Towards a conservation strategy for wild *Hordeum* spp.: using niche modelling

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Why conserve wild *Hordeum*?

- Crop wild relatives (CWR) are an important source of genetic diversity for use in crop breeding.

- Over the next couple of decades, use of CWR relatives in crop improvement will rise due to:
  - Improved and increased gene transfer technology and ability.
  - As a consequence of global climate change (Maxted & Kell, 2009).

- Wild *Hordeum* species have already been used extensively in improving cultivated barley.
Use of wild *Hordeum*

- *H. bulbosum* - resistance against: rice blast fungus, leaf rust and powdery mildew, scald and Russian wheat aphid and greenbug (Bothmer & Komatsuda, 2010)

- *H. murinum* - subspecies *glaucum* and *leporinum* show strong resistance to barley scald (Bothmer & Komatsuda, 2010)

- *H. cordobense* - resistance to common root rot and spot blotch (Bothmer & Komatsuda, 2010)

- *H. jubatum* - resistance to stem rust and tolerance to saline environments (Bothmer & Komatsuda, 2010)

- *H. marinum* - high tolerance for saline environments, waterlogging tolerance and oxygen deficiency (Bothmer & Komatsuda, 2010)

- *H. chilense* - ability to cross with other members of the *Triticeae* tribe such as durum wheat to make an interesting new crop *Tritordeum* (Martín et al., 2003)
Genetic Gap Analysis Methodology

Step 1: Circumscription of target taxon and target area

Step 2: Natural *in situ* diversity
2a - Taxonomic Diversity Assessment
2b - Genetic Diversity Assessment
2c - Ecogeographic Diversity Assessment
2d - Threat Assessment

Step 3: Current conservation strategies
3a - *In situ* techniques
3b - *Ex situ* techniques

Step 4: Setting priorities for conservation action
4a - *In situ* conservation priorities
4b - *Ex situ* conservation priorities

Maxted *et al.* (2008)
Project aim


- Identification of *in situ* conservation priorities
- Identification of *ex situ* conservation priorities
Hordeum taxa

- *Hordeum* has 32 species and 45 taxa (Bothmer, 1995)

- Centres of diversity for *Hordeum* are:
  - Southwest and central Asia
  - Southern South America
  - Western North America

- Centre of diversity for gene pool 1 (*H. vulgare* subsp. *spontaneum*) is the Fertile Crescent

- Centre of diversity for gene pool 2 (*H. bulbosum*) is in the Mediterranean centred around Greece and Turkey
Data collation

Accession passport data sources:
- ICARDA gene bank: 16,716
- IPK gene bank: 1,280
- Nordic gene bank: 1,333
- EURISCO: 5,646
- PGRC: 56,309
- USDA: 30,617
- Von Bothmer data set: 2,763

Original total of accessions = 114,664

But, after duplicate removal and deletion of unusable data…

Total reduced = 17,169 germplasm and herbarium accessions
The ecogeographic database

- Contains data on accession name and identifiers, collectors name and date and collection location
- Compared data sets, checking for duplicates, deleting exact matches and updating any missing information (where possible)
- Updated rows with longitude, latitude and elevation data using GoogleEarth and online gazetteers
Issues related to data collation

• Inaccurate/ old data
• Gazetteers possibly incomplete/ inaccurate
• Human error
• Poor formatting = more manual inputting
• Duplicates that differed for important information.
• Finding duplicate accessions
• Are the accessions viable?
• Misidentified species
Global geographical spread of all *Hordeum* species

N = 17,169 accessions
Hordeum vulgare GP1 and GP2 distribution
Hordeum Species Richness: South America
Hordeum Species Richness: Europe and Asia
Hordeum Species Richness: America
**Hordeum Species and Observation Richness**

- South America has the largest diversity of *Hordeum* species with 21 species.
- Richest areas in Middle East / Asia are Tajikistan / Uzbekistan, Armenia, Turkey and Iran with either 5 or 6 species being present in grid cells.
- Eastern Mediterranean has the most collections but not highest species richness.
Frequency of species collection
Accessions and species per region
Gap analysis of *H. vulgare* subsp. *spontaneum* (GP1b)
Gap analysis of *H. bulbosum* (GP2)
In situ Gap Analysis

In situ gap analysis involved comparing known National Protected Areas with actual distribution points to see which accessions currently have passive protection

- 25 species are globally present in national reserves
- The USA and Israel have the most accessions in national reserves with 25 and 12 reserves respectively

There are 7 wild species that are not represented in protected areas:

- *H. erectifolium* (1 accession)
- *H. euclaston* (20 accessions)
- *H. flexuosum* (24 accessions)
- *H. guatemalense* (1 accession)
- *H. procerum* (14 accessions)
- *H. cordobense* (9 accessions)
- *H. stenostachys* (79 accessions)
In situ Gap Analysis cont.

There are several protected areas where maintenance of *Hordeum* diversity is included in their management plans:

- Ammiad, Israel
- Kaz Dag, Turkey
- Ceylanpinar, Turkey
- Amanos, Turkey
- Haffeh, Syria
- Ham, Lebanon
- Erebuni, Armenia
Reserve Selection Algorithm

- DIVA-GIS was used to designate the optimal location of *in situ* reserves globally based upon the accessions in the *Hordeum* database.

- The algorithm DIVA-GIS employs attempts to conserve maximum species diversity of an entire genus in a minimum number of 100km x100 km grid cells.

- 12 grid cells were required to represent all 32 *Hordeum* species.
*Hordeum* Reserve Selection: South American hotspots
Hordeum Reserve Selection: American Hotspots
Hordeum Reserve Selection: Asian Hotspots
Reserve Selection: South African Hotspot
Hordeum priority (GP1b + GP2) species hotspots
**Ex situ Conservation Priority Species**

Species <50 accessions have *ex situ* collection priority:

<table>
<thead>
<tr>
<th>H. tetraploidum</th>
<th>H. roshevitzii</th>
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<tbody>
<tr>
<td>H. pusillum</td>
<td>H. procerum</td>
</tr>
<tr>
<td>H. intercedens</td>
<td>H. halophilum</td>
</tr>
<tr>
<td>H. guatemalense</td>
<td>H. flexuosum</td>
</tr>
<tr>
<td>H. euclaston</td>
<td>H. erectifolium</td>
</tr>
<tr>
<td>H. depressum</td>
<td>H. cordobense</td>
</tr>
<tr>
<td>H. capense</td>
<td>H. arizonicum</td>
</tr>
</tbody>
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Populations of *H. guatemalense* and *H. erectifolium* are so rare, there may be little new diversity gained from further collections.
In situ conservation for the whole genus

DIVA identified Argentina as the country with the most species diversity, a location in west central Argentina (slightly east of Mendoza) near the Chilean border would be optimal reserve for conserving species richness.

A reserve should be established near Bahia Blanca to conserve those species not found in any protected area.

A genetic reserve should be set up near Chiantla, Guatemala for H. guatemalense.
In situ conservation for the priority species alone
Allied analysis: Complementarity Analysis of priority *Aegilops* species (White and Maxted, 2006)
Allied analysis: Complementarity Analysis of priority Avena species (Patsiou and Maxted, 2007)
Next Steps -

- Further genetic gap analysis of cereal data
- Targeted *ex situ* collection
- Establishment of genetic reserves in existing protected areas
- Establishment of novel protected areas
- Integration of genetic reserves into FAO Global CWR Network