



# Crop wild relatives in Lebanon: mapping the distribution of Poaceae and Fabaceae priority taxa for conservation planning

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**Abstract** Lebanon is a part of the Fertile Crescent recognized for its agrobiodiversity wealth in terms of both cultivated plants and crop wild relatives (CWR) diversity. Within the context of climate change and its adverse effect on agrobiodiversity, conservation of CWRs in Lebanon is essential to prevent the loss of potentially useful genetic diversity and to facilitate their use in crop breeding. To establish a comprehensive conservation plan for Lebanese CWR belonging to Poaceae and Fabaceae, in this study we prioritized 16 taxa based on their value for world security and local economy, gene pool (primary and secondary) and genome type (A, B and D

for *Triticum* genera). Georeferenced occurrence data of populations belonging to the prioritized taxa list were retrieved from different sources and imported into QGIS to visualize by mapping their distribution in-situ and ex-situ on the Lebanese territory, highlighting sites with highest density per genus and sites characterised by the highest taxa richness. The analysis allowed to identify Lebanese areas that still need further surveying actions (mainly the south-west parts of the country) and showed that priority taxa had different distribution pattern independently from genus. Bekaa and Baalbak governorates were evaluated to include sites represented with highest taxa richness, which makes them preliminary contenders to be included within in-situ conservation actions. This study provided a foundation for further research into the conservation planning of crop wild relatives belonging to Poaceae and Fabaceae in Lebanon by identifying areas with highest taxa richness.

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Eliane Sayde and Lorenzo Raggi have equally contributed to this work and should be both considered first authors.

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## Introduction

A crop wild relative (CWR) is defined as a wild taxon that is more or less closely related to a particular crop and to which it might contribute with genetic material (Heywood et al. 2007). This relationship can be defined using the “Gene Pool” or the “Taxon Group”

concept. Aiming at a rational classification of cultivated plants, Harlan and de Wet (1971) established the “Gene Pool” concept. they designated germplasm resources as primary gene pool (GP-1) the cultigen itself and any wild forms that breeding tests show to be conspecific with it (i.e. the same biological species), as secondary gene pool (GP-2) those taxa for which gene flow with the cultigen is possible via interspecific hybrids and tertiary gene pool (GP-3) those taxa for which hybridization with the cultigen is possible but the hybrids themselves are infertile, inviable or anomalous and do not allow gene flow by normal introgressive processes. Remarking that the gene pool concept has limitations (Maxted et al. 1997a, b), the Taxon Group was conceptualized in the following manner (Maxted et al. 2006): Taxon Group 1a—crop, Taxon Group 1b—same species as crop, Taxon Group 2—same series or section as crop, Taxon Group 3—same subgenus as crop, Taxon Group 4—same genus and Taxon Group 5—same tribe but different genus to crop.

CWRs are a vital source of genes for increasing the diversity of the cultivated gene pool of many crops; they are particularly rich with genes for resistance to diseases, pests and stresses such as drought and extreme temperature (Fonseka et al. 2020); indeed, their great value in bringing “game changing” characteristics to the breeding pool through hybridization is well recognized by breeders and could be particularly relevant in mitigating the impact of climate change on agricultural systems through the development of improved varieties that are genetically tolerant or resistant to the new range of abiotic and biotic challenges (Kilian et al. 2021). A major proportion (80%) of traits transferred from CWRs into cultivated crop varieties includes resistance to diseases and pests (Hajjar and Hodgkin 2007; Bohra et al. 2021) but they have been also used to increase the nutritional value and protein content in durum wheat (Saini et al. 2022) and chickpea (Sharma et al. 2021); the development of nutrient-rich crop cultivar can be relevant to combat malnutrition through biofortification.

When still present in nature, CWR are subjected to natural selection that allows them to maintain a high degree of adaptability and a rich pool of genetic diversity; since gene transfer can occur between cultivated plants and their wild relatives, they are good candidates in crop enhancement for novel traits (Allaby et al. 2019). Germplasm is likely to reflect the

selection pressures of the environment in which it is developing. Environmental parameters describing the sites can be thus used as selection criteria to improve the probability of uncovering useful variation. The focused identification of germplasm strategy (FIGS) is an efficient method to explore plant agro-biodiversity for climate change adaptive traits. The correlation between the geographic distribution of resistance genes and environmental variables at collection sites enabled accurate prediction of novel sources of resistance against stem rust (Bari et al. 2012) and stripe rust (Bari et al. 2014) from wheat landraces stored in the genebank at the International Center for Agricultural Research in the Dry Areas (ICARDA). A similar approach also worked for the identification of stripe rust resistance genes in a global spring wheat panel including landraces and improved accessions (Elbasyoni et al. 2019). Gene transfer can also occur when the crop and the wild species are characterised by different chromosome number and even by a different ploidy level. In this case the gene can overcome the natural sex compatibility barrier through the formation of an initial hybrid naturally experiencing successive backcrosses that allow to restore fertility to a certain degree. The weedy *Aegilops cylindrica* Host. have been identified as a valuable source for herbicide resistance gene that can be transferred for breeding new varieties of the polyploid soft wheat (*Triticum aestivum* L.) (Wang et al. 2001; Guadagnuolo et al. 2001).

The need of conservation comes from the continuous degradation of habitats and extinction of CWR holding possibly unique and valuable genetic diversity. Therefore, there is an urgent need to address a continued maintenance and conservation of CWR at global, regional, national and local levels in order to (i) minimize the vulnerability of areas rich in CWR and (ii) maximize the availability of plant genetic resources for crop improvement, to increase productivity and food security; this also applies to agricultural systems of the most vulnerable farmers and rural people in developing countries (FAO 2001). Therefore, one of the most important aspects of agrobiodiversity to be emphasized is the state of the genetic resources that are currently conserved and utilized in agricultural production systems (OECD 2001). In those regions where biodiversity and agrobiodiversity still exist, and especially in the areas where they are particularly threatened or affected by widespread

industrial and agricultural activities, high population density, and the effects of climate fluctuation (Pacicco et al. 2018), conservation plans are of great relevance and urgently required.

For an appropriate and systematic conservation of agrobiodiversity, CWRs and landraces that are its main components, both in-situ and ex-situ approaches should be considered and pursued (Maxted et al. 2006). The ex-situ strategy allows the conservation of components of biological diversity outside their natural habitats involving localising, sampling, transfer and storage of samples of the target taxa away from their native habitat in gene banks or in field gene banks as living collections (CBD 1992; Maxted et al. 1997a, b). Whereas in-situ conservation involves the maintenance of genetic variation at the location where it is encountered, either in the wild or in traditional farming systems (CBD 1992; Hopkins and Maxted 2010). The benefit of in-situ conservation approach is that it allows taxa to remain genetically dynamic and continue to evolve in response to both natural and artificial selection, thereby enhancing their adaptation to the environments in which they are grown (Bohra et al. 2021).

There is no single best method for planning CWR conservation (Magos Brehm et al. 2022) but a basic pattern has been suggested (Magos Brehm et al. 2017; Maxted et al. 1997a, b). The process starts with the generation of a CWR checklist, followed by a prioritization of CWR taxa to be the focus of conservation action, available baseline ecogeographic data are then collected and threat assessment and gap analysis are performed. Based on the results of the above-mentioned steps in-situ and ex-situ actions are recommended that form the basis of a national CWR strategy. Additionally, the conservation action requires continuous monitoring of CWR diversity and promoting the use of CWR.

The first step of conservation planning is the creation of a checklist, an inventory including all the species present in a certain area (normally a country), to provide a logical organization of diversity information presented in a retrievable way, and to avoid duplication of efforts (Maxted et al. 2015). The CWR checklist is usually created before prioritization. For each considered taxa, priority level is generally assessed by considering its geographic presence with information related to nomenclature, the applied Gene Pool or Taxon Group concepts with actual and potential utilization of

the CWR for crop improvement, biology, habitats, ecogeography, direct uses, threats and threat status, current conservation actions and legislation (Maxted et al. 2013). Prioritized list of wild plants of socio-economic interest has been developed for Italy (Ciancaleoni et al. 2021) as well as for other countries (El Mokni et al. 2022 and references therein). Gap analysis is a systematic method of analysing the degree of conservation of taxa (Ramírez-Villegas et al. 2010) aiming at identify those locations, taxa, and particular traits such as adaptations and presence or absence in secured conservation systems (Maxted et al. 2008). Gap analysis techniques assists a pragmatical collecting and conservation by emphasizing target localities where sets of species absent from existing collections can be obtained with least effort and cost, assessing which areas are not well collected or fully conserved based on distribution of a taxon; locating which regions have the greatest or most dissimilar species richness compared with other regions, and defining the ecological amplitudes of each species (Nabhan 1990).

Lebanon is a part of the Fertile Crescent recognized for its agrobiodiversity wealth in terms of both cultivated plants and CWR diversity. Lebanon has 2,606 vascular plants (Mouterde 1970). Located at the Eastern shore of the Mediterranean Basin, Lebanon represents one of the most important agrobiodiversity hotspots, not only for wild species diversity, but also for cultivated plant diversity (Talhouk et al. 2018). The country is also well recognized for its wealth in CWRs (Nair 2019; Vincent et al. 2013) with a large share of Poaceae and the Fabaceae families (Zair et al. 2018).

As a first step towards a comprehensive conservation plan for Lebanese CWR, in this study we aimed to (i) review the CWR species occurring in Lebanon and identify those that are priority for global food security and local economic significance, (ii) study the distribution of priority species and identify sites for new collections to fill the gaps in genebanks and (iii) identify the areas richest in priority species CWR diversity to be target of future ad hoc designed conservation activities.

## Material and methods

### Elaboration of a taxa list and prioritization

Since the products of the major cereals and legumes account for a large part of carbohydrate and protein

for human nutrition, we decided to focus our investigation on CWR taxa of Poaceae (formerly called Gramineae) and Fabaceae (also known as Leguminosae) families present in Lebanon. First a desk analysis was performed to create a checklist of the taxa belonging to the following genera of the above-mentioned families: *Aegilops* (now included in *Triticum*), *Avena*, *Triticum*, *Hordeum*, *Pisum*, *Lens* and *Cicer*, which are considered of primary importance at worldwide level (Vincent et al. 2013). Since we wanted to focus on CWR taxa known to be present in-situ and/or ex-situ in Lebanon, the list was developed using data from Mouterde (1966, 1970, 1986), the International Center for Agricultural Research in the Dry Areas (ICARDA-Lebanon) genebank's database and from the online databases GBIF and GENESYS.

GBIF is an international network and data infrastructure aimed at providing open access to chorological data of all types of life on Earth and coming from genebanks, botanic gardens, museums, and universities. Fed by numerous national and international data providers, GENESYS is a database holding information on ex-situ accessions conserved in genebanks worldwide. Once developed, the taxa list was validated and checked for synonymous relying on: (i) Plants Of the World Online (<https://powo.science.kew.org/>); (ii) World Flora Online (<http://www.worldfloraonline.org/>) and (iii) Euro+Med (<https://www.emplantbase.org/home.html>) databases. The taxa nomenclature used in this study, followed the taxa list provided by the gene bank database to avoid the confusion on the accession level.

Identified taxa were then prioritized according to the following criteria (i) taxa relevance for Lebanese economy and food security, (ii) level of fertility with the corresponding crop and (iii) genome type, this criterion was only applied to taxa belonging to the genus *Triticum*. Evaluation of the first criterion was performed using data available on FAOSTAT (2019). For the application of the second criterion, we relied on the gene pool concept (Harlan and de Wet 1971), only the taxa belonging to the primary (GP-1) and secondary (GP-2) gene pools of the related crop were included in the prioritized list; some specific cases of CWR taxa belonging to the tertiary (GP-3) were also taken into consideration. As for the third (criterion), only *Triticum* and *Aegilops* taxa holding A, B or D genomes, that are the genomes of *T. aestivum*, the most cultivated species in the world (FAO 2019),

were included. Each priority taxon was also assessed through literature review for their importance in breeding, valuable traits and nutritional value.

As for the main characteristics of the three *Triticum* genomes considered, chromosomes of A genome carry important genes related to milling yield (Parker et al. 1999), flour colour (Parker and Langridge 2000), supernumerary spikelet (SS) (Peng et al. 1998), pre-harvest sprouting resistance (Zanetti et al. 2000), total florets per spike (Zheng et al. 1993) and yield traits such as tiller number, heading date and plant height (Yuanwu and Yujian 1995). The B genome was identified to contain a considerable portion of alleles able to increase the expression of relevant agronomic traits such as the ability to extend root system when subjected to drought stress (Ahmadi et al. 2018). D-genome was revealed to carry QTL(s) associated with photosynthetic pigments content, chlorophyll fluorescence, shoot biomass, and tolerance indexes of these traits, additionally to drought tolerance (Osipova et al. 2016).

#### Occurrence data collation and quality verification

Georeferenced occurrence data of populations belonging to the taxa included in the prioritized list were retrieved from different sources. For each considered taxa two list of records were created:

- in-situ *list*, including records from ICARDA's genebank, GBIF and Genesys
- ex-situ *list*, including records from ICARDA's genebank and Genesys

To get the most accurate data and eliminate possible errors, collected data went through filtering and cleaning process using some of the parameters suggested by Rubio Teso et al. 2020 (Table 1). Records dated before 1950 were also removed and duplicates simplified keeping the records with locality field information, most recent and informative.

The application of described filters allowed to generate an operative high-quality CWR occurrences database for the geographic area of the study, using both geographic and temporal criteria. Noting that ICARDA's database and Genesys both represent ex-situ data, therefore their data could contain similarities, we prioritized the Genesys data when deleting duplicates as

**Table 1** Filtering and cleaning steps applied to select high quality CWR occurrence data; records belonging to the categories listed in the Table were deleted

Applied filter	GBIF	Genesys
Whose coordinates do not match with the reported country	X	X
With coordinates in the sea	X	X
In country centroids, capital cities, botanic gardens, or a GBIF headquarter	X	X
Cultivated origin or cultivated in botanic gardens	X	X
Susceptible to be of low quality or not trustable according to the GBIF issues flags or coming from unreliable source (e.g., iNaturalist)	X	X
Coming from the SINGER database, better updated and available in the Genesys database	X	–

The “X” indicates that the filter has been applied to records retrieved from the corresponding database while the “–” that the filter was not applicable

they described more details related to location and environmental aspects of the collection site.

#### Mapping taxa distribution and density

After filtering procedure, data were imported into QGIS software v3.16.15-Hannover (QGIS Development Team 2021) specifying the geographic reference system WGS84 (EPSG: 4326) not projected, compliant with the LAT/LONG DD format.

Distribution through the Lebanon territory of the populations belonging to the different CWR taxa considered was graphically elaborated by species. A density analysis was also performed by genus as described in Raggi et al. (2022), to the purpose a grid of cells of 0.025 degrees side was used (each cell covering about 5 km<sup>2</sup>). Cells including  $\geq 1$  CWR population record were identified, the number of records per cell calculated using the “Count Points in Polygon” available in QGIS; analysis results were graphically elaborated. Areas characterised by the highest taxa richness were identified by applying the same methodology on a grid of cells of 0.05 degrees side (each cell covering about 20 km<sup>2</sup>). The distribution of sites: i) hosting CWR populations in-situ and ii) where ex-situ conserved materials were collected was compared by overlaying occurrence data using QGIS. The analysis also allowed the identification of Lebanese areas that could be candidates for future collection missions.

## Results

### List development and prioritized taxa

As for CWR taxa present in Lebanon belonging to Poaceae and Fabaceae, 42 taxa resulted from ICARDA’s database, 33 from GENESYS database and 40 from GBIF. After checking for synonyms, to eliminate similarities and unify the nomination, a total of 40 unique CWR taxa of primary relevance were identified (Table 2).

The prioritization process allowed the selection of 16 taxa to focus on belonging to the *Aegilops*, *Triticum*, *Cicer*, *Hordeum*, *Lens* and *Pisum* genera which are recorded to have traits of great interest (Table 3). It is noteworthy that in the process *Triticum parvicoccum* was discarded since it is suspected to be extinct (Kislev 1980); additionally, all taxa belonging to *Avena* were also eliminated as they are less valuable for the Lebanese economy and food security (FAO 2019). Finally, even though *Lens ervoides* belongs to *L. culinaris* GP-3, this taxon was included being common in Lebanon and being considered a good source of traits for lentil breeding including traits related to growth habit, biomass production and seed characteristics.

**Table 2** List of the identified 40 CWR taxa of primary importance present in Lebanon

Taxa	Genome	GP*	Related crop*	Common name
<i>Aegilops biuncialis</i> Vis	UM	GP-2	<i>T. aestivum</i> L	Soft wheat
<i>Aegilops caudata</i> L. subsp. <i>caudata</i>	C	GP-2	<i>T. aestivum</i> L	Soft wheat
<i>Aegilops columnaris</i> var. <i>glabriuscula</i> Eig	C	GP-2	<i>T. aestivum</i> L	Soft wheat
<i>Aegilops crassa</i> Boiss	D	GP-2	<i>T. aestivum</i> L	Soft wheat
<i>Aegilops cylindrica</i> Host	CD	GP-2	<i>T.</i>	Soft wheat
<i>Aegilops geniculata</i> Roth	MMUU	GP-2	<i>T. aestivum</i> L	Soft wheat
<i>Aegilops kotschyi</i> Boiss	US	–	<i>T. aestivum</i> L	Soft wheat
<i>Aegilops peregrina</i> (Hack.) Maire & Weiller subsp. <i>peregrina</i>	UUS	GP-2	<i>T. aestivum</i> L	Soft wheat
<i>Aegilops searsii</i> Feldman & Kislev	B	GP-2	<i>T. aestivum</i> L	Soft wheat
<i>Aegilops sharonensis</i> Eig	D	GP-2	<i>T. aestivum</i> L	Soft wheat
<i>Aegilops speltoides</i> subsp. <i>ligustica</i> (Savign.) Zhuk	BB	GP-2	<i>T. aestivum</i> L	Soft wheat
<i>Aegilops triuncialis</i> L. subsp. <i>triuncialis</i>	CU	GP-2	<i>T. aestivum</i> L	Soft wheat
<i>Aegilops umbellulata</i> Zhuk	U	GP-2	<i>T. aestivum</i> L	Soft wheat
<i>Aegilops uniaristata</i> Vis	N	GP-2	<i>T. aestivum</i> L	Soft wheat
<i>Aegilops vavilovii</i> (Zhuk.) Chennav	DMS	GP-2	<i>T. aestivum</i> L	Soft wheat
<i>Aegilops ventricosa</i> Tausch	D	GP-2	<i>T. aestivum</i> L	Soft wheat
<i>Triticum boeoticum</i> Boiss	AA	GP-1	<i>T. aestivum</i> L	Soft wheat
<i>Triticum dicoccoides</i> (Asch. & Graebn.) Schweinf	AABB	GP-1	<i>T. aestivum</i> L	Soft wheat
<i>Triticum parvicoccum</i> Kislev	AB	–	–	–
<i>Triticum timopheevii</i> (Zhuk.) Zhuk	AAGG	GP-1	<i>T. aestivum</i> L	Soft wheat
<i>Triticum urartu</i> Thumanjan ex Gandilyan	AA	GP-1	<i>T. aestivum</i> L	Soft wheat
<i>Avena eriantha</i> Durieu	–	GP-3	<i>A. sativa</i> L	Oat
<i>Avena sterilis</i> L. subsp. <i>sterilis</i>	–	GP-1	<i>A. sativa</i> L	Oat
<i>Avena barbata</i> Link subsp. <i>barbata</i>	–	GP-3	<i>A. sativa</i> L	Oat
<i>Avena barbata</i> subsp. <i>wiestii</i> (Steud.) Mansf	–	GP-3	<i>A. sativa</i> L	Oat
<i>Avena clauda</i> Durieu	–	GP-3	<i>A. sativa</i> L	Oat
<i>Avena fatua</i> L. subsp. <i>fatua</i>	–	GP-1	<i>A. sativa</i> L	Oat
<i>Avena fatua</i> subsp. <i>meridionalis</i> Malzev	–	GP-1	<i>A. sativa</i> L	Oat
<i>Hordeum bulbosum</i> L	–	GP-2	<i>H. vulgare</i> L	Barley
<i>Hordeum marinum</i> Huds	–	GP-3	<i>H. vulgare</i> L	Barley
<i>Hordeum murinum</i> L	–	GP-3	<i>H. vulgare</i> L	Barley
<i>Hordeum spontaneum</i> K.Koch	–	GP-1	<i>H. vulgare</i> L	Barley
<i>Cicer incisum</i> var. <i>libanoticum</i> (Boiss.) Bornm	–	GP-3	<i>C. arietinum</i> L	Chickpea
<i>Cicer judaicum</i> Boiss	–	GP-2	<i>C. arietinum</i> L	Chickpea
<i>Cicer pinnatifidum</i> Jaub. & Spach	–	GP-2	<i>C. arietinum</i> L	Chickpea
<i>Lens culinaris</i> Medik. subsp. <i>culinaris</i>	–	GP-1	<i>L. culinaris</i> Medik	Lentil
<i>Lens culinaris</i> subsp. <i>odemensis</i> (Ladiz.) M. E. Ferguson & al	–	GP-1	<i>L. culinaris</i> Medik	Lentil
<i>Lens culinaris</i> subsp. <i>orientalis</i> (Boiss.) Ponert	–	GP-1	<i>L. culinaris</i> Medik	Lentil
<i>Lens ervoides</i> (Brign.) Grande**	–	GP-3	<i>L. culinaris</i> Medik	Lentil
<i>Pisum sativum</i> subsp. <i>elatius</i> (M. Bieb.) Asch. & Graebn	–	GP-1	<i>P. sativum</i> L	Pea

\*As from <https://www.cwrdiversity.org>

\*\*Cultivated species but also found in the wild

**Table 3** List of the 16 taxa prioritised in the study

Priority taxa list	Traits of interest
<i>Ae. crassa</i>	Cytoplasmic male sterility (Murai and Tsunewaki 1993); yield, seed quality and salinity tolerance (Liu et al. 2002)
<i>Ae. cylindrica</i>	Resistance to frost (Stankova et al. 1995)
<i>A. searsii</i>	Resistance to stem rust (Liu et al. 2011); resistance to powdrey mildew (Liu et al. 2017)
<i>Ae. sharonensis</i>	Drought tolerance (Waines et al. 1993)
<i>Ae. ventricosa</i>	Resistance to leaf rust and stripe rust (Bariana and McIntosh 1993); Resistance to Cyst nematode (Delibes et al. 1993)
<i>T. boeoticum</i>	Resistance to powdery mildew and leaf rust (Dorofeev et al. 1979); nutritional value e.g., higher protein quality and amino-acid content, and resistance to biotic stresses (Bahraei & Jaradat 1998; Anker & Niks 2001)
<i>T. dicoccoides</i>	Rich source for agronomic traits related to grain quality and abiotic/biotic stress (Xie and Nevo 2008)
<i>T. timopheevii</i>	Important source resistance to leaf rust (Brown-Guedira et al. 2003)
<i>T. urartu</i>	Adaptation alleles to local conditions (Qiu et al. 2005; Brunazzi et al. 2018)
<i>C. judaicum</i>	Resistance to <i>Helicoverpa</i> in chickpea (Sharma et al. 2006); good resistance to stem rot
<i>C. pinnatifidum</i>	Resistance to stem rot, resistance to <i>Ascochyta</i> blight (Collard et al. 2001)
<i>H. spontaneum</i>	Adaptation to drought-prone environments (Talame et al. 2004; Abulfaraj et al. 2022)
<i>L. culinaris</i> subsp. <i>odemensis</i>	Variation in root traits, including nodulation and root distribution in soil (Gorim & Vandenberg 2017)
<i>L. culinaris</i> subsp. <i>orientalis</i>	Variation in seed size and number of seeds and pods (Fratini et al. 2007; Gupta & Sharma 2006)
<i>L. ervoides</i>	Good source of growth habit, biomass production, and seed traits (Fiala et al. 2009; Tullu et al. 2011, 2013)
<i>P. sativum</i> subsp. <i>elatius</i>	Nutritional value traits (Clemente et al. 2015)

For each taxa, some of the most relevant traits for breeding is also reported

## Occurrences

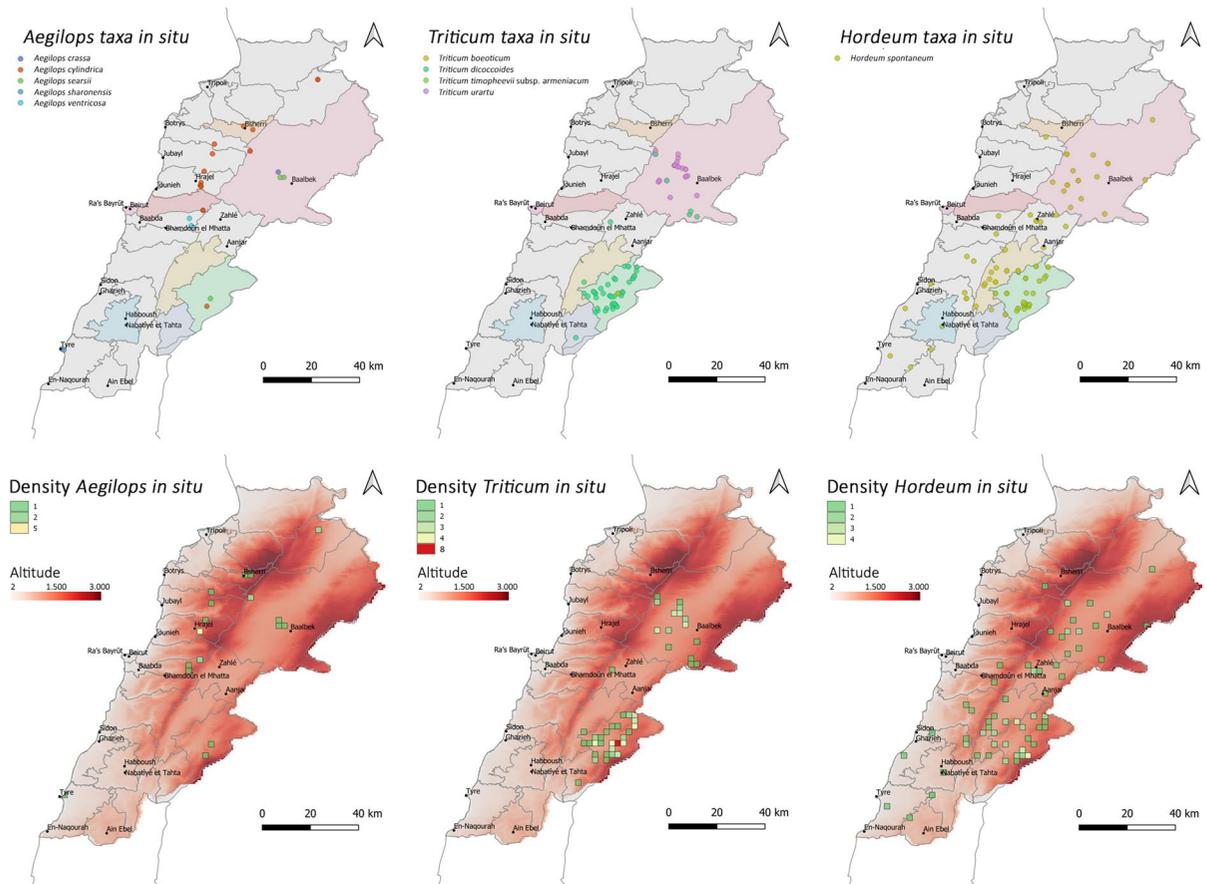
We were able to retrieve data on 878 occurrences from GBIF that result in 26 occurrences after the application of described data quality filtering process, the major part of the data was discarded in this case due to records coming from SINGER or not having accurate coordinates; accordingly, the final adopted occurrences can be considered of high-quality. 1,066 occurrences were retrieved from Genesys online database, that also list data related to collections for ex-situ, to end up after filtering with 208 occurrences for priority taxa. The ICARDA's gene bank database referring to collections for ex-situ conservation counted 237 occurrence points; after filtering and cleaning we ended with 23 high quality occurrence data. The foremost cause for discarding a major part of the ex-situ data was removing the duplicates. All collected data were organised in two different databases: 1. *Priority taxa in-situ database*, this database includes all the 257 occurrence points retrieved from the 3 used data sources (GBIF + ICARDA + Genesys). Indeed, we consider that all the populations, included

those listed in ICARDA and Genesys, are ought to have occurred in the nature, therefore they are all considered as a part of the in-situ *database*. The complete list of occurrences in the database is available in Table S1 (Supplementary Materials). 2. *Priority taxa ex-situ database*, this database includes 231 ex-situ occurrences (ICARDA + Genesys). The database is available in Table S2 (Supplementary Materials).

## Mapping taxa distribution and genus density

Occurrence data stored in the two developed databases were mapped using QGIS software; results of the distribution and density analyses are shown in Fig. 1. A map displaying Governorates and districts of Lebanon is available in Figure S1 (Supplementary Materials).

Our targeted *Aegilops* taxa show different distribution preferences on the Lebanese territory: *Ae. cylindrica* is distributed mainly in Mount Lebanon and North-Lebanon, while the scattering of the rest of *Aegilops* taxa cannot be fully judged due to the limited number of populations per taxa. The highest



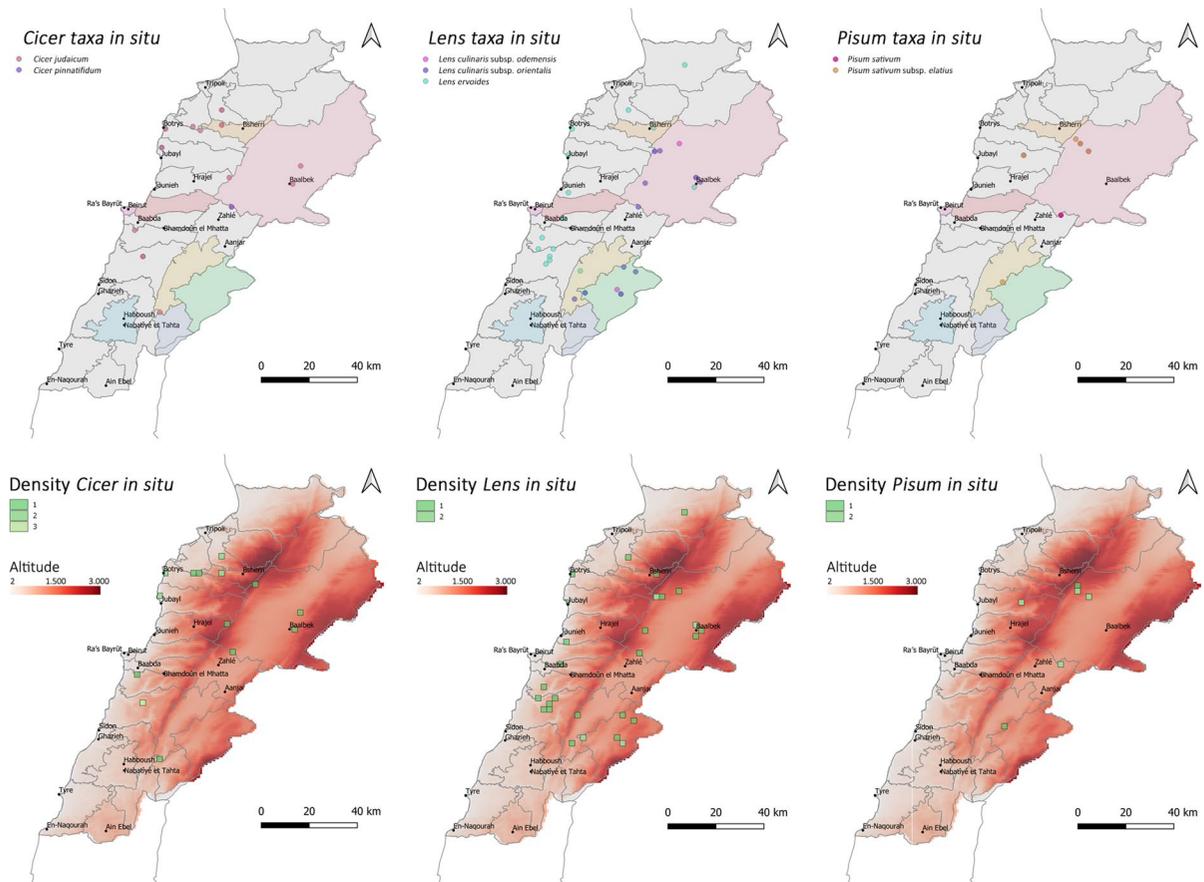
**Fig. 1** Distribution (top) and density (bottom) maps of cereals priority taxa belonging to *Aegilops*, *Triticum* and *Hordeum* genera. In the distribution maps, main regions hosting CWR

populations are highlighted; in density maps, cell and map colours are displayed according to the “density” and “altitude” scales, respectively

occurrence density for targeted *Aegilops* taxa was found in the “Matn” region (5 occurrences in an area of about 5 km<sup>2</sup>), fair lower density was recorded for all the other sites hosting taxa of this genus. *Triticum* taxa showed a more localized distribution, as *T. urartu* was mainly found in “Baalbak” region, while *T. dicoccoides* in eastern “Bekaa” (in “Rashaya” in particular) and in “Baalbak”. Even though *T. boeoticum* and *T. timopheevii* subsp. *armeniaticum* have a low number of occurrences, they are also mainly located in “Rashaya” area. As for density, the area that corresponds to Rashaya-Mt. Hermon scored the highest values: one cell characterised by having 8 occurrences, four by having 4 occurrences each and others with lower numbers are located in the area. Lower *Triticum* population density values characterise the Baalbak area (Fig. 1). According to our results,

*Hordeum spontaneum* is very widely present all along the eastern and internal sides of Lebanon, while still being less frequently present on the West-Eastern range of the country. The Bekaa region was also characterized with the highest density for *H. spontaneum*.

Legume taxa were distributed in distinctive manners (Fig. 2); *Cicer judaicum* is scattered on the Western coastal area mainly in the North-West while, due to the low number of occurrence and data deficiency, it is hard to infer *C. pinnatifidum* distribution across the Lebanese territory. The site with highest *Cicer* genus density is in Mount Lebanon-Chouf even if densities never reach high values for this genus. *Lens* taxa also showed some distribution preferences, as *L. ervoides* was found in the western side of the country where it is more humid and warmer due to the sea mitigation effect on temperatures, while *L. culinaris* subsp.



**Fig. 2** Distribution (top) and density (bottom) maps of legumes priority taxa belonging to *Cicer*, *Lens* and *Pisum* genera. In the distribution maps, main regions hosting CWR popula-

tions are highlighted; in density maps, cell and map colours are displayed according to the “density” and “altitude” scales, respectively

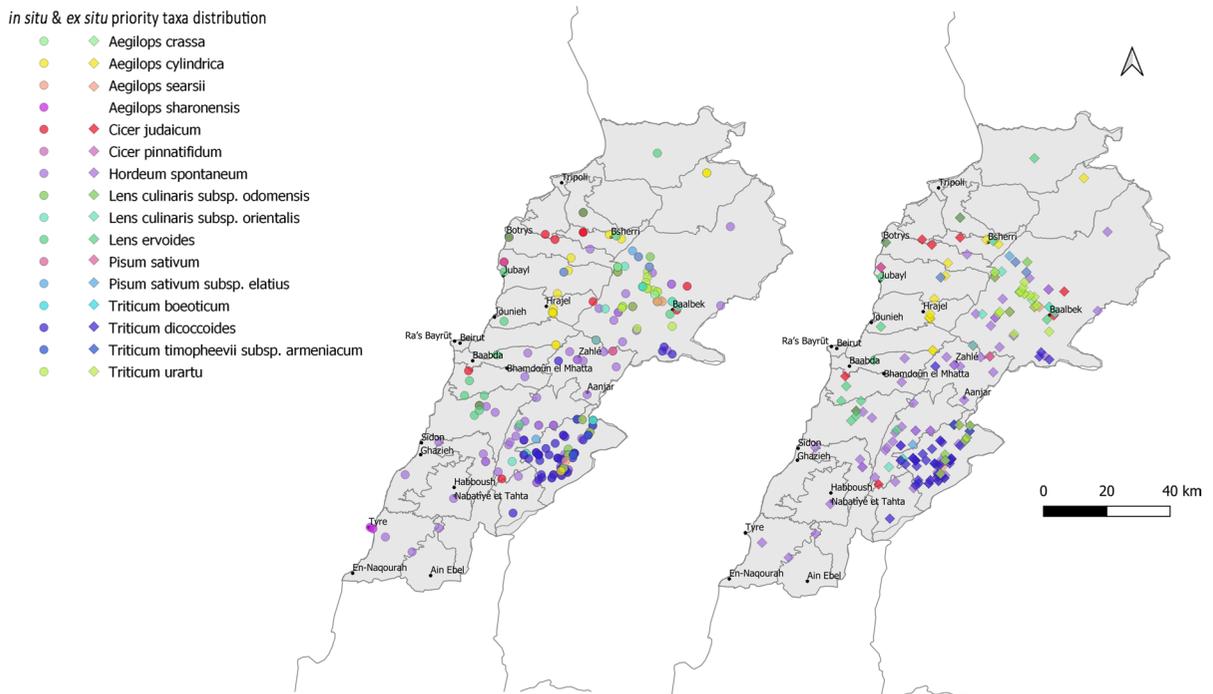
*orientalis* seems to prefer the more internal and eastern side of Lebanon known for its moderate humidity and harsh snowy winter. Cells located in Baalbek and Rashaya areas are characterised by the highest density values even if, similarly to what observed for *Cicer*, densities do not reach high values. *Pisum sativum* subsp. *elatius* distribution was most noticeable in Baalbak region, and this result is validated with the density analysis as 2 sites in this area had the highest *Pisum* density.

According to our results and based on the elevation maps, Poaceae taxa preferred elevation higher than sea level but not the highest elevation areas that are poor in Poaceae taxa. The Fabaceae taxa showed distinctive distribution patterns per genus regarding the elevation factor. *Cicer* and *Lens* taxa shows presence from sea side level up to high elevation higher than

1500 m, while *Pisum* was absent on sea side elevation and more abundant on mountainous areas.

#### Comparison of in-situ and ex-situ databases

Results of the comparison of the geographical location of sites (i) where CWR population occur in-situ and (ii) were the target of collection missions for ex-situ conservation are summarised in Fig. 3. Comparison analysis results showed that a few populations, known to be present in-situ, have not been the target of ex-situ collections: *H. spontaneum* (11 occurrences), *C. judaicum* (6), *T. urartu* (4) and *Ae. sharonensis* (2) for which no records are present in the developed *Priority taxa ex-situ database*. Indeed Fig. 3 clearly shows how most of the sites known to hold in-situ populations in Lebanon have been



**Fig. 3** Distribution of in-situ (circles, left map) and ex-situ (diamonds, right map) priority taxa across Lebanon. Each taxa corresponds to a different color as depicted in figure legend.

No symbol is associated to *Aegilops sharonensis* in ex-situ distribution map being this taxon absent from ex-situ collection

already the target of collection activities. Additionally, both maps show that most of the occurrences are on the eastern side of the country, while the western side appears to be populated by a lower number of priority taxa populations.

#### Mapping areas of highest taxa richness

Results of priority species richness analysis are summarised in Fig. 4. Most of the sites characterised by the highest values are concentrated in Rachaya-Mount Hermon area were also the sites hosting the highest number of different CWR priority taxa is located (6 priority taxa). The second site, in term of number of CWR priority taxa (5), is in the northwest of Baalbek region (Fig. 4). Three sites in Rachaya area are home for 4 CWR targeted taxa each while ten sites in different regions included 3 priority CWR taxa. Overall, a quite relevant proportion of the Lebanese territory hosts a CWR priority taxa at least. Based on the collected data and data analysis results, the eastern part of Lebanon clearly holds most of the sites where

priority CWR taxa occur that are also characterised by high taxa richness indexes.

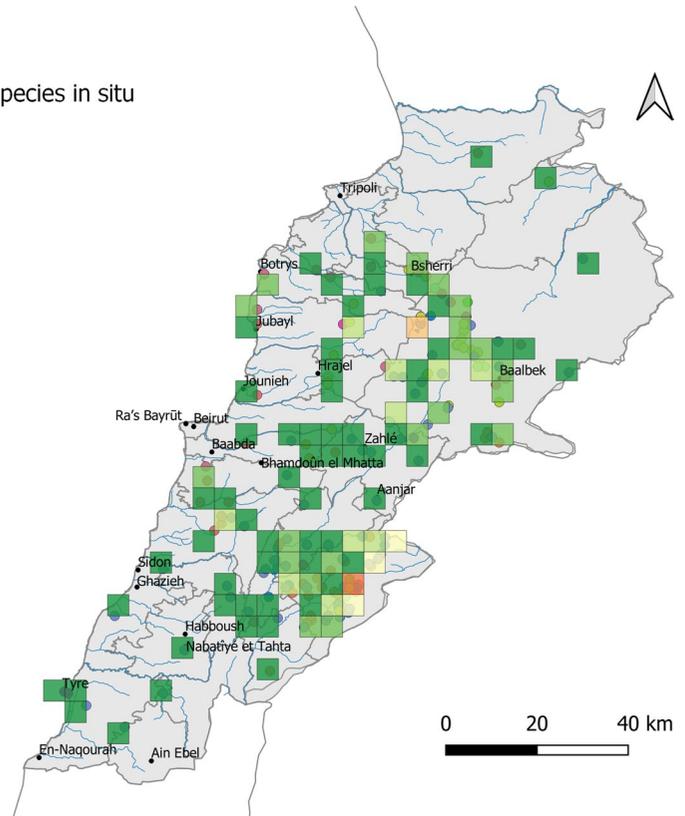
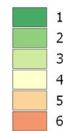
#### Discussion

This study provides a baseline for assessing the distribution in-situ and the diversity of CWR taxa in Lebanon with the final goal of giving inputs to their diversity long-term conservation. It also sheds light on priority CWR taxa distribution and sites of high taxa density and richness; all this information is relevant for the identification of areas of priority for collecting CWR of different key taxa and fill the gaps in genebank collections. The study is also the first in depth analysis of the distribution of different CWR belonging to relevant genera in Lebanon that can help in identifying the gaps in their assessment across the country territory.

As for the taxa considered, cereals are among the most widely consumed and most valuable crops for humankind (FAO 2019) while grain legumes, including pea, chickpea, and lentil, are primary sources

**Fig. 4** Mapping taxa richness of priority CWR sites, the different colours as shown in the legend describe the value of species richness in cells

RICHNESS - Priority species in situ



of nutritional protein for approximately 30% of the world's human population (Afshin et al. 2014). Accordingly, we focused our analysis on the distribution of CWR taxa that are of high importance at the global level as well as for Lebanon.

Distribution of *Aegilops cylindrica* populations shows that this species is present in different areas of the country; its main agglomeration on western side and partial presence on the eastern side could be due to the fact that *Ae. cylindrica* is preferential for grazing by sheep and goat most commonly present in the eastern side of the country (Baalbaki et al. 2006). The low number of occurrences for the rest of the *Aegilops* taxa is a subject to further surveying. At this regard some preliminary data on surveys carried out in 2022 seems to suggest that several sites hosting *Aegilops* populations have been disturbed due to anthropization also in the west part of the country.

*Hordeum spontaneum* is the only wild species in the barley primary genepool (GP1) (Zohary et al. 2012) that makes the species of high value for barley breeding and thus deserving a special attention

for both conservation and use. Results of our analyses show that most of the known populations of this species occurring in Lebanon has been already the object of collection suggesting that there is no urgent need for additional collection efforts at the current time. At this regard it should be noted that ICARDA holds a rich collection of wild *Hordeum* species including *H. spontaneum*. Apart from being considered an invasive plant, a recent study from Elouadi et al. (2021) showed that *H. spontaneum* accessions are high in  $\beta$ -glucan and high in Zinc, Iron, and Selenium, making this taxon relevant for the development of biofortified barley germplasm. Indeed, this species has been also already successfully used for the introgression of resistance traits in the cultivated forms.

*Triticum* taxa showed selective distribution patterns. According to our data, *T. boeoticum* has a limited number of occurrences in-situ; however, since a previous study showed that the relative genetic distances among *T. boeoticum* accessions is not correlated with geographical distances of places of their origins (i.e., indicating that populations relatively

close can be genetically different) (Malaki et al. 2006; Naghavi et al. 2009), each accession of this species could hold unique diversity and being thus of a certain interest for conservation. *T. dicoccoides* is mainly present in the eastern side of the country and in Bekaa and Baalbak governorates in particular; both sites should be thoroughly considered for the genetic assessment of this taxa, as previous studies shows that seed storage-protein differentiation was significantly correlated with the altitude of the collecting sites (Ciaffi et al. 2013), therefore it is expected ecogeographic-climatic aspects to have a substantial effect on the diversity and on some traits of interest of this taxa. At this regard it should be noted that the identified distribution area is quite diverse when altitude is considered.

*Cicer judaicum* and *Cicer pinnatifidum* are taxa considered underrepresented in worldwide genebank collections (Berger et al. 2003); this is quite alarming considering that, with *C. bijugum*, these are the only 3 species in *C. arietinum* GP2 (Nguyen et al. 2004 and references therein). Even though our results shows that *C. judaicum* is mainly clustered in the coastal Lebanese side, it also occurred dispersedly in different types of habitats all over the country according to previous studies (Ben-David et al. 2010), suggesting adaptive responses to stress intensity, imposed by climate and soil type. The relatively low number of occurrences retrieved for these two important species suggest the need of new surveying missions across the country that most likely holds a much higher number of populations. As for the importance of this species, it should also be considered that genes for resistance to botrytis grey mold has been already identified in *C. judaicum* (Singh et al. 1982) and that biotic stresses have been reported among the mong the major constraints to chickpea productivity. Having been classically considered among the ‘orphans’ crops from the genomics revolution, the tremendous progress in the development of large scale genomic resources achieved in recent years for chickpea—including genetic maps and whole-genome transcription profiling—will certainly increases the values of wild relatives and the possibility to access the diversity.

Not all *Lens* priority taxa survived to the filtering process, that was necessary to build solid datasets. On the other hand, *L. ervoides* was included in the study even though it belongs to the tertiary genepool due to its high presence in Lebanon and because it

is considered as a good source of important trait for breeding including growth habit, biomass production as well as different seed-related traits (Fiala et al. 2009; Tullu et al. 2011, 2013). The distribution of this species shows a preference to the coastal areas with a more humid climate, which is the same distribution pattern observed in neighbouring Mediterranean countries like Syria and Turkey (Redden et al. 2007). *Lens culinaris* subsp. *orientalis*, is believed to be the progenitor of the cultivated lentil, with preference to more dry areas on higher elevation (Davies et al. 2007; Singh et al. 2014). The density and distribution maps show a wide distribution of this taxa in Lebanon, but most studies focused on its distribution in other countries such as Syria and Turkey, hence national initiatives are encouraged to be implemented in characterizing the Lebanese wild *Lens* in more depth. Wild populations of *Lens* are generally poor competitors and highly palatable to grazing animals making them prone to genetic erosion (Ferguson and Erskine 2001), therefore their collection and active conservation is essential and possibly quite urgent.

Due to the limited amount of data and the erratically distribution pattern, mapping the distribution of *Pisum sativum* subsp. *elatius* was not possible in the present study and specific conclusion can hardly be drawn for this taxon; such evidence suggests that more botanical surveys and studies targeting this taxon are required. Considering that wild peas hold wide genetic diversity and have less than 3% representation in different national collections, there is a strong need to increase the current sampled diversity also considering that, as for many other CWRs, natural habitats hosting wild peas are being lost due to increased human population, grazing pressure, conversion of marginal areas to agriculture (Kneller et al 2011). Furthermore, the different wild pea populations spread in the vast habitat range (from the Mediterranean through the Middle East and central Asia) are expected to contain genetic diversity for abiotic stress tolerance and more investigations have been particularly advocated for *P. sativum* subsp. *elatius* (Smýkal et al. 2012).

In-situ GAP analysis results, defined by the comparison of mapping all taxa distributions in-situ and ex-situ, showed insignificant differences suggesting that the populations in situ are quite well represented ex situ. This could be the consequence of data cleaning and filtering that resulted in few data of in-situ

occurrences; therefore, the gene bank data was the main source of occurrences; however, filtering and cleaning were necessary to produce a trustable dataset. On the other hand, this evidence encourages to further planning of botanical survey and collection missions with the purpose of re-targeting the sites of previous collections and to acquire new data on the priority CWR taxa in additional sites. At the same time, we can see the main effort of surveys and collections was focused on the North-eastern side of the country, providing information on the need to put more efforts on targeting the south-western regions with botanical surveys. The deficiency of occurrences in coastal areas could be attributed to the higher presence of anthropized areas including cities developed nearby the coast (mainly at the sea level).

Taxa richness map is of great service to select sites most suitable for pragmatically survey and collection missions, so that multiple taxa per site can be targeted in a single mission. In addition, sites characterised by the highest number of different taxa in a limited area are of great value for setting future genetic reserves for CWR (Maxted et al. 2013) where different taxa can be protected at the same time. Interestingly, a study by Maxted et al. (2011), targeting both the legumes and cereals, showed the area at the northern end of the Bekaa Valley in Lebanon to be a target for in-situ and ex-situ conservation action for both wild legumes and cereals. Our analysis showed that, in addition to the Northern Bekaa valley, the western Bekaa side is also of significant importance.

CWR play an important role in both bio-conservation and food security, therefore emphasising their conservation in their native habitats in Lebanon helps to preserve the valuable genetic resource for future generations, ensuring the continuation of food production in the face of changing environmental conditions and emerging pest and disease pressures. A study conducted by Sharma et al. (2021) showed that *C. judaicum* accessions collected from different countries including Lebanon, were found to be promising for multiple seed nutrients as these accessions have high seed Fe, Cu, Mn, Ca and Mg concentration compared with other wild *Cicer* accessions; in the light of these results, the biofortification of chickpea through the use of wild species offers the potential to create a staple food crop that improves diets and prevents disease for millions of people, particularly in the developing world. By promoting the cultivation

and use of CWRs in the local diet, communities can reduce their dependence on imported foods, which can be vulnerable to price spikes and supply chain disruptions. This can help to ensure food security, especially for the most vulnerable populations, by increasing the availability and accessibility of nutritious, locally-sourced foods. CWR play a crucial role in both bio-conservation and food security in Lebanon, and targeted management and conservation of these species in protected areas can help to ensure their long-term survival and the benefits they provide to local communities.

## Conclusion

This study prioritized CWR taxa of major interest for world security and local economy present in Lebanon and contributes to a first localization of areas suitable for new collection missions as well as for putting in place *in-situ* conservation actions. Presented data show that a general greater effort is needed to fully collect Lebanese diversity of target species and, on the other hand, not been properly surveyed yet, the South-West of Lebanon arises as an interesting target for future missions. Indeed, access to full range CWR diversity is crucial for plant breeders to breed climate change resilient varieties, while making the use of CWR more effective is the path to provide sustainability to conservation actions. At this regard, future studies are required to further analyse the distribution pattern of each taxon individually for a better understanding of the traits potentially present in the different populations. Collate additional georeferenced data points for the priority CWR through ecogeographic-botanical surveys and a comprehensive data analysis, also based on the use of ad hoc developed Ecogeographical Land Characterization (ELC) maps, will shed further light on those sites potentially encompassing the widest ranges of diversity; once identified, such sites will be excellent candidates for the establishment of genetic reserves where effective, active long-term in-situ conservation can be put in place.

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