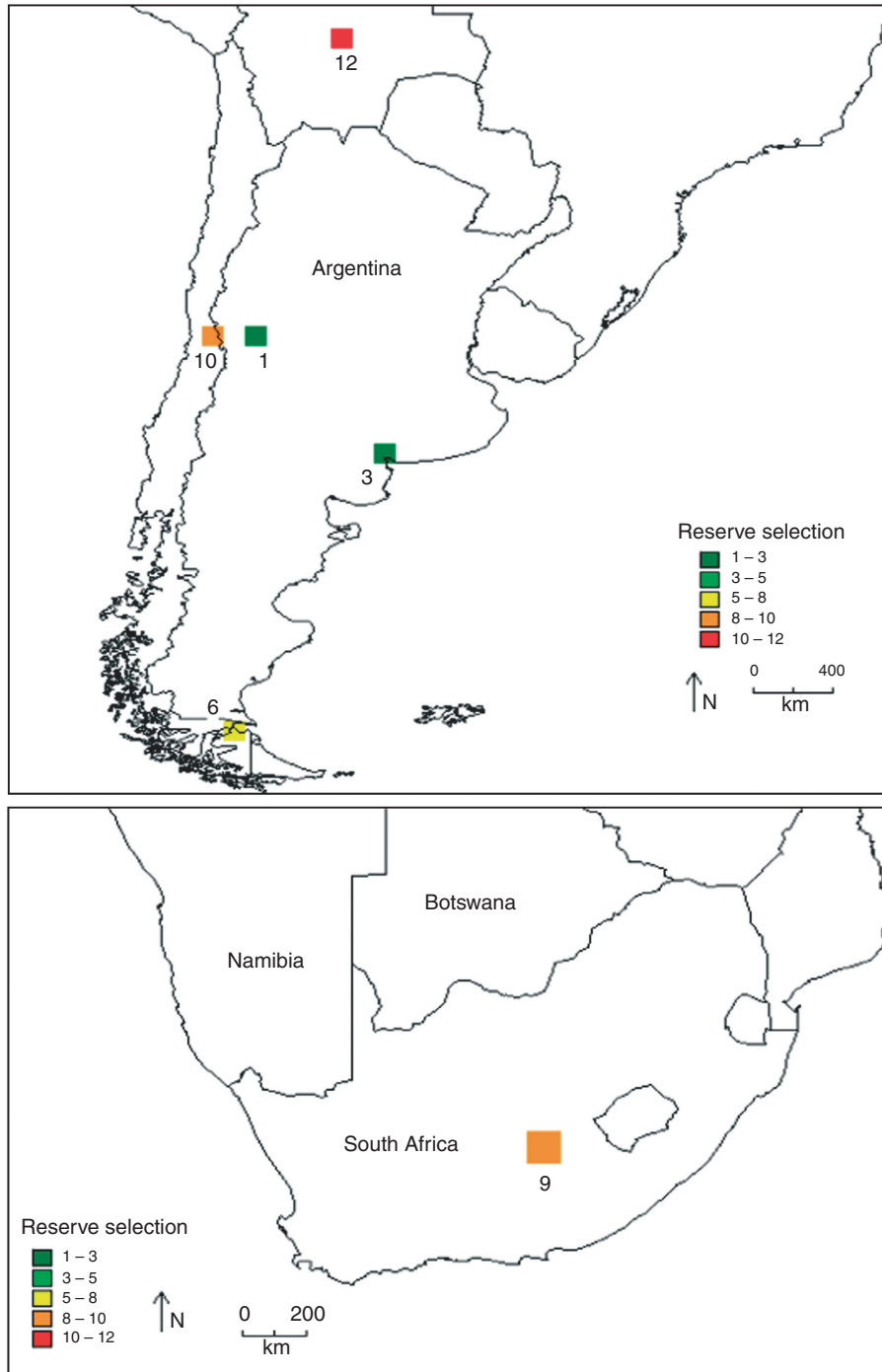


Fig. 1. Complementary analysis of 100 km × 100 km grid cells in order of priority for *in situ* conservation, highlighting South America and Southern Africa (where 1=high priority and 12=low priority).

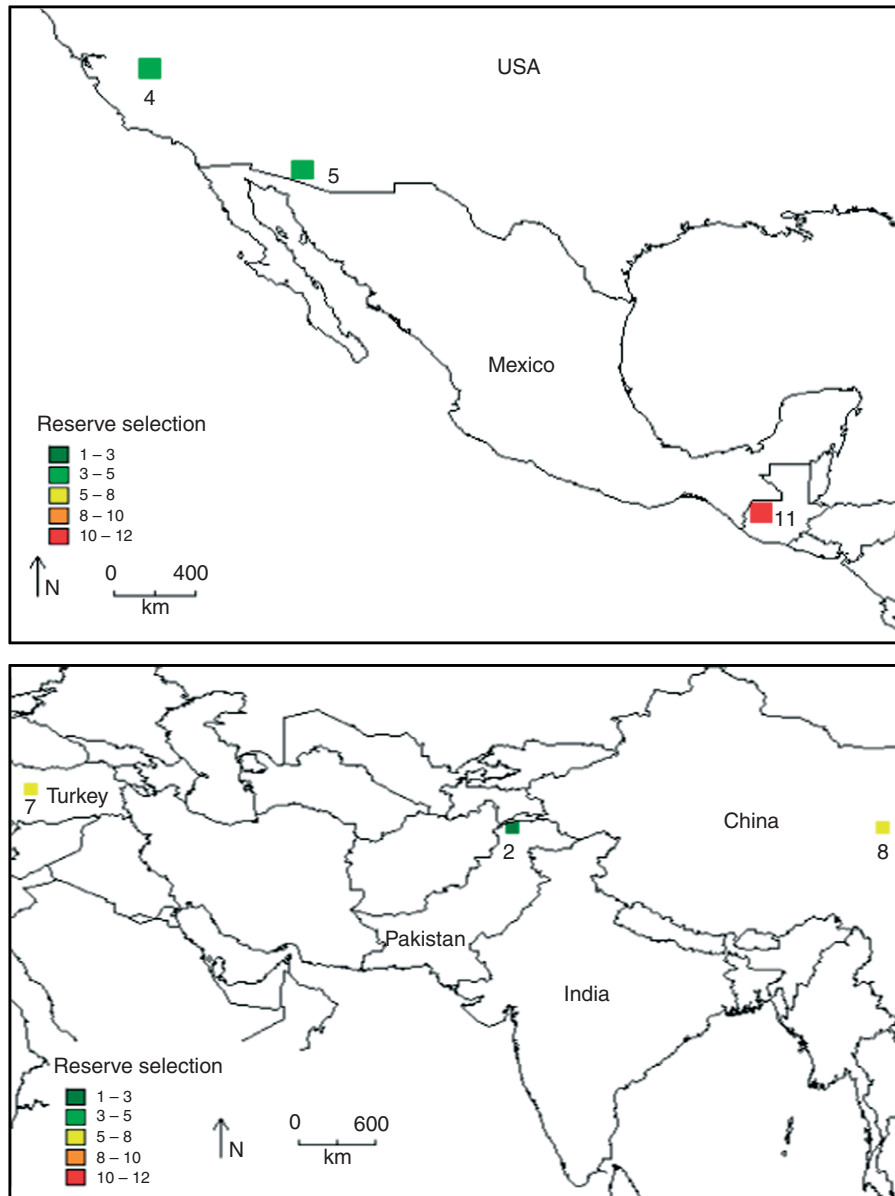


Fig. 2. Complementary analysis of 100 km × 100 km grid cells in order of priority for *in situ* conservation, highlighting North America and Asia (where 1=high priority and 12=low priority).

Ex situ conservation gap analysis

All 32 species of *Hordeum* are represented as *ex situ* germplasm accessions in the survey; however, some are represented very poorly in terms of frequency, with the number of accessions ranging from 1 for *H. erectifolium* and *H. guatemalense* to 13,258 for *H. vulgare* subsp. *spontaneum*. To assess which species require further germplasm collection, the distribution maps of the *Hordeum* database accessions need to be studied along with the predicted distribution maps produced in DIVA-GIS. The results of the gap analysis are documented

in Supplementary Table S1 (available online only at <http://journals.cambridge.org>).

In situ species richness and complementary analysis

The most species-rich area is in southern South America, mainly Argentina, as the area with the highest species richness. The main hotspot is in western Argentina, in the Mendoza Province, and contains 11 *Hordeum* species. The analysis highlights California, USA, as being the most species-rich area in North America with

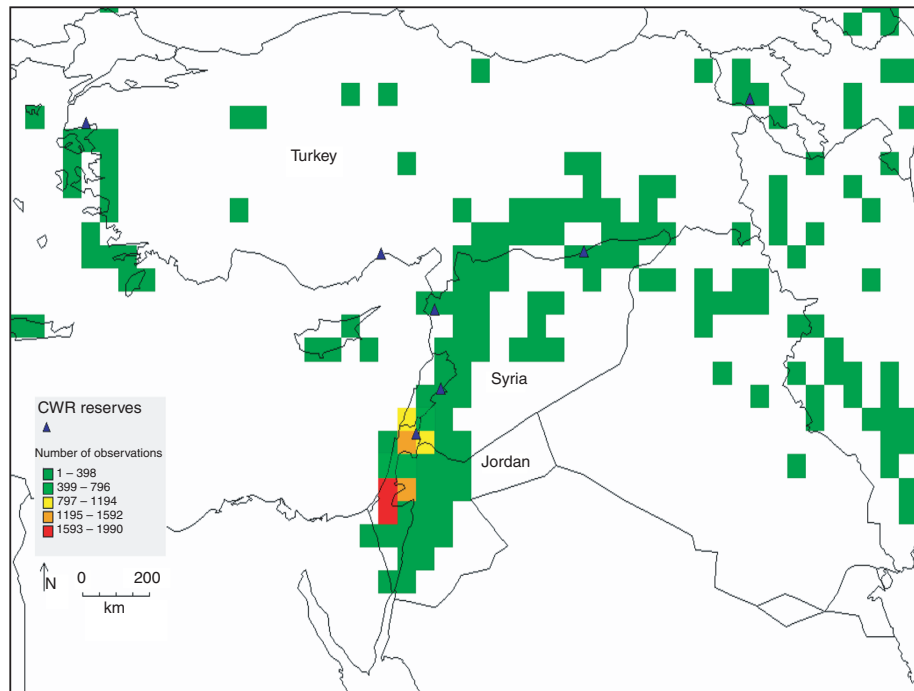


Fig. 3. Observation richness for *Hordeum vulgare* subsp. *spontaneum* using a 50 km × 50 km resolution, also showing known crop wild relative (CWR) reserves.

six species in the richest hotspot; however, two of these species, *Hordeum marinum* and *Hordeum murinum* are introduced species from Europe and have become invasive weeds in several parts of the world, not least North America. In Asia and Europe, the richest areas in terms of the number of species are northern Iran, western Tajikistan, eastern Azerbaijan, central Turkey and Armenia. The observation richness map shows that Israel, Jordan, Syria and Lebanon are the countries where most collections have occurred. The main observation hotspot covering central to western Israel, the West Bank, and a very small part of Jordan and Egypt contains 3,828 accessions which constitutes 22.3% of the total accessions in the database.

To designate the optimal location of *in situ* reserves globally based upon the accessions in the *Hordeum* database, DIVA-GIS employs the Rebelo algorithm which attempts to conserve maximum species diversity in a minimum number of map grid cells. As a result, a total of 12 grid cells were required to represent all 32 species of the *Hordeum* genus. This number is rather high due to the global spread of *Hordeum* species and the narrow distribution of endemic species. Five of the grid cells produced by the reserve selection algorithm were found in South America where 21 species are located according to the data in the *Hordeum* database. The priority site (iteration 1 of the 'reserve selection' algorithm) for a genetic reserve also matches with the species richness results, indicating that the Mendoza Province of Argentina is the ideal area for a reserve. Two grid cells

were located in south-western USA and one in Guatemala. Three grid cells are present in Asia with one in Turkey, one in central China and one in Pakistan. The final grid cell is located in South Africa, south-west of Lesotho (Figs 1 and 2).

The taxa in gene pools 1B (*H. vulgare* subsp. *spontaneum*) and 2 (*H. bulbosum*) were analysed separately due to their importance in barley breeding. Figures 3 and 4 show the richness of observations for *H. vulgare* subsp. *spontaneum* and *H. bulbosum*, respectively, along with known existing sites where CWR are being conserved. The central regions of Israel are highlighted (Fig. 3) as being the area with most observations of *H. vulgare* subsp. *spontaneum*. The other areas of high observations are as follows: the West Bank from Jerusalem to the border of Jordan, the northern region of Israel and across the borders into southern Lebanon, the south-western point of Syria and the north-western tip of Jordan. The Izmir area of Turkey has the most observations of *H. bulbosum* (Fig. 4) with Gaziantep and Urfa, also in Turkey, having high richness.

National protected areas

To compare the reserve sites identified previously with current *in situ* conservation activities, the World Database on Protected Areas (WDPA) (IUCN and UNEP-WCMC, 2010) that contains polygon shapefiles of the world's different protected areas was used. Supplementary

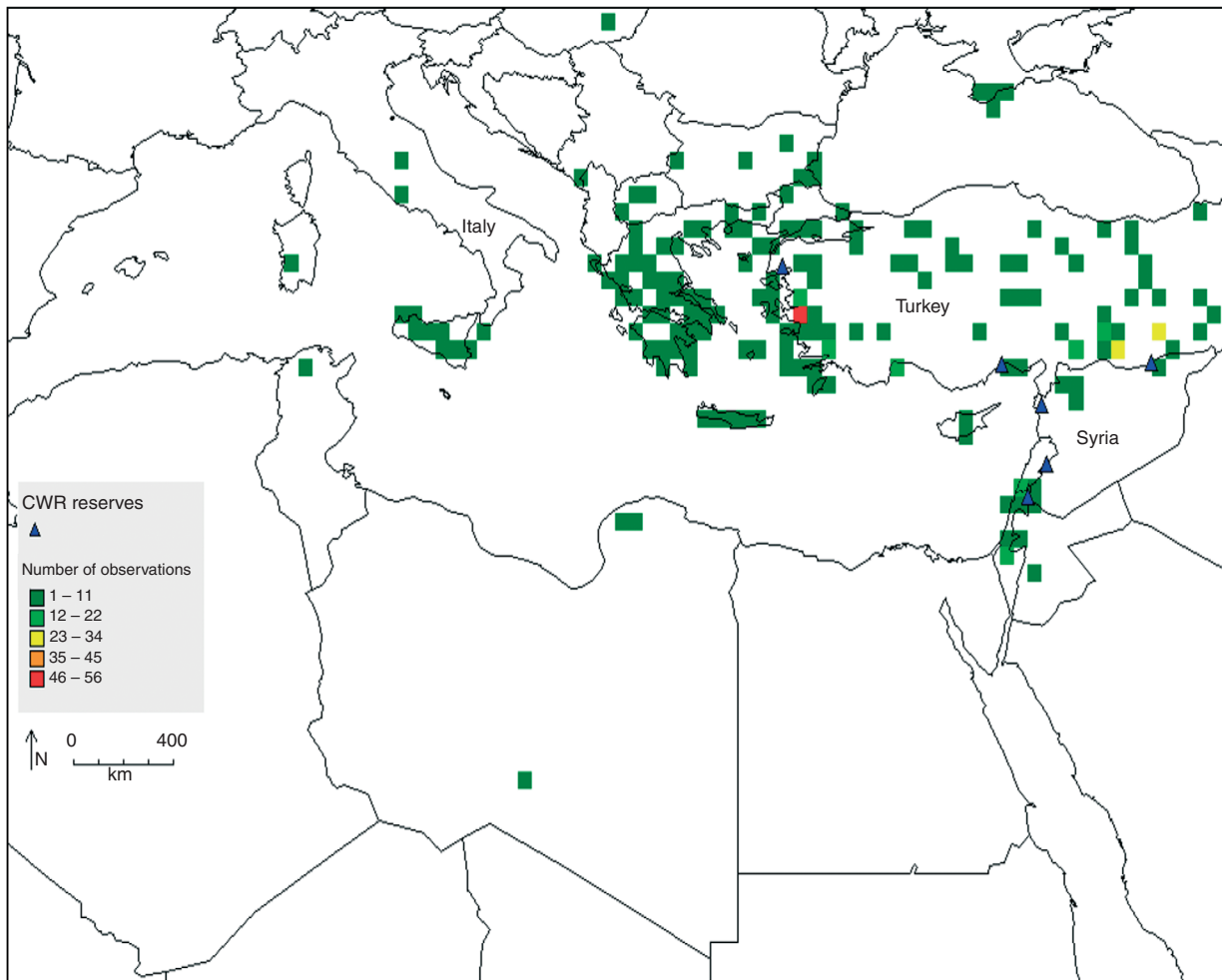


Fig. 4. Observation richness for *Hordeum bulbosum* using a 50 km × 50 km resolution, also showing known crop wild relative (CWR) reserves.

Table S2 (available online only at <http://journals.cambridge.org>) shows that 11 out of 12 hotspots identified have national protected areas within them. Further analysis was conducted, listing every country where an occurrence of *Hordeum* species was present and when any accession was found within a protected site; the reserve name and the species were recorded too. This highlighted that the USA and Israel have the most accessions within national protected areas and, globally, 25 out of 32 species are represented at least once in a national protected area.

Discussion

Assessment of current conservation strategies

In situ conservation assessment

After reviewing online material and literature, several established genetic reserves were found that actively

conserve *Hordeum* species, centred near the Fertile Crescent. There is a reserve in Ammiad, Galilee that includes wild *Hordeum* species in its management plan (Anikster *et al.*, 1997), and there are three genetic reserves in Turkey, one in the Kaz Dag area, another in Ceylanpinar and the last in the Amanos region, that include wild *Hordeum* species in their management plans (Ertug and Tan, 1997). The reserves in Haffeh, Syria and Ham, Lebanon also conserve wild *Hordeum* species. The Erebuni reserve in Armenia is located 8–10 km from Yerevan and holds several species of wild *Hordeum* (Avagyan, 2008). In addition to this, the distribution of the accessions in the *Hordeum* database was compared with the WDPA, and it was found that there are over 100 national protected areas in which *Hordeum* species potentially exist. This suggests that passive *in situ* conservation (where there is no active population management of the target species) is occurring for 25 species of *Hordeum* across the geographic range of the genus. The species not covered even

passively are *H. cordobense*, *H. erectifolium*, *H. euclaston*, *H. flexuosum*, *H. guatemalense*, *H. procerum* and *H. stenostachys*. It is important, however, that target sites receive active *in situ* conservation and *Hordeum* species are incorporated into active management plans to ensure the species' future protection.

Ex situ conservation assessment

The Results section details where each species of *Hordeum* could be further collected. Overall, South America contains a wealth of *Hordeum* diversity which may prove to hold important genes for the future of barley breeding and the region has not been conserved sufficiently in *ex situ* collections; the 21 species (66% of species) found in this area account only for 7.2% of the accessions in the *Hordeum* database. Of the wild taxa, *H. vulgare* subsp. *spontaneum* has the highest number of accessions in the primary gene pool of cultivated barley; however, further collection of this taxon would still be advised but in varied ecological niches to ensure that the full diversity of the species is conserved. *H. bulbosum* is also reasonably well represented in *ex situ* collections with 792 accessions; this is most likely due to the relative ease of breeding useful traits from *H. bulbosum* into cultivated barley compared with other wild relatives (excluding *H. vulgare* subsp. *spontaneum*). Additionally, some perennial and outcrossing species are more difficult to conserve *ex situ*, therefore their conservation is limited in genebanks. The gap analysis indicates that the majority of *Hordeum* species are under-represented and require further collection.

Formulating conservation strategies

In situ conservation priorities

Hordeum species with highest priority for *in situ* conservation are the ones with the highest socio-economic value, these being *H. brevisubulatum*, *H. bulbosum*, *H. chilense*, *H. cordobense*, *H. jubatum*, *H. marinum*, *H. murinum* and *H. vulgare* subsp. *spontaneum*. This is due to the fact that these species have a particularly good prospect for utilization in wheat and barley breeding (Xu and Snape, 1988; Kindler and Springer, 1991; Vaz Patto *et al.*, 2001; Martín *et al.*, 2000; Knüpffer, 2009; Bothmer and Komatsuda, 2010).

A genetic reserve in South America, either in Chile or Argentina, is required as a large amount of *Hordeum* diversity is native to this region. The species richness analysis and reserve selection identify Mendoza near the Chilean border as the best place to establish a reserve. However, further investigation is required to identify the three distinct ecotypes of *H. chilense* to ensure that all of them are conserved adequately. *H. chilense* does

appear in five national protected areas; so, as an interim measure before a reserve is set up for this species, these protected areas could alter their management plans to include *H. chilense* conservation.

In the Middle East, several areas seem likely places to establish further reserves, the first being near Izmir in Turkey (for *H. bulbosum*) and the second (for *H. vulgare* subsp. *spontaneum*) being the Israel/Jordan area (DIVA-GIS suggests east of Jerusalem) where the crop was first domesticated; however, a network of several reserves in the Israel/Jordan region would be more desirable, to more effectively conserve the genetic diversity of this important taxon. Using Fig. 3, the following places would be good sites to establish reserves for *H. vulgare* subsp. *spontaneum*: near Be'er Sheva, Israel, between Hebron and Jerusalem in the West Bank, and finally the area around Irbid, Jordan. Although there is already a genetic reserve conserving wild *Hordeum* in Ammiad, Israel, this region is the centre of diversity for the primary gene pool of cultivated barley and could possibly benefit from another genetic reserve being established or at least incorporating wild *Hordeum* into the management plans of the 12 protected areas in Israel where species have a georeferenced accession. However, the genetic diversity of populations of both priority taxa should be examined to further determine that the proposed sites are conserving as much genetic diversity as possible. Additional sites should be set up in Europe and Asia to conserve *H. bulbosum* and *H. vulgare* subsp. *spontaneum* (covering the range of habitats *H. brevisubulatum*, *H. bulbosum*, *H. chilense*, *H. cordobense*, *H. jubatum*, *H. marinum*, *H. murinum* and *H. vulgare* subsp. *spontaneum* in which these species occur); however, this requires further ecological analysis and, ideally, the use of molecular marker techniques to ensure the conservation of genetically distinct populations.

A further genetic reserve should also be established (or existing protected area management plans amended) in California, USA to ensure protection of the endemic species found there, as they are threatened by anthropogenic disturbance more than other *Hordeum* species (Bothmer *et al.*, 1995). The gap analysis suggests that south of Bootjack, next to the Sierra National forest, would be a good place to establish such a genetic reserve.

Genetic reserves should also be created to conserve populations of *H. guatemalense* and *H. erectifolium* in Guatemala: Departamento de Huehuetenango, Chiantla, Llano de Pacquix and Argentina: Buenos Aires, Buenos Aires Provincia, Bahía Blanca Partido, respectively. As these are endemic and have small populations, it is better to set up *in situ* reserves than collect further seed for *ex situ* storage, as over-collecting could damage the populations and the existing collections in genebanks most probably already contain the majority

of the genetic diversity of the species. Also, being endemic and such small populations, there is a greater threat of extinction, so setting up *in situ* reserves would hopefully offer better protection.

All prospective sites for reserves should be checked to actually establish that the target taxa are present and ensure viable population size before any steps to establish reserves or alter management plans are taken.

Ex situ conservation priorities

It has been argued by Ford-Lloyd *et al.* (2008) that: ‘... species must be prioritised so that those which require the most urgent attention and conservation planning can be dealt with as soon as possible...’. The gap analysis used a simple prioritization technique based upon perceived threat (inferred from narrow geographical distribution) and relative numbers of *ex situ* conserved accessions. The species are ranked as follows:

High priority – *Hordeum* species represented by less than 50 *ex situ* accessions and/or species poorly represented in their known and predicted geographical range.

Medium priority – species that are well represented across the known and predicted geographical range with less than 100 accessions stored *ex situ*.

Low priority – species well represented throughout their geographical range with more than 100 accessions stored *ex situ*.

See Table 1 for the priority ranking for *ex situ* collection for *Hordeum* species.

For a more effective *ex situ* and *in situ* conservation of population diversity (genetic diversity), the gap analysis on the basis of species richness, geographical distribution, should be complemented with genetic diversity analysis of existing accessions using mainly molecular marker techniques. An example of such a studies is the series of papers on *H. marimum* (Jakob *et al.*, 2007), Patagonian species (Jakob *et al.*, 2010) and the (South) American diploids (Jakob and Blattner, 2010), but these studies require extension to the entire gene-pool. Targeting valuable traits for *ex situ* and *in situ* conservation can also add another important dimension to concentrate the conservation efforts on populations’ adaptive traits such as heat, drought and salt tolerance.

Conclusion

In conclusion, the majority of wild *Hordeum* taxa are under-represented in genebanks globally with 14 wild species having less than 50 accessions stored *ex situ*. There is an additional need for further investigation

into the ecological environments that *Hordeum* species occupy to ensure that any adaptive traits expressed are fully conserved, particularly in the case of *H. vulgare* subsp. *spontaneum* and *H. bulbosum*.

Genetic reserves should ideally be established in Argentina, Guatemala and the USA to cover both the threatened endemics and high species diversity in the Americas. An important network of reserves should also be set up across the Fertile Crescent in Israel, Palestine, Syria, Jordan, Lebanon and Turkey to provide effective conservation within the centres of diversity for gene pools 1B and 2. Although there are several existing genetic reserves that claim to be actively conserving *in situ* *Hordeum* diversity, it would be expedient to review the conservation procedures in place and ensure that they conform to current international standards (Iriondo *et al.*, 2008, 2012).

Finally, studies are required to genetically characterize existing collections and to test the viability of rare species accessions held in genebanks to determine whether further *ex situ* collections are required alongside the proposed *in situ* conservation.

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